

130045

STIC-Biotech/ChemLib

From: Duffy, Patricia  
Sent: Monday, August 16, 2004 5:49 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search 10/063546

Importance: High

CREF

In re:

10/063,546

Please search SEQ ID NO:38 and oligomers thereof.

Please include both a commercial and interference database search.

Please print out top ~~100~~ hits in each category.

70 scores

Thank you,

Patricia A. Duffy, Ph.D.

Art Unit 1645, Remsen 3B05

571-272-0855

\*\*\*\*\*

STAFF USE ONLY

Searcher: SHAY  
Searcher Phone: 2-  
Date Searcher Picked up: 8/16/04  
Date Completed: 8/16/04  
Searcher Prep/Rev. Time:      
Online Time:    

\*\*\*\*\*

Type of Search

NA Sequence: #      
AA Sequence: #      
Structure: #      
Bibliographic:      
Litigation:      
Patent Family:      
Other:    

\*\*\*\*\*

Vendors and cost where applicable

STN:      
DIALOG:      
QUESTEL/ORBIT:      
LEXIS/NEXIS:      
SEQUENCE SYSTEM: MS?  
WWW/Internet:      
Other(Specify):

Duffy, Patricia

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Thank you,

*Patricia A. Duffy, Ph.D.*  
*Art Unit 1645, Remsen 3B05*  
*571-272-0855*

PRO 1344  
Abs.



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## OM protein - protein search, using sw model

Run on: August 18, 2004, 16:25:34 ; Search time 63 Seconds

(without alignments)  
3229.114 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 720  
Sequence: 1 MELGCTQLGLTFLQLLLIS.....LSTAFKVLKLPFKDIERNMK 720Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 700 summaries

Database : A Geneseq 29Jan04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	720	100.0	720	3	AAy66695 Membrane-
2	720	100.0	720	4	AAU29108 Human PRO
3	720	100.0	720	4	AAH87544 Human PRO
4	720	100.0	720	4	AAH65218 Human PRO
5	720	100.0	720	5	ABG95869 Human sec
6	720	100.0	720	5	ABU58484 Human PRO
7	720	100.0	720	6	ABU88032 Novel hum
8	720	100.0	720	6	ABU84347 Human sec
9	720	100.0	720	6	ABR66221 Human sec
10	720	100.0	720	6	ABR65511 Human sec
11	720	100.0	720	6	ABU95551 Human sec
12	720	100.0	720	6	ABU58033 Human PRO
13	720	100.0	720	6	ABU59111 Novel hum
14	720	100.0	720	6	ABU82623 Human sec
15	720	100.0	720	6	ABU82790 Human PRO
16	720	100.0	720	6	ABU89911 Novel hum
17	720	100.0	720	6	ABR68160 Human sec
18	720	100.0	720	6	ABU60542 Human sec
19	720	100.0	720	6	ABU96213 Novel hum
20	720	100.0	720	6	ABU92644 Human sec
21	720	100.0	720	6	ABO08721 Human sec
22	720	100.0	720	6	ABO02773 Human sec
23	720	100.0	720	6	ABR74927 Human sec
24	720	100.0	720	6	ABR94689 Human sec
25	720	100.0	720	6	ABU13924 Human PRO

26	720	100.0	720	6	ABU85662 Human PRO
27	720	100.0	720	6	ABU98822 Novel hum
28	720	100.0	720	6	ABU98037 Novel hum
29	720	100.0	720	6	ABU91743 Novel hum
30	720	100.0	720	6	ABU89436 Human PRO
31	720	100.0	720	6	ABU86277 Human sec
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34	720	100.0	720	6	ABU72509 Novel hum
35	720	100.0	720	6	ABU90894 Novel hum
36	720	100.0	720	6	ABO33953 Human sec
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83	720	100.0	720	6	ABU83127 Human sec
84	720	100.0	720	6	ABU94983 Novel hum
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86	720	100.0	720	6	ABU84042 Human sec
87	720	100.0	720	6	ABU93693 Novel hum
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104	720	100.0	720	6	ABR59815	AbR59815 Human SEC	177	720	100.0	720	6	ABO21537	ABO21537 Human DEC
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114	720	100.0	720	6	ABU86887	AbU86887 Novel HUM	187	720	100.0	720	6	ABR92859	AbR92859 Human DEC
115	720	100.0	720	6	ABU94676	AbU94676 Human PRO	188	720	100.0	720	6	ABO24620	ABO24620 Human DEC
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117	720	100.0	720	6	ABR70352	AbR70352 Human SEC	190	720	100.0	720	6	ABM11631	ABM11631 Human DEC
118	720	100.0	720	6	ABU92342	AbU92342 Novel HUM	191	720	100.0	720	6	ABM02732	ABM02732 Human DEC
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120	720	100.0	720	6	ABR65916	AbR65916 Human SEC	193	720	100.0	720	6	ABO27589	ABO27589 Human DEC
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122	720	100.0	720	6	ABU59407	AbU59407 Novel HUM	195	720	100.0	720	6	ABM07056	ABM07056 Human DEC
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125	720	100.0	720	6	ABU95908	AbU95908 Human PRO	198	720	100.0	720	6	ABO41366	ABO41366 Human DEC
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127	720	100.0	720	6	ABU90221	AbU90221 Novel HUM	200	720	100.0	720	6	ABO43710	ABO43710 Human PRO
128	720	100.0	720	6	ABO09636	ABO09636 Human SEC	201	720	100.0	720	6	ABM76410	ABM76410 Human DEC
129	720	100.0	720	6	ABO10908	ABO10908 Human SEC	202	720	100.0	720	6	ABM76106	ABM76106 Human DEC
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132	720	100.0	720	6	ABU87570	AbU87570 Human PRO	205	720	100.0	720	6	ADA21428	ADa21428 Human DEC
133	720	100.0	720	6	ABU91438	AbU91438 Human PRO	206	720	100.0	720	6	ABO03383	ABO03383 Human DEC
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135	720	100.0	720	6	ABU84652	AbU84652 Human SEC	208	720	100.0	720	6	ABO44257	ABO44257 Human DEC
136	720	100.0	720	6	ABR69742	AbR69742 Human SEC	209	720	100.0	720	6	ABR90639	ABR90639 Human DEC
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139	720	100.0	720	6	ABU92173	AbU92173 Novel HUM	212	720	100.0	720	6	ABR94384	ABR94384 Human DEC
140	720	100.0	720	6	ABU93388	AbU93388 Human PRO	213	720	100.0	720	6	ABR75891	ABR75891 Human DEC
141	720	100.0	720	6	ABO09941	ABO09941 Human SEC	214	720	100.0	720	6	ABR71267	ABR71267 Human DEC
142	720	100.0	720	6	ABO09026	ABO09026 Human SEC	215	720	100.0	720	6	ABR93164	ABR93164 Human DEC
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144	720	100.0	720	6	ABU10879	AbU10879 Human PRO	217	720	100.0	720	6	ADA10215	ADa10215 Human DEC
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157	720	100.0	720	6	ABR35604	AbR35604 Human SEC	230	720	100.0	720	6	ABO52387	ABO52387 Human PRO
158	720	100.0	720	6	ABR80901	AbR80901 Human SEC	231	720	100.0	720	6	ADA11900	ADa11900 Novel HUM
159	720	100.0	720	6	ABR81206	AbR81206 Human SEC	232	720	100.0	720	6	ABO23705	ABO23705 Human CTR
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164	720	100.0	720	6	ABO31554	ABO31554 Human SEC	237	720	100.0	720	6	ABM11021	ABM11021 Human DEC
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170	720	100.0	720	6	ABM24810	AbM24810 Human SEC	243	720	100.0	720	6	ABM22370	ABM22370 Human DEC
171	720	100.0	720	6	ABO03078	ABO03078 Human SEC	244	720	100.0	720	6	ABM07666	ABM07666 Human DEC

Ab-90334 Human DEC	AbM17248 Human DEC	Ab-94594 Human DEC	Ab-95299 Human DEC	ADb17095 Human CTR	ABO21537 Human DEC	ABR97801 Human DEC	ABR87589 Human DEC	ABR77630 Human DEC	ABM27860 Human DEC	ABM06141 Human DEC	ABM03647 Human DEC	ABM03509 Human DEC	ABM26335 Human DEC	ABO48117 Human DEC	ABR92859 Human DEC	ABO24620 Human DEC	ADA37742 Human DEC	ABM11631 Human DEC	ABM02732 Human DEC	ABM16028 Human DEC	ABO27589 Human DEC	ABM29080 Human DEC	ABM07056 Human DEC	ABM21150 Human DEC	ABM09496 Human DEC	ABO41366 Human DEC	ABO36181 Human PRO	ABO43710 Human PRO	ABM76410 Human DEC	ABM76106 Human DEC	ABM25725 Human DEC	ABM26030 Human DEC	ADA21428 Human DEC	ABO03383 Human DEC	ABO02468 Human DEC	ABR90639 Human DEC	ABR73707 Human DEC	ABO16595 Human DEC	ABR94384 Human DEC	ABR75891 Human DEC	ABR71267 Human DEC	ABR93164 Human DEC	ABR93469 Human DEC	ADA10215 Human DEC	ABR87894 Human DEC	ABO27894 Human DEC	ABO30029 Human DEC	ABO33338 Human PRO	ABM04926 Human DEC	ABM08886 Human DEC	ABO36486 Human DEC	ABO35571 Human PRO	ABO39536 Human DEC	ABM10411 Human DEC	ABM11936 Human DEC	ABO52082 Human PRO	ABO52387 Human PRO	ADA11900 Novel HUM	ABO23705 Human CTR	ADB17283 Human PRO	ADA17759 Human CTR	ABR97191 Human DEC	ABR86979 Human DEC	ABM11021 Human DEC	ABR28165 Human DEC	ABO32164 Human DEC	ABM15291 Human DEC	ABM06446 Human DEC	ABM04257 Human DEC	ABM22370 Human DEC	ABM07666 Human DEC
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263	720	100.0	720	6	ABM10106	ABM10106 Human sec	336	720	100.0	720	6	ABM24200	ABM24200 Human sec
264	720	100.0	720	6	ABO38621	ABO38621 Human sec	337	720	100.0	720	6	ABM14681	ABM14681 Human sec
265	720	100.0	720	6	ABM32861	ABM32861 Human sec	338	720	100.0	720	6	ABM04562	ABM04562 Human sec
266	720	100.0	720	6	ABM2875	ABM2875 Human sec	339	720	100.0	720	6	ABM06751	ABM06751 Human sec
267	720	100.0	720	6	ABM74886	ABM74886 Human sec	340	720	100.0	720	6	ABM09191	ABM09191 Human sec
268	720	100.0	720	6	ADA79714	ADA79714 Human sec	341	720	100.0	720	6	ABO39231	ABO39231 Human sec
269	720	100.0	720	6	ABR96276	ABR96276 Human sec	342	720	100.0	720	6	ABM75496	ABM75496 Human sec
270	720	100.0	720	6	ABM02427	ABM02427 Human sec	343	720	100.0	720	6	ABM25420	ABM25420 Human sec
271	720	100.0	720	6	ABR86369	ABR86369 Human sec	344	720	100.0	720	6	ABM19930	ABM19930 Human sec
272	720	100.0	720	6	ABR86674	ABR86674 Human sec	345	720	100.0	720	6	ABO46836	ABO46836 Human PRO
273	720	100.0	720	6	ABM16638	ABM16638 Human sec	346	720	100.0	720	6	ABO47141	ABO47141 Human PRO
274	720	100.0	720	6	ABM29690	ABM29690 Human sec	347	720	100.0	720	6	ADA83239	ADA83239 Human sec
275	720	100.0	720	6	ABO29114	ABO29114 Human sec	348	720	100.0	720	6	ABR71572	ABR71572 Human sec
276	720	100.0	720	6	ABM23895	ABM23895 Human sec	349	720	100.0	720	6	ABR72182	ABR72182 Human sec
277	720	100.0	720	6	ABM23285	ABM23285 Human sec	350	720	100.0	720	6	ABR98521	ABR98521 Human sec
278	720	100.0	720	6	ABM22065	ABM22065 Human sec	351	720	100.0	720	6	ABO06891	ABO06891 Human sec
279	720	100.0	720	6	ABO37706	ABO37706 Human sec	352	720	100.0	720	6	ABR84844	ABR84844 Human sec
280	720	100.0	720	6	ABM28470	ABM28470 Human sec	353	720	100.0	720	6	ABR73402	ABR73402 Human sec
281	720	100.0	720	6	ABM28775	ABM28775 Human sec	354	720	100.0	720	6	ABR76496	ABR76496 Human sec
282	720	100.0	720	6	ABM66419	ABM66419 Human sec	355	720	100.0	720	6	ABR73097	ABR73097 Human sec
283	720	100.0	720	6	ABM75801	ABM75801 Human sec	356	720	100.0	720	6	ABM18163	ABM18163 Human sec
284	720	100.0	720	6	ABM34081	ABM34081 Human sec	357	720	100.0	720	6	ABO20622	ABO20622 Human sec
285	720	100.0	720	6	ABM34386	ABM34386 Human sec	358	720	100.0	720	6	ABO25365	ABO25365 Human PRO
286	720	100.0	720	6	ABO20317	ABO20317 Human sec	359	720	100.0	720	6	ABO25670	ABO25670 Human PRO
287	720	100.0	720	6	ABO21232	ABO21232 Human sec	360	720	100.0	720	6	ABR94079	ABR94079 Human sec
288	720	100.0	720	6	ABO22147	ABO22147 Human sec	361	720	100.0	720	6	ADA92793	ADA92793 Human sec
289	720	100.0	720	6	ADA20072	ADA20072 Novel hum	362	720	100.0	720	6	ABR79986	ABR79986 Human sec
290	720	100.0	720	6	ABO34185	ABO34185 Human sec	363	720	100.0	720	6	ABM11326	ABM11326 Human sec
291	720	100.0	720	6	ABR96581	ABR96581 Human sec	364	720	100.0	720	6	ABO32933	ABO32933 Human PRO
292	720	100.0	720	6	ADA94447	ADA94447 Human sec	365	720	100.0	720	6	ABO30639	ABO30639 Human sec
293	720	100.0	720	6	ABR85759	ABR85759 Human sec	366	720	100.0	720	6	ABO30944	ABO30944 Human sec
294	720	100.0	720	6	ABR9741	ABR9741 Human sec	367	720	100.0	720	6	ABM27250	ABM27250 Human sec
295	720	100.0	720	6	ABM00597	ABM00597 Human sec	368	720	100.0	720	6	ABM29995	ABM29995 Human sec
296	720	100.0	720	6	ABM00292	ABM00292 Human sec	369	720	100.0	720	6	ABM05531	ABM05531 Human sec
297	720	100.0	720	6	ABO29724	ABO29724 Human sec	370	720	100.0	720	6	ABM05851	ABM05851 Human sec
298	720	100.0	720	6	ABM23590	ABM23590 Human sec	371	720	100.0	720	6	ABO42281	ABO42281 Human sec
299	720	100.0	720	6	ABO29385	ABO29385 Human sec	372	720	100.0	720	6	ABO38011	ABO38011 Human sec
300	720	100.0	720	6	ABO38316	ABO38316 Human sec	373	720	100.0	720	6	ABO45921	ABO45921 Human PRO
301	720	100.0	720	6	ABO45616	ABO45616 Human PRO	374	720	100.0	720	6	ABM66724	ABM66724 Human sec
302	720	100.0	720	6	ABM20540	ABM20540 Human sec	375	720	100.0	720	6	ADB20282	ADB20282 Human sec
303	720	100.0	720	6	ADA81441	ADA81441 Human sec	376	720	100.0	720	6	ABM19625	ABM19625 Human sec
304	720	100.0	720	6	ABO16654	ABO16654 Human sec	377	720	100.0	720	6	ABO49337	ABO49337 Human sec
305	720	100.0	720	6	ABO18280	ABO18280 Human sec	378	720	100.0	720	6	ABO49337	ABO49337 Human sec
306	720	100.0	720	6	ABO22707	ABO22707 Human PRO	379	720	100.0	720	6	ADA78534	ADA78534 Human sec
307	720	100.0	720	6	ABO23012	ABO23012 Human PRO	380	720	100.0	720	6	ABR88199	ABR88199 Human sec
308	720	100.0	720	6	ABR92554	ABR92554 Human sec	381	720	100.0	720	6	ADA00369	ADA00369 Human sec
309	720	100.0	720	6	ABR81511	ABR81511 Human sec	382	720	100.0	720	6	ABM25945	ABM25945 Human sec
310	720	100.0	720	6	ABM77935	ABM77935 Human sec	383	720	100.0	720	6	ABM03342	ABM03342 Human sec
311	720	100.0	720	6	ABR89724	ABR89724 Human sec	384	720	100.0	720	6	ABO39841	ABO39841 Human sec
312	720	100.0	720	6	ABM26640	ABM26640 Human sec	385	720	100.0	720	6	ABO49947	ABO49947 Human sec
313	720	100.0	720	6	ABM13766	ABM13766 Human sec	386	720	100.0	720	7	ABO50862	ABO50862 Human sec
314	720	100.0	720	6	ABO28504	ABO28504 Human sec	387	720	100.0	720	7	ABO05318	ABO05318 Human sec
315	720	100.0	720	6	ABO30314	ABO30314 Human sec	388	720	100.0	720	7	ABR74622	ABR74622 Human sec
316	720	100.0	720	6	ABM07361	ABM07361 Human sec	389	720	100.0	720	7		
317	720	100.0	720	6	ABM03952	ABM03952 Human sec	390	720	100.0	720	7	ABR77101	ABR77101 Human sec

391	720	100.0	720	7	ABM17858	Human	sec	464	720	100.0	720	7	ABM14986	Human	sec	Abm14986	Human	sec
392	720	100.0	720	7	ABR95909	Human	sec	465	720	100.0	720	7	ABO41061	Human	sec	AbO41061	Human	sec
393	720	100.0	720	7	ABO21842	Human	sec	466	720	100.0	720	7	ABO36791	Human	sec	AbO36791	Human	sec
394	720	100.0	720	7	ABO20012	Human	sec	467	720	100.0	720	7	ABO37401	Human	sec	AbO37401	Human	sec
395	720	100.0	720	7	ABO24315	Human	sec	468	720	100.0	720	7	ABM75191	Human	sec	Abm75191	Human	sec
396	720	100.0	720	7	ABR86064	Human	sec	469	720	100.0	720	7	ABM33471	Human	sec	Abm33471	Human	sec
397	720	100.0	720	7	ABM10716	Human	sec	470	720	100.0	720	7	ABO46526	Human	sec	AbO46526	Human	sec
398	720	100.0	720	7	ABM75715	Human	sec	471	720	100.0	720	7	ADA82605	Human	sec	AdA82605	Human	sec
399	720	100.0	720	7	ABR89419	Human	sec	472	720	100.0	720	7	ADB85611	Novel	hum	AdB85611	Novel	hum
400	720	100.0	720	7	ABM12546	Human	sec	473	720	100.0	720	7	ADB966239	Human	sec	AdB966239	Human	sec
401	720	100.0	720	7	ABM05836	Human	sec	474	720	100.0	720	7	ABM31825	Human	sec	Abm31825	Human	sec
402	720	100.0	720	7	ABO34961	Human	sec	475	720	100.0	720	7	ABM31215	Human	sec	Abm31215	Human	sec
403	720	100.0	720	7	ABM03037	Human	sec	476	720	100.0	720	7	ADB85913	Human	sec	AdB85913	Human	sec
404	720	100.0	720	7	ABM19015	Human	sec	477	720	100.0	720	7	ABM32130	Human	sec	Abm32130	Human	sec
405	720	100.0	720	7	ABM19320	Human	sec	478	720	100.0	720	7	ABM32435	Human	sec	Abm32435	Human	sec
406	720	100.0	720	7	ABO46531	Human	sec	479	720	100.0	720	7	ADB68290	Human	sec	AdB68290	Human	sec
407	720	100.0	720	7	ABO49032	Human	sec	480	720	100.0	720	7	ADB68097	Human	sec	AdB68097	Human	sec
408	720	100.0	720	7	ABR69075	Human	sec	481	720	100.0	720	7	ABM31520	Human	sec	Abm31520	Human	sec
409	720	100.0	720	7	ABR89114	Human	sec	482	720	100.0	720	7	ABM30910	Human	sec	Abm30910	Human	sec
410	720	100.0	720	7	ABR72487	Human	sec	483	720	100.0	720	7	ADB90914	Human	sec	AdB90914	Human	sec
411	720	100.0	720	7	ABR74317	Human	sec	484	720	100.0	720	7	ADC57711	Human	sec	AdC57711	Human	sec
412	720	100.0	720	7	ABO18585	Human	sec	485	720	100.0	720	7	ADC55075	Human	sec	AdC55075	Human	sec
413	720	100.0	720	7	ABR80291	Human	sec	486	720	100.0	720	7	ADC11942	Human	sec	AdC11942	Human	sec
414	720	100.0	720	7	ABM01512	Human	sec	487	720	100.0	720	7	ADC06994	Human	sec	AdC06994	Human	sec
415	720	100.0	720	7	ABM02122	Human	sec	488	720	100.0	720	7	ADC56364	Human	sec	AdC56364	Human	sec
416	720	100.0	720	7	ABR87284	Human	sec	489	720	100.0	720	7	ADC17173	Human	sec	AdC17173	Human	sec
417	720	100.0	720	7	ABM12851	Human	sec	490	720	100.0	720	7	ADC07419	Human	sec	AdC07419	Human	sec
418	720	100.0	720	7	ABM30605	Human	sec	491	720	100.0	720	7	ADC11409	Human	sec	AdC11409	Human	sec
419	720	100.0	720	7	ABM24505	Human	sec	492	720	100.0	720	7	ADC14871	Novel	hum	AdC14871	Novel	hum
420	720	100.0	720	7	ABO29419	Human	sec	493	720	100.0	720	7	ADC52366	Novel	hum	AdC52366	Novel	hum
421	720	100.0	720	7	ABO31249	Human	sec	494	720	100.0	720	7	ADC14531	Novel	hum	AdC14531	Novel	hum
422	720	100.0	720	7	ABM14376	Human	sec	495	720	100.0	720	7	ADC08063	Novel	hum	AdC08063	Novel	hum
423	720	100.0	720	7	ABM09801	Human	sec	496	720	100.0	720	7	ADC81988	Human	sec	AdC81988	Human	sec
424	720	100.0	720	7	ABO38926	Human	sec	497	720	100.0	720	7	ADC07530	Novel	hum	AdC07530	Novel	hum
425	720	100.0	720	7	ABM34691	Human	sec	498	720	100.0	720	7	ADC82421	Novel	hum	AdC82421	Novel	hum
426	720	100.0	720	7	ABO51167	Human	sec	499	720	100.0	720	7	ADC05643	Novel	hum	AdC05643	Novel	hum
427	720	100.0	720	7	ABO03993	Human	sec	500	720	100.0	720	7	ADC08601	Novel	hum	AdC08601	Novel	hum
428	720	100.0	720	7	ABO10463	Human	sec	501	720	100.0	720	7	ADC06680	Novel	hum	AdC06680	Novel	hum
429	720	100.0	720	7	ABO53170	Human	sec	502	720	100.0	720	7	ADC83097	Human	sec	AdC83097	Human	sec
430	720	100.0	720	7	ABR77706	Human	sec	503	720	100.0	720	7	ADC55204	Human	sec	AdC55204	Human	sec
431	720	100.0	720	7	ABR78916	Human	sec	504	720	100.0	720	7	ADC36042	Novel	hum	AdC36042	Novel	hum
432	720	100.0	720	7	ABO24010	Human	sec	505	720	100.0	720	7	ADC56162	Human	sec	AdC56162	Human	sec
433	720	100.0	720	7	ABR93774	Human	sec	506	720	100.0	720	7	ADC54600	Human	sec	AdC54600	Human	sec
434	720	100.0	720	7	ABM01817	Human	sec	507	720	100.0	720	7	ADC526754	Novel	hum	AdC526754	Novel	hum
435	720	100.0	720	7	ABM78240	Human	sec	508	720	100.0	720	7	ADC56221	Novel	hum	AdC56221	Novel	hum
436	720	100.0	720	7	ABR90029	Human	sec	509	720	100.0	720	7	ADC52176	Novel	hum	AdC52176	Novel	hum
437	720	100.0	720	7	ADA22354	Human	sec	510	720	100.0	720	7	ADC74307	Human	sec	AdC74307	Human	sec
438	720	100.0	720	7	ABM27555	Human	sec	511	720	100.0	720	7	ADC74919	Human	sec	AdC74919	Human	sec
439	720	100.0	720	7	ABM13156	Human	sec	512	720	100.0	720	7	ADC70531	Human	sec	AdC70531	Human	sec
440	720	100.0	720	7	ABO31859	Human	sec	513	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
441	720	100.0	720	7	ABM14071	Human	sec	514	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
442	720	100.0	720	7	ABM08276	Human	sec	515	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
443	720	100.0	720	7	ABO40146	Human	sec	516	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
444	720	100.0	720	7	ABM74581	Human	sec	517	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
445	720	100.0	720	7	ABM33776	Human	sec	518	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
446	720	100.0	720	7	ABM20235	Human	sec	519	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
447	720	100.0	720	7	ABO48727	Human	sec	520	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
448	720	100.0	720	7	ABO22540	Human	sec	521	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
449	720	100.0	720	7	ABR72792	Human	sec	522	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
450	720	100.0	720	7	ABO15434	Human	sec	523	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
451	720	100.0	720	7	ABR85149	Human	sec	524	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
452	720	100.0	720	7	ABO15129	Human	sec	525	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
453	720	100.0	720	7	ABO17264	Human	sec	526	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
454	720	100.0	720	7	ABM17553	Human	sec	527	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
455	720	100.0	720	7	ADA06520	Human	sec	528	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
456	720	100.0	720	7	ADA39213	Human	sec	529	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
457	720	100.0	720	7	ABR85454	Human	sec	530	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
458	720	100.0	720	7	ABM77020	Human	sec	531	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
459	720	100.0	720	7	ABO28199	Human	sec	532	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
460	720	100.0	720	7	ABM22980	Human	sec	533	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
461	720	100.0	720	7	ABM30300	Human	sec	534	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
462	720	100.0	720	7	ABM21760	Human	sec	535	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec
463	720	100.0	720	7	ABM21455	Human	sec	536	720	100.0	720	7	ADC70532	Human	sec	AdC70532	Human	sec

537	9	1.2	30	2	AA76945	AA76945	UK-t-PA h	610	7	1.0	76	4	AAU67610	AAU67610	Proponib
538	9	1.2	30	2	AA93590	AA93590	UK t-PA h	611	7	1.0	76	6	ABM62991	ABM62991	Proponib
539	9	1.2	30	2	AA93593	AA93593	UK t-PA h	612	7	1.0	76	6	ABM64129	ABM64129	Proponib
540	9	1.2	30	2	AA93588	AA93588	UK t-PA h	613	7	1.0	79	5	ABE20816	ABE20816	Human gen
541	9	1.2	101	2	AA92896	AA92896	CUB domai	614	7	1.0	79	5	ABG64651	ABG64651	Human ald
542	9	1.2	110	2	AA927043	AA927043	Amino aci	615	7	1.0	81	6	ABM64695	ABM64695	Proponib
543	9	1.2	730	1	AA980618	AA980618	Human Bon	616	7	1.0	103	3	AA903800	AA903800	Human sec
544	9	1.2	730	2	AA980618	AA980618	C-protein	617	7	1.0	105	3	AA944590	AA944590	Nonclass
545	9	1.2	788	2	AA975919	AA975919	C-protein	618	7	1.0	107	5	ABP66753	ABP66753	Human ORF
546	9	1.2	970	5	AA979188	AA979188	Human tol	619	7	1.0	108	4	AAU27656	AAU27656	Human pro
547	9	1.2	986	2	AA913670	AA913670	C-protein	620	7	1.0	111	2	AA991113	AA991113	Bovine ze
548	9	1.2	986	5	AA980755	AA980755	Human Tum	621	7	1.0	116	2	AA999115	AA999115	Human zet
549	9	1.2	986	6	AA954462	AA954462	Human tum	622	7	1.0	117	3	AA926792	AA926792	Zea may
550	9	1.2	992	5	AA979187	AA979187	Human tol	623	7	1.0	121	3	AA951373	AA951373	Arabidops
551	9	1.2	1015	3	AA932240	AA932240	Human tol	624	7	1.0	121	3	AA926791	AA926791	Zea may
552	9	1.2	1464	3	AA971111	AA971111	Drosophi	625	7	1.0	128	3	AA911631	AA911631	Arabidops
553	9	1.1	11	5	AA977068	AA977068	AC2885 an	626	7	1.0	128	3	AA951372	AA951372	Arabidops
554	9	1.1	50	6	AA936802	AA936802	Human epi	627	7	1.0	142	3	AA926790	AA926790	Zea may
555	9	1.1	51	3	AA976087	AA976087	mutRI fra	628	7	1.0	144	2	AA941967	AA941967	Flea seri
556	9	1.1	51	4	AA956026	AA956026	Skin cell	629	7	1.0	144	4	AA950629	AA950629	Flea seri
557	9	1.1	51	5	AA972226	AA972226	Murine pr	630	7	1.0	148	4	AAU64494	AAU64494	Proponib
558	9	1.1	88	3	AA956553	AA956553	Partial p	631	7	1.0	148	4	AAU64103	AAU64103	Proponib
559	9	1.1	94	3	AA979331	AA979331	Human EGF	632	7	1.0	151	3	AA951371	AA951371	Arabidops
560	9	1.1	95	6	AA927159	AA927159	Human ger	633	7	1.0	172	6	AA939246	AA939246	Protein e
561	9	1.1	95	6	AA927158	AA927158	Human ger	634	7	1.0	172	6	AA939246	AA939246	Protein e
562	9	1.1	96	6	AA95905	AA95905	Human A10	635	7	1.0	184	3	AA951370	AA951370	Arabidops
563	9	1.1	124	4	AA980399	AA980399	Human mus	636	7	1.0	187	7	AA927109	AA927109	E. faeciu
564	9	1.1	124	6	AA980399	AA980399	Novel hum	637	7	1.0	194	4	AAU25597	AAU25597	Human G p
565	9	1.1	126	6	AA977064	AA977064	AC2885 an	638	7	1.0	200	4	AA929491	AA929491	Human G p
566	9	1.1	127	6	AA957370	AA957370	AntI-TRAI	639	7	1.0	200	5	AA960779	AA960779	Novel G p
567	9	1.1	128	3	AA956718	AA956718	Amino aci	640	7	1.0	202	4	AA985610	AA985610	Drosophi
568	9	1.1	152	3	AA976009	AA976009	Murine TG	641	7	1.0	209	4	AA945202	AA945202	Proponib
569	9	1.1	152	4	AA955948	AA955948	Skin cell	642	7	1.0	209	6	AA941721	AA941721	Proponib
570	9	1.1	152	5	AA972148	AA972148	Murine pr	643	7	1.0	210	2	AA935451	AA935451	Chlamydia
571	9	1.1	155	3	AA979314	AA979314	The kappa	644	7	1.0	210	2	AA977599	AA977599	Protein e
572	9	1.1	155	6	AA935906	AA935906	Human 2.1	645	7	1.0	211	6	AA949962	AA949962	Protein e
573	9	1.1	235	6	AA970774	AA970774	Human adi	646	7	1.0	212	4	AA94556	AA94556	E. coli c
574	9	1.1	467	3	AA979332	AA979332	Human EGF	647	7	1.0	212	6	AA931486	AA931486	Protein e
575	9	1.1	596	6	AA92131	AA92131	Protein e	648	7	1.0	212	6	AA948063	AA948063	Protein e
576	9	1.1	859	5	AA968935	AA968935	Human pol	649	7	1.0	212	6	AA915066	AA915066	Protein e
577	9	1.1	1019	2	AA943394	AA943394	Singapore	650	7	1.0	212	6	AA945471	AA945471	Protein e
578	9	1.1	1019	2	AA905750	AA905750	Horrethoe	651	7	1.0	213	5	AA9854972	AA9854972	Lactococc
579	9	1.1	1019	2	AA943302	AA943302	Horrethoe	652	7	1.0	213	6	AA940559	AA940559	Protein e
580	9	1.1	1019	3	AA942490	AA942490	Recombina	653	7	1.0	221	4	AA985059	AA985059	Drosophi
581	9	1.1	1019	4	AA960935	AA960935	Horrethoe	654	7	1.0	227	4	AA951369	AA951369	Arabidops
582	9	1.1	1019	6	AA972332	AA972332	Horrethoe	655	7	1.0	227	4	AA982525	AA982525	Human pro
583	9	1.1	1019	6	AA972332	AA972332	Horrethoe	656	7	1.0	227	6	AA940124	AA940124	Protein e
584	9	1.1	1083	2	AA905749	AA905749	Singapore	657	7	1.0	228	3	AA915809	AA915809	Arabidops
585	9	1.1	1083	2	AA905749	AA905749	Horrethoe	658	7	1.0	228	6	AA915809	AA915809	Arabidops
586	9	1.1	1083	3	AA943301	AA943301	Horrethoe	659	7	1.0	230	3	AA933373	AA933373	Protein e
587	9	1.1	1083	3	AA943301	AA943301	Horrethoe	660	7	1.0	231	6	AA927062	AA927062	Protein e
588	9	1.1	1083	4	AA960934	AA960934	Horrethoe	661	7	1.0	232	4	AA933655	AA933655	Pseudomon
589	9	1.1	1083	4	AA972333	AA972333	Horrethoe	662	7	1.0	232	6	AA915506	AA915506	Protein e
590	9	1.1	1238	6	AA962022	AA962022	Drosophi	663	7	1.0	232	6	AA941957	AA941957	Flea seri
591	9	1.1	1316	4	AA94754	AA94754	Human pro	664	7	1.0	234	3	AA951368	AA951368	Arabidops
592	9	1.1	3570	7	AA937944	AA937944	Human CGD	665	7	1.0	235	3	AA915808	AA915808	Arabidops
593	9	1.1	3571	5	AA920146	AA920146	Human C3b	666	7	1.0	237	3	AA933372	AA933372	Zea may
594	9	1.0	30	2	AA971665	AA971665	Modified	667	7	1.0	239	6	AA949459	AA949459	Protein e
595	9	1.0	43	6	AA978761	AA978761	N. gonorr	668	7	1.0	241	3	AA933371	AA933371	Zea may
596	9	1.0	49	4	AA923855	AA923855	Human EST	669	7	1.0	254	7	AA973285	AA973285	Human 1BT
597	9	1.0	49	7	AA933279	AA933279	Human nov	670	7	1.0	257	4	AA938252	AA938252	Salmonell
598	9	1.0	50	4	AA906451	AA906451	Human foe	671	7	1.0	257	6	AA945762	AA945762	Acinetoba
599	9	1.0	54	4	AA991460	AA991460	C glutami	672	7	1.0	258	3	AA915807	AA915807	Arabidops
600	9	1.0	56	2	AA902522	AA902522	Clone sel	673	7	1.0	259	2	AA911545	AA911545	Human thr
601	9	1.0	59	6	AA971422	AA971422	Staphyloc	674	7	1.0	259	6	AA960565	AA960565	Human thr
602	9	1.0	62	4	AA948293	AA948293	Proponib	675	7	1.0	259	6	AA960563	AA960563	Human thr
603	9	1.0	62	6	AA944812	AA944812	Proponib	676	7	1.0	265	2	AA972891	AA972891	Mycobact
604	9	1.0	63	4	AA944063	AA944063	Peptide #	677	7	1.0	265	2	AA921908	AA921908	Amino aci
605	9	1.0	63	4	AA975756	AA975756	Human bon	678	7	1.0	266	5	AA917669	AA917669	B tropica
606	9	1.0	63	4	AA957494	AA957494	Human liv	679	7	1.0	266	5	AA917668	AA917668	B tropica
607	9	1.0	63	4	AA935189	AA935189	Human dea	680	7	1.0	268	4	AA952510	AA952510	Flea seri
608	9	1.0	74	4	AA966472	AA966472	Proponib	681	7	1.0	268	4	AA961421	AA961421	Proponib
609	9	1.0	76	4	AA966472	AA966472	Proponib	682	7	1.0	280	4	AA961421	AA961421	Proponib

683	7	1.0	280	6	ABM57940	Abm57940	Propionib
684	7	1.0	284	3	AAy82700	AAy82700	Tick deri
685	7	1.0	295	2	AAr74778	AAr74778	Mutant ch
686	7	1.0	295	2	AAr76033	AAr76033	Mutant ch
687	7	1.0	295	2	AAr74776	AAr74776	Mutant ch
688	7	1.0	295	2	AAr76038	AAr76038	Mutant ch
689	7	1.0	295	2	AAr76039	AAr76039	Mutant ch
690	7	1.0	295	2	AAr74779	AAr74779	Mutant ch
691	7	1.0	295	2	AAr76035	AAr76035	Mutant ch
692	7	1.0	295	2	AAr74775	AAr74775	Wild-type
693	7	1.0	295	2	AAr74780	AAr74780	Mutant ch
694	7	1.0	295	2	AAr76036	AAr76036	Mutant ch
695	7	1.0	295	2	AAr74777	AAr74777	Mutant ch
696	7	1.0	295	2	AAr76034	AAr76034	Mutant ch
697	7	1.0	295	2	AAr76040	AAr76040	Mutant ch
698	7	1.0	295	2	AAr76037	AAr76037	Mutant ch
699	7	1.0	295	2	AAW22892	AAW22892	Human mat
700	7	1.0	295	3	AAb08633	AAb08633	Amino aci

## ALIGNMENTS

## RESULT 1

AAy66695 standard; protein; 720 AA.

ID	AAy66695	standard; protein; 720 AA.
AC	AAy66695;	
XX	05-APR-2000	(first entry)
XX	05-APR-2000	
DE	Membrane-bound protein PRO1344.	
XX	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;	
KW	pharmaceutical; receptor immunoadhesin; gene mapping.	
XX	Homo sapiens.	
PN	MO9963088-A2.	
XX	09-DEC-1999.	
XX	02-JUN-1999;	99MO-US012252.
XX	02-JUN-1998;	98US-0087607P.
PR	02-JUN-1998;	98US-0087609P.
PR	02-JUN-1998;	98US-0087759P.
PR	03-JUN-1998;	98US-0087827P.
PR	04-JUN-1998;	98US-0088021P.
PR	04-JUN-1998;	98US-0088025P.
PR	04-JUN-1998;	98US-0088028P.
PR	04-JUN-1998;	98US-0088029P.
PR	04-JUN-1998;	98US-0088030P.
PR	04-JUN-1998;	98US-0088033P.
PR	05-JUN-1998;	98US-0088167P.
PR	05-JUN-1998;	98US-0088167P.
PR	05-JUN-1998;	98US-0088202P.
PR	05-JUN-1998;	98US-0088212P.
PR	05-JUN-1998;	98US-0088217P.
PR	09-JUN-1998;	98US-0088655P.
PR	10-JUN-1998;	98US-0088722P.
PR	10-JUN-1998;	98US-0088730P.
PR	10-JUN-1998;	98US-0088734P.
PR	10-JUN-1998;	98US-0088738P.
PR	10-JUN-1998;	98US-0088740P.
PR	10-JUN-1998;	98US-0088741P.
PR	10-JUN-1998;	98US-0088742P.
PR	10-JUN-1998;	98US-0088810P.
PR	10-JUN-1998;	98US-0088811P.
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PR	10-JUN-1998;	98US-0088825P.
PR	10-JUN-1998;	98US-0088826P.
PR	11-JUN-1998;	98US-0088858P.

PR	11-JUN-1998;	98US-0088861P.
PR	11-JUN-1998;	98US-0088863P.
PR	11-JUN-1998;	98US-0088876P.
PR	12-JUN-1998;	98US-0089090P.
PR	12-JUN-1998;	98US-0089105P.
PR	16-JUN-1998;	98US-0089440P.
PR	16-JUN-1998;	98US-0089512P.
PR	16-JUN-1998;	98US-0089514P.
PR	17-JUN-1998;	98US-0089532P.
PR	17-JUN-1998;	98US-0089538P.
PR	17-JUN-1998;	98US-0089598P.
PR	17-JUN-1998;	98US-0089599P.
PR	17-JUN-1998;	98US-0089600P.
PR	17-JUN-1998;	98US-0089653P.
PR	18-JUN-1998;	98US-0089801P.
PR	18-JUN-1998;	98US-0089907P.
PR	18-JUN-1998;	98US-0089908P.
PR	19-JUN-1998;	98US-0089947P.
PR	19-JUN-1998;	98US-0089948P.
PR	19-JUN-1998;	98US-0089952P.
PR	22-JUN-1998;	98US-0090246P.
PR	22-JUN-1998;	98US-0090252P.
PR	22-JUN-1998;	98US-0090254P.
PR	23-JUN-1998;	98US-0090349P.
PR	23-JUN-1998;	98US-0090355P.
PR	24-JUN-1998;	98US-0090423P.
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PR	24-JUN-1998;	98US-0090444P.
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PR	25-JUN-1998;	98US-0090557P.
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PR	25-JUN-1998;	98US-0090690P.
PR	25-JUN-1998;	98US-0090691P.
PR	25-JUN-1998;	98US-0090694P.
PR	25-JUN-1998;	98US-0090695P.
PR	25-JUN-1998;	98US-0090696P.
PR	26-JUN-1998;	98US-0090862P.
PR	26-JUN-1998;	98US-0090863P.
PR	01-JUL-1998;	98US-0091358P.
PR	01-JUL-1998;	98US-0091360P.
PR	02-JUL-1998;	98US-0091478P.
PR	02-JUL-1998;	98US-0091486P.
PR	02-JUL-1998;	98US-0091519P.
PR	02-JUL-1998;	98US-0091544P.
PR	02-JUL-1998;	98US-0091626P.
PR	02-JUL-1998;	98US-0091628P.
PR	02-JUL-1998;	98US-0091633P.
PR	02-JUL-1998;	98US-0091646P.
PR	02-JUL-1998;	98US-0091673P.
PR	07-JUL-1998;	98US-0091978P.
PR	07-JUL-1998;	98US-0091982P.
PR	09-JUL-1998;	98US-0092182P.
PR	10-JUL-1998;	98US-0092472P.
PR	20-JUL-1998;	98US-0093139P.
PR	30-JUL-1998;	98US-0094651P.
PR	04-AUG-1998;	98US-0095282P.
PR	04-AUG-1998;	98US-0095285P.
PR	04-AUG-1998;	98US-0095301P.
PR	04-AUG-1998;	98US-0095302P.
PR	04-AUG-1998;	98US-0095318P.
PR	04-AUG-1998;	98US-0095321P.
PR	10-AUG-1998;	98US-0095325P.
PR	10-AUG-1998;	98US-0095916P.
PR	10-AUG-1998;	98US-0095929P.
PR	10-AUG-1998;	98US-0096012P.

PR 11-AUG-1998; 98US-0096143P.  
 PR 11-AUG-1998; 98US-0096146P.  
 PR 12-AUG-1998; 98US-0096329P.  
 PR 17-AUG-1998; 98US-0096757P.  
 PR 17-AUG-1998; 98US-0096766P.  
 PR 17-AUG-1998; 98US-0096768P.  
 PR 17-AUG-1998; 98US-0096773P.  
 PR 17-AUG-1998; 98US-0096791P.  
 PR 17-AUG-1998; 98US-0096867P.  
 PR 17-AUG-1998; 98US-0096891P.  
 PR 17-AUG-1998; 98US-0096894P.  
 PR 17-AUG-1998; 98US-0096895P.  
 PR 17-AUG-1998; 98US-0096897P.  
 PR 18-AUG-1998; 98US-0096949P.  
 PR 18-AUG-1998; 98US-0096950P.  
 PR 18-AUG-1998; 98US-0096959P.  
 PR 18-AUG-1998; 98US-0096960P.  
 PR 18-AUG-1998; 98US-0097022P.  
 PR 19-AUG-1998; 98US-0097141P.  
 PR 20-AUG-1998; 98US-0097218P.  
 PR 24-AUG-1998; 98US-0097661P.  
 PR 26-AUG-1998; 98US-0097951P.  
 PR 26-AUG-1998; 98US-0097952P.  
 PR 26-AUG-1998; 98US-0097954P.  
 PR 26-AUG-1998; 98US-0097955P.  
 PR 26-AUG-1998; 98US-0097971P.  
 PR 26-AUG-1998; 98US-0097974P.  
 PR 26-AUG-1998; 98US-0097978P.  
 PR 26-AUG-1998; 98US-0097979P.  
 PR 26-AUG-1998; 98US-0097986P.  
 PR 26-AUG-1998; 98US-0098014P.  
 PR 31-AUG-1998; 98US-0098525P.  
 PR 16-SEP-1998; 98US-0100634P.  
 PR 12-JAN-1999; 99US-0115365P.

(GETH ) GENENTECH INC.

PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 PI Wood WJ, Yuan J;

DR WPI; 2000-072883/06.  
 DR N-PSDB; AAZ65034.

PT Membrane-bound proteins and related nucleotide sequences.

PS Claim 12; Fig 159; 822BP; English.

XX The invention provides membrane-bound PRO polypeptides and  
 CC polynucleotides encoding them. The PRO sequences of the invention were  
 CC identified based on extracellular domain homology screening. The PRO  
 CC sequences have homology with proteins including LDL receptors, TIE  
 CC ligands and various enzymes. The membrane-bound proteins and receptor  
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 CC immunoadhesins, for instance, can be used as therapeutic agents to block  
 CC receptor-ligand interactions. The membrane-bound proteins can also be  
 CC employed for screening of potential peptide or small molecule inhibitors  
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
 CC are useful as hybridization probes, in chromosome and gene mapping and in  
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will  
 CC also be useful for the preparation of PRO polypeptides, especially by  
 CC recombinant techniques

XX Sequence 720 AA;

Query Match 100.0%; Score 720; DB 3; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MELGCMTOLGTLTLLTLLTSSLPREYTVINACPGAENINMCECEYDQIEVCQPGKRE 60  
 DB 1 MELGCMTOLGTLTLLTLLTSSLPREYTVINACPGAENINMCECEYDQIEVCQPGKRE 60  
 OY 61 VVGTTIPCCRNEMNEEDSCLIHPGCTIFENCKSCRNMGWGLTDFYVKGFFCAECRAGW 120

DB 61 VVGTTIPCCRNEMNEEDSCLIHPGCTIFENCKSCRNMGWGLTDFYVKGFFCAECRAGW 120  
 OY 121 YGGDCRCRCGVTLAPAPGQIILLESYPLNANCERTTHAKPGVIGTQRTVYMLSLFEDYMCQYD 180  
 DB 121 YGGDCRCRCGVTLAPAPGQIILLESYPLNANCERTTHAKPGVIGTQRTVYMLSLFEDYMCQYD 180  
 OY 181 YVEVRDGDNDGQITKRVCGNERPAPIQSISSLSLHVLPHSDGSKNPFDPFAIYEETPACS 240  
 DB 181 YVEVRDGDNDGQITKRVCGNERPAPIQSISSLSLHVLPHSDGSKNPFDPFAIYEETPACS 240  
 OY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGQRCEMLLEBRNCSDPGPNVGYQKITGGFGLI 300  
 DB 241 SSPCFHDGTCVLDKAGSYKACLAGYTGQRCEMLLEBRNCSDPGPNVGYQKITGGFGLI 300  
 OY 301 NGRHAKIGTVVSFCNNSTYLSGNEKRTCCQNMENSGKQICIKACREPKISDLVRRVL 360  
 DB 301 NGRHAKIGTVVSFCNNSTYLSGNEKRTCCQNMENSGKQICIKACREPKISDLVRRVL 360  
 OY 361 PMQVSRRTPLAQLYSAFQKQLOSAPTKPPALPFQDLPMGYQHLHTQLOVECTISPFYR 420  
 DB 361 PMQVSRRTPLAQLYSAFQKQLOSAPTKPPALPFQDLPMGYQHLHTQLOVECTISPFYR 420  
 OY 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRMPQAAIYRRTSGVHDGSL 480  
 DB 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRMPQAAIYRRTSGVHDGSL 480  
 OY 481 HKGAPLVCSGALVNETTVVAACHCTDGLKQVMIKRADIKVYLGRKYRDDDRREKTIQS 540  
 DB 481 HKGAPLVCSGALVNETTVVAACHCTDGLKQVMIKRADIKVYLGRKYRDDDRREKTIQS 540  
 OY 541 LQISAILHPNYPDILDDADIAITKLDKARISTRVOPICLAASRDISTFOESHITVAG 600  
 DB 541 LQISAILHPNYPDILDDADIAITKLDKARISTRVOPICLAASRDISTFOESHITVAG 600  
 OY 601 MNVLADVRSPGKNDTLRSGVSVSDSLCEQHEHDGIPVSVTDNNFCASWEPTAPSDI 660  
 DB 601 MNVLADVRSPGKNDTLRSGVSVSDSLCEQHEHDGIPVSVTDNNFCASWEPTAPSDI 660  
 OY 661 CTAFETGGTAAVSPGRASPEPRWHLMGLVMSVDKTCSHRLSTFTVLPFKQMIERNMK 720  
 DB 661 CTAFETGGTAAVSPGRASPEPRWHLMGLVMSVDKTCSHRLSTFTVLPFKQMIERNMK 720

RESULT 2

ID AAU29108 standard; protein; 720 AA.

AC AAU29108;

DT 18-DEC-2001 (first entry)

XX Human PRO polypeptide sequence #85.

DE PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

OS Homo sapiens.

XX MO200168848-A2.

XX PD 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2000; 2000WO-US005601.

XX 02-MAR-2000; 2000WO-US005841.

XX 03-MAR-2000; 2000US-0187202P.

XX 06-MAR-2000; 2000US-0186968P.

XX 14-MAR-2000; 2000US-0189320P.

XX 14-MAR-2000; 2000US-0189328P.



PR 15-MAR-2000; 2000MO-US006884.  
 PR 21-MAR-2000; 2000US-0190828P.  
 PR 21-MAR-2000; 2000US-0191007P.  
 PR 21-MAR-2000; 2000US-0191048P.  
 PR 21-MAR-2000; 2000US-0191314P.  
 PR 28-MAR-2000; 2000US-0192655P.  
 PR 29-MAR-2000; 2000US-0193032P.  
 PR 29-MAR-2000; 2000US-0193053P.  
 PR 30-MAR-2000; 2000MO-US008439.  
 PR 04-APR-2000; 2000US-0194449P.  
 PR 04-APR-2000; 2000US-0194647P.  
 PR 11-APR-2000; 2000US-0195975P.  
 PR 11-APR-2000; 2000US-0196000P.  
 PR 11-APR-2000; 2000US-0196187P.  
 PR 11-APR-2000; 2000US-0196690P.  
 PR 11-APR-2000; 2000US-0196820P.  
 PR 18-APR-2000; 2000US-0198121P.  
 PR 18-APR-2000; 2000US-0198585P.  
 PR 25-APR-2000; 2000US-0199397P.  
 PR 25-APR-2000; 2000US-0199550P.  
 PR 25-APR-2000; 2000US-0199654P.  
 PR 03-MAY-2000; 2000US-0201516P.  
 PR 17-MAY-2000; 2000MO-US013705.  
 PR 22-MAY-2000; 2000MO-US014042.  
 PR 30-MAY-2000; 2000MO-US014941.  
 PR 02-JUN-2000; 2000MO-US015264.  
 PR 05-JUN-2000; 2000US-0209832P.  
 PR 28-JUL-2000; 2000MO-US020710.  
 PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000MO-US023328.  
 PR 08-NOV-2000; 2000MO-US030952.  
 PR 01-DEC-2000; 2000MO-US032678.  
 PR 20-DEC-2000; 2000MO-US034956.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WT, Zhang Z;  
 XX  
 DR N-PSDB; AAS646009.  
 XX  
 PT MPI: 2001-602746/68.  
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumors, such as prostate and breast tumors, in mammals and to  
 PT screen for modulators of the compounds.  
 XX  
 PS Claim 11; Fig 170; 774pp; English.  
 CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
 CC The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumor in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of  
 CC expression in the test sample indicates the presence of a tumor in the  
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
 CC and rabbits but are preferably human. The polypeptides can be used to  
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
 CC when contacted with it. A specific polypeptide can be used to stimulate  
 CC the proliferation or differentiation of chondrocyte cells. The PRO  
 CC proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders  
 CC  
 SO Sequence 720 AA;  
 Query Match 100.0%; Score 720; DB 4; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MELGCTQTGLTFLQLLISLPREYTVINEACPGAEWNIMCRECCBYDQIECVCGKRE 60  
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Db 1 MELGCTQTGLTFLQLLISLPREYTVINEACPGAEWNIMCRECCBYDQIECVCGKRE 60  
 QY 61 VVGYYTIPCCRNENECDSCLHPGCTIENCKSCGNSWGTLDPFYKGFCAECRAGW 120  
 Db 61 VVGYYTIPCCRNENECDSCLHPGCTIENCKSCGNSWGTLDPFYKGFCAECRAGW 120  
 QY 121 YGGDCMRGQVLRAPKQILLSESYPLNAHCEWTIAKKGFPYQLRFWMLSEFDYMCYD 180  
 Db 121 YGGDCMRGQVLRAPKQILLSESYPLNAHCEWTIAKKGFPYQLRFWMLSEFDYMCYD 180  
 QY 181 YVEVDGDNRDGQIIKRVCGNERPAPISIGSSLHLVLFHSDGSKXNFDGPHAIYEETACS 240  
 Db 181 YVEVDGDNRDGQIIKRVCGNERPAPISIGSSLHLVLFHSDGSKXNFDGPHAIYEETACS 240  
 QY 241 YVEVDGDNRDGQIIKRVCGNERPAPISIGSSLHLVLFHSDGSKXNFDGPHAIYEETACS 240  
 Db 241 YVEVDGDNRDGQIIKRVCGNERPAPISIGSSLHLVLFHSDGSKXNFDGPHAIYEETACS 240  
 QY 241 SSPCFHDGTCVLDKXGSKYKCAAGYTQRCNLLSEBNCSDPGAPVNGYQKITGCGPGLI 300  
 Db 241 SSPCFHDGTCVLDKXGSKYKCAAGYTQRCNLLSEBNCSDPGAPVNGYQKITGCGPGLI 300  
 QY 301 NGRHAKIGTVVSFFCNSYVLSGNEKRTCOQNGESGKQPTICIKAREPKISDLVRRVL 360  
 Db 301 NGRHAKIGTVVSFFCNSYVLSGNEKRTCOQNGESGKQPTICIKAREPKISDLVRRVL 360  
 QY 361 PMQVSRRETPHLQLYSAAPSKOKLOSAPTKKPPALPFGDLPMGYQHLHTQLOYECSIPFYR 420  
 Db 361 PMQVSRRETPHLQLYSAAPSKOKLOSAPTKKPPALPFGDLPMGYQHLHTQLOYECSIPFYR 420  
 QY 421 RIGSSRRCTLTGKSGRASPCTIPCGKIENTAKTGTGLRPMQAAIYRRSGVHDSL 480  
 Db 421 RIGSSRRCTLTGKSGRASPCTIPCGKIENTAKTGTGLRPMQAAIYRRSGVHDSL 480  
 QY 481 HKGAMFLVCSGALVNERTVVAHACVTDLGKVTMIKTADLKVVLGKPYRDDDRDEKTIQS 540  
 Db 481 HKGAMFLVCSGALVNERTVVAHACVTDLGKVTMIKTADLKVVLGKPYRDDDRDEKTIQS 540  
 QY 541 LQISAIIILHPNYDPIILLADIAIILKLDKARISTRVQDPCIAASDLSTSPQESHITVAG 600  
 Db 541 LQISAIIILHPNYDPIILLADIAIILKLDKARISTRVQDPCIAASDLSTSPQESHITVAG 600  
 QY 601 WNVLDVSPGPKNDTLRSVVSVDLSLCEBQHDHGIPIVSTVDMFCASWEPAPSDI 660  
 Db 601 WNVLDVSPGPKNDTLRSVVSVDLSLCEBQHDHGIPIVSTVDMFCASWEPAPSDI 660  
 QY 661 CTAETGGIAAIVSFPGRASPEPRMHLGLVSWSYDKTCSHRLSTAFKYLPEKDWIERNMK 720  
 Db 661 CTAETGGIAAIVSFPGRASPEPRMHLGLVSWSYDKTCSHRLSTAFKYLPEKDWIERNMK 720  
 RESULT 3  
 AAB87544  
 ID AAB87544 standard; protein; 720 AA.  
 AC AAB87544;  
 XX  
 DT 15-MAY-2001 (first entry)  
 XX  
 DE Human PRO1344.  
 XX  
 KW Human; PRO protein; mapping.  
 OS Homo sapiens.  
 XX  
 PN WO200116318-A2.  
 XX  
 PD 08-MAR-2001.  
 XX  
 PF 24-AUG-2000; 2000MO-US023328.  
 XX  
 PR 01-SEP-1999; 99MO-US020111.  
 PR 15-SEP-1999; 99MO-US021090.  
 PR 07-DEC-1999; 99US-0169495P.  
 PR 09-DEC-1999; 99US-0170262P.  
 PR 11-JAN-2000; 2000US-0175481P.  
 PR 18-FEB-2000; 2000MO-US004341.



PR 18-FEB-2000; 2000MO-US004342.  
 PR 22-FEB-2000; 2000MO-US004414.  
 PR 01-MAR-2000; 2000MO-US005601.  
 PR 03-MAR-2000; 2000US-0187202P.  
 PR 21-MAR-2000; 2000US-0191007P.  
 PR 30-MAR-2000; 2000MO-US008439.  
 PR 25-APR-2000; 2000US-019397P.  
 PR 22-MAY-2000; 2000MO-US014042.  
 PR 05-JUN-2000; 2000US-0209832P.

XX (GETH ) GENENTECH INC.

XX Eason DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;  
 PI WPI; 2001-183260/18.

DR N-PSDB; AAF92076.

XX Eighty four nucleic acids encoding PRO polypeptides, useful in molecular  
 PT biology, including use as hybridization probes, and in chromosome and  
 PT gene mapping.

PS Claim 12, Fig 38; 278bp; English.

XX The present sequence is a human PRO polypeptide (secreted and  
 CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or  
 CC anti-PRO antibodies are useful for preparation of a medicament useful in  
 CC the treatment of a condition which is responsive to the PRO protein,  
 CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be  
 CC employed as molecular weight markers for protein electrophoresis. The PRO  
 CC coding sequence has applications in molecular biology, including use as  
 CC hybridization probes, and in chromosome and gene mapping

XX Sequence 720 AA;

Query Match 100.0%; Score 720; DB 4; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELCGWQLGTLFQQLLISLPREYTYINACPGAEENINRCCECEQDIECCPGRE 60  
 DB 1 MELCGWQLGTLFQQLLISLPREYTYINACPGAEENINRCCECEQDIECCPGRE 60  
 QY 61 VVGTYIPCCRNENECDSCLHPGCTIFENCKSCNNGSGGTLDFYKGFYCAECRAGW 120  
 DB 61 VVGTYIPCCRNENECDSCLHPGCTIFENCKSCNNGSGGTLDFYKGFYCAECRAGW 120  
 QY 121 YGGDCMRGCVLRAPKQIILBSYPLNAHCETTHAKGFIYQLRFVNLSEFDYMCQYD 180  
 DB 121 YGGDCMRGCVLRAPKQIILBSYPLNAHCETTHAKGFIYQLRFVNLSEFDYMCQYD 180  
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 DB 121 YGGDCMRGCVLRAPKQIILBSYPLNAHCETTHAKGFIYQLRFVNLSEFDYMCQYD 180  
 QY 181 YVEVADGNGNRGOITIKRVCGNERPAPISIGSSILHLFHSNGSKNPFDFHAYEETNCS 240  
 DB 181 YVEVADGNGNRGOITIKRVCGNERPAPISIGSSILHLFHSNGSKNPFDFHAYEETNCS 240  
 QY 241 SSPCFHDTGCVLDKASGYKCAAGYTGQRCENLLEENNCSDPGGPNVNGYKITGGPGLI 300  
 DB 241 SSPCFHDTGCVLDKASGYKCAAGYTGQRCENLLEENNCSDPGGPNVNGYKITGGPGLI 300  
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 DB 301 NGRNAKIGTVVSFFCNNSYVLSGNEKRTCCQNGEWSGQPIICIRACRPKISDLVRRVYL 360  
 QY 301 NGRNAKIGTVVSFFCNNSYVLSGNEKRTCCQNGEWSGQPIICIRACRPKISDLVRRVYL 360  
 DB 301 NGRNAKIGTVVSFFCNNSYVLSGNEKRTCCQNGEWSGQPIICIRACRPKISDLVRRVYL 360  
 QY 361 PMOVOSRETPHLQYLSAFAFSKOKLOSAPTKKPLAPFGDLPMGYOHLHTQLQYECISPFYR 420  
 DB 361 PMOVOSRETPHLQYLSAFAFSKOKLOSAPTKKPLAPFGDLPMGYOHLHTQLQYECISPFYR 420  
 QY 421 RLGSRRRTCLRTGKMSGRAPSCIPICGKIENITAPKTGSLMPWQALYRRTSGVHDSGL 480  
 DB 421 RLGSRRRTCLRTGKMSGRAPSCIPICGKIENITAPKTGSLMPWQALYRRTSGVHDSGL 480  
 QY 481 HKGAMFLVCSGALVNERTVVAACHVTLGKVTMTKTADLVAVVGLKFRDDREKTIQS 540  
 DB 481 HKGAMFLVCSGALVNERTVVAACHVTLGKVTMTKTADLVAVVGLKFRDDREKTIQS 540

DB 481 HKGAMFLVCSGALVNERTVVAACHVTLGKVTMTKTADLVAVVGLKFRDDREKTIQS 540  
 QY 541 LQISATILHBNYDPIILDADIALTKLIDKARISTRVOPICLAASRDLSTSFQSHITVAG 600  
 DB 541 LQISATILHBNYDPIILDADIALTKLIDKARISTRVOPICLAASRDLSTSFQSHITVAG 600  
 QY 601 MNTLADVRSPGKNDTLRSQVSVSDSLCEQHEHGHIPVSYTDNMFCAWSWEPASDI 660  
 DB 601 MNTLADVRSPGKNDTLRSQVSVSDSLCEQHEHGHIPVSYTDNMFCAWSWEPASDI 660  
 QY 661 CTATGTGIAAVSPGRASPEPRNHLGLVSWSDTKCSHLSLTAFTKYLFPKMIERNMK 720  
 DB 661 CTATGTGIAAVSPGRASPEPRNHLGLVSWSDTKCSHLSLTAFTKYLFPKMIERNMK 720

RESULT 4  
 AAB65218  
 ID AAB65218 standard; protein: 720 AA.

XX AAB65218;

XX 02-APR-2001 (first entry)

XX Human PRO1344 (UNG699) protein sequence SEQ ID NO:231.

XX Human; secreted and transmembrane protein; PRO; cytosolic; cell death;  
 KW cancer; chromosomal mapping; gene mapping; tissue typing;  
 KW diagnostic assay.

XX Homo sapiens.

XX WO200073454-A1.

XX 07-DEC-2000.

XX 30-MAR-2000; 2000MO-US008439.

XX 02-JUN-1999; 99MO-US012252.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0143048P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145658P.  
 PR 28-JUL-1999; 99US-0146222P.  
 PR 17-AUG-1999; 99US-0149326P.  
 PR 15-SEP-1999; 99MO-US021090.  
 PR 15-SEP-1999; 99MO-US021547.  
 PR 08-OCT-1999; 99US-0158663P.  
 PR 30-NOV-1999; 99MO-US028313.  
 PR 01-DEC-1999; 99MO-US028301.  
 PR 16-DEC-1999; 99MO-US030095.  
 PR 20-DEC-1999; 99MO-US030911.  
 PR 05-JAN-2000; 2000MO-US000219.  
 PR 06-JAN-2000; 2000MO-US000376.  
 PR 11-FEB-2000; 2000MO-US003565.  
 PR 18-FEB-2000; 2000MO-US004341.  
 PR 22-FEB-2000; 2000MO-US004414.  
 PR 24-FEB-2000; 2000MO-US004914.  
 PR 24-FEB-2000; 2000MO-US005004.  
 PR 02-MAR-2000; 2000MO-US005841.  
 PR 15-MAR-2000; 2000MO-US005884.  
 PR 20-MAR-2000; 2000MO-US007377.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eason DL;  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi CJ, Gurney AL, Kijavlin IV, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;  
 DR WPI; 2001-032160/04.  
 DR N-PSDB; AAF44180.



PR	24-SEP-1998	98US101916P
PR	30-SEP-1998	98US101925P
PR	06-OCT-1998	98US101934P
PR	08-MAY-1999	99MO-US005028
PR	14-MAY-1999	99MO-US010733
PR	02-JUN-1999	99MO-US012252
PR	01-SEP-1999	99MO-US020111
PR	15-SEP-1999	99MO-US021090
PR	15-SEP-1999	99MO-US021194
PR	22-DEC-1999	99MO-US030720
PR	18-FEB-2000	2000MO-US003431
PR	18-FEB-2000	2000MO-US004342
PR	22-FEB-2000	2000MO-US004614
PR	01-MAR-2000	2000MO-US005601
PR	30-MAR-2000	2000MO-US008439
PR	02-MAY-2000	2000MO-US014042
PR	02-JUN-2000	2000MO-US015264
PR	23-AUG-2000	2000MO-US023522
PR	24-AUG-2000	2000MO-US023328
PR	01-NOV-2000	2000MO-US030873
PR	01-DEC-2000	2000MO-US033778
PR	20-DEC-2000	2000MO-US034956
PR	28-FEB-2001	2001MO-US005620
PR	01-MAR-2001	2001MO-US006666
PR	30-MAY-2001	2001MO-US017443
PR	01-JUN-2001	2001MO-US017800
PR	20-JUN-2001	2001MO-US019692
PR	29-JUL-2001	2001MO-US021066
PR	09-JUL-2001	2001MO-US021735

PA (GETH ) GENENTECH INC.

PI Eaton DL, Filvaroff E, Geriltsen ME, Goddard A, Godowski FJ,  
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

DR WPI; 2002-731348/79.  
DR N-PSDB; ABS74396.

PT New isolated secreted and transmembrane PRO polypeptide useful for modulating biological activity of a cell, or for treating sports-related joint problems, osteoarthritis or rheumatoid arthritis.

PS Claim 20; Fig 38; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO polypeptide having 80 % sequence identity to a sequence appearing as AB695851-AB695934 or their associated signal peptide, or a sequence of an extracellular domain of the proteins with their associated signal peptide or lacking its associated signal peptide. Also included are the nucleic acids encoding the proteins, vectors, host cells, fusion proteins and antibodies which specifically bind to the proteins. The proteins are useful for detecting a polypeptide designated as A, B, C or D in a sample suspected of containing an A, B, C or D polypeptide, by contacting the sample with a polypeptide designated as E, F, G, H or I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide conjugate in the sample, where the formation of the conjugate is indicative of the presence of an A, B, C or D polypeptide in the sample, where A is PRO10772 polypeptide, B is a PRO20110 polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO50501 polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with a detectable label or is attached to a solid support. The proteins are useful for linking a bioactive molecule to a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies against them are useful for modulating a biological activity of a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H, or I. The cell is killed. The proteins are useful for identifying agonists or antagonists, for the preparation of a medicament useful in the treatment of a condition which is responsive to the proteins, as molecular weight markers for protein electrophoresis

XX 15-APR-2003 (first entry)  
DT Human PRO polypeptide #85.  
XX  
DE Human PRO polypeptide #85.  
XX  
KW Human; PRO; cytosolic; tumour; cancer; breast; lung; stomach; liver;  
dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;  
KM antibody-dependent enzyme mediated prodrug therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2003027272-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 21-JUN-2002; 2002US-00176492.  
XX  
PR 18-SEP-1997; 97US-0059263P.  
PR 18-SEP-1997; 97US-0059266P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 21-OCT-1997; 97US-0063486P.  
PR 24-OCT-1997; 97US-0063120P.  
PR 24-OCT-1997; 97US-0063121P.  
PR 28-OCT-1997; 97US-0063540P.  
PR 28-OCT-1997; 97US-0063541P.  
PR 28-OCT-1997; 97US-0063544P.  
PR 28-OCT-1997; 97US-0063564P.  
PR 29-OCT-1997; 97US-0063734P.  
PR 31-OCT-1997; 97US-0063870P.  
PR 31-OCT-1997; 97US-0064103P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 21-NOV-1997; 97US-0066120P.  
PR 24-NOV-1997; 97US-0066466P.  
PR 24-NOV-1997; 97US-0066772P.  
PR 11-DEC-1997; 97US-0069335P.  
PR 12-DEC-1997; 97US-0069425P.  
PR 17-DEC-1997; 97US-0069870P.  
PR 18-DEC-1997; 97US-0068017P.  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
PR 11-MAR-1998; 98US-0077649P.  
PR 20-MAR-1998; 98US-0078886P.  
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PR 31-MAR-1998; 98US-0080107P.  
PR 31-MAR-1998; 98US-0080194P.  
PR 01-APR-1998; 98US-0080327P.  
PR 01-APR-1998; 98US-0080333P.  
PR 08-APR-1998; 98US-0081049P.  
PR 08-APR-1998; 98US-0081070P.  
PR 09-APR-1998; 98US-0081195P.  
PR 15-APR-1998; 98US-0081838P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082797P.  
PR 28-APR-1998; 98US-0083222P.  
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PR 29-APR-1998; 98US-0083496P.  
PR 29-APR-1998; 98US-0083496P.  
PR 07-MAY-1998; 98US-0084640P.  
PR 07-MAY-1998; 98US-0084643P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 18-MAY-1998; 98US-0086023P.  
PR 22-MAY-1998; 98US-0086392P.  
  
PR 22-MAY-1998; 98US-0086486P.  
PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 02-JUN-1998; 98US-0087509P.  
PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088025P.  
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PR 09-JUN-1998; 98US-0088655P.  
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PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088740P.  
PR 10-JUN-1998; 98US-0088811P.  
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PR 11-JUN-1998; 98US-0088863P.  
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PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 19-JUN-1998; 98US-0089952P.  
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PR 25-JUN-1998; 98US-0090696P.  
PR 26-JUN-1998; 98US-009105413.  
PR 26-JUN-1998; 98US-0090862P.  
PR 26-JUN-1998; 98US-0090863P.  
PR 26-JUN-1998; 98US-0091010P.  
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PR 01-JUL-1998; 98US-0091544P.  
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PR 02-JUL-1998; 98US-0091486P.  
PR 02-JUL-1998; 98US-0091626P.  
PR 02-JUL-1998; 98US-0091628P.  
PR 02-JUL-1998; 98US-0091632P.  
PR 02-JUL-1998; 98US-0094006P.  
PR 04-AUG-1998; 98US-0095282P.  
PR 10-AUG-1998; 98US-0095988P.  
PR 10-AUG-1998; 98US-0096012P.  
PR 17-AUG-1998; 98US-0096575P.  
PR 17-AUG-1998; 98US-0096766P.  
PR 17-AUG-1998; 98US-0096867P.  
PR 17-AUG-1998; 98US-0096891P.  
PR 17-AUG-1998; 98US-0096897P.  
PR 18-AUG-1998; 98US-0096949P.  
PR 18-AUG-1998; 98US-0096959P.

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PR 18-AUG-1998; 98US-0097022P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0098602P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
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PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98US-0101751P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
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PR 23-SEP-1998; 98US-0101471P.
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 Best Local Similarity 100.0%; Pred. No. 0;  
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## RESULT 7

ABU88032 standard; protein; 720 AA.

ABU88032;

07-JUL-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO1344.

KW Human; secreted and transmembrane protein: PRO; gene therapy;  
 tumour necrosis factor-alpha release; TNF-alpha release;  
 chondrocyte proliferation; chondrocyte differentiation; tumour;  
 adrenal tumour; lung tumour; colon tumour; breast tumour;  
 prostate tumour; rectal tumour; cervical tumour; liver tumour.

OS Homo sapiens.

US2003032127-A1.

13-FEB-2003.

26-JUN-2002; 2002US-00183012.

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XX DT 05-AUG-2003 (first entry)  
XX DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
XX KW Human; PRO: secreted protein; transmembrane protein;  
KW extracellular domain; tumour necrosis factor- $\alpha$ ; TNF- $\alpha$ ;  
KW chondrocyte; proliferation; differentiation; cartilage disorder;  
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
KW antirheumatic; vulnery; gene therapy.  
XX OS Homo sapiens.  
XX PN US2003036159-A1.  
XX PD 20-FEB-2003.  
XX PF 02-JUL-2002; 2002US-0018773.  
XX PR 18-SEP-1997; 97US-0059263P.  
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QY 121 YGGGCMRCGQVLRAPKQITLESYPLNACHCMTTHAKRGFTYQLRPWLSEFPYMCQYD 180
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QY 181 YVEVDDGNDRDGQITIKRVCNERNPAPISQISSLSLHVLPHSDGSKNFGFPAHYEITRACS 240
DB 181 YVEVDDGNDRDGQITIKRVCNERNPAPISQISSLSLHVLPHSDGSKNFGFPAHYEITRACS 240

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## RESULT 11

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ABU99551;

ABU99551; (first entry)

Human secreted/transmembrane protein (PRO) #85.

Human; secreted and transmembrane protein; PRO; TNF-alpha;

tissue typing. factor alpha; chondrocyte cell; tumour; gene therapy;

Homo sapiens.

US2003040070-A1.

27-FEB-2003.

27-JUN-2002; 2002US-00184627.

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RESULT 12  
 ABUS8033

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 XX 14-APR-2003 (first entry)  
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 XX Human PRO polypeptide #65.  
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 KW horse; dog; cat; sheep; pig; goat; rabbit; ADAPT;  
 KW antibody-dependent enzyme mediated prodruq therapy.  
 OS  
 XX Homo sapiens.  
 XX  
 XX US2003027163-A1.  
 XX  
 XX 06-FEB-2003.  
 XX  
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 PR 24-JUN-1998; 98US-0090542P.  
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 PR 25-JUN-1998; 98US-0090676P.  
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 PR 25-JUN-1998; 98US-0090694P.  
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 PR 01-JUL-1998; 98US-0091360P.  
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 PR 02-JUL-1998; 98US-0091478P.  
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 PR 02-JUL-1998; 98US-0091628P.  
 PR 02-JUL-1998; 98US-0091633P.  
 PR 02-JUL-1998; 98US-0091646P.  
 PR 02-JUL-1998; 98US-0091673P.  
 PR 07-JUL-1998; 98US-0091978P.  
 PR 07-JUL-1998; 98US-0091982P.  
 PR 09-JUL-1998; 98US-0092182P.  
 PR 20-JUL-1998; 98US-0092472P.  
 PR 20-JUL-1998; 98US-0093339P.  
 PR 30-JUL-1998; 98US-0094651P.  
 PR 04-AUG-1998; 98US-0095282P.  
 PR 04-AUG-1998; 98US-0095285P.  
 PR 04-AUG-1998; 98US-0095301P.  
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 PR 04-AUG-1998; 98US-0095321P.  
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 PR 19-AUG-1998; 98US-0097141P.  
 PR 20-AUG-1998; 98US-0097218P.  
 PR 24-AUG-1998; 98US-0097661P.  
 PR 26-AUG-1998; 98US-0097952P.  
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 PR 26-AUG-1998; 98US-0098014P.  
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 PR 02-JUN-1999; 98US-0100658P.  
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 PR 15-MAR-2000; 98US-0100658P.  
 PR 20-MAR-2000; 98US-0100658P.  
 PR 30-MAR-2000; 98US-0100658P.  
 PR 15-MAY-2000; 98US-0100658P.  
 PR 17-MAY-2000; 98US-0100658P.  
 PR 22-MAY-2000; 98US-0100658P.  
 PR 30-MAY-2000; 98US-0100658P.  
 PR 02-JUN-2000; 98US-0100658P.  
 PR 23-JUN-2000; 98US-0100658P.  
 PR 28-JUL-2000; 98US-0100658P.  
 PR 11-AUG-2000; 98US-0100658P.  
 PR 23-AUG-2000; 98US-0100658P.  
 PR 24-AUG-2000; 98US-0100658P.  
 PR 07-SEP-2000; 98US-0100658P.

Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGCTQGLTFLQLLISSLPREYVINEACGAEWNINCRCEYDQIEYCPGRRE 60  
 DB 1 MELGCTQGLTFLQLLISSLPREYVINEACGAEWNINCRCEYDQIEYCPGRRE 60  
 QY 61 VVGTTIPCCRNENECOSCLHPCTTIPENCKSCRNSWGTLDDFYVKGFPYCAECRPGW 120  
 DB 61 VVGTTIPCCRNENECOSCLHPCTTIPENCKSCRNSWGTLDDFYVKGFPYCAECRPGW 120  
 QY 121 YGSDCMRCGQVLRAPKQIILLESYPLNAHCWTHAKGFIQLRFWLSLEFDMCQYD 180  
 DB 121 YGSDCMRCGQVLRAPKQIILLESYPLNAHCWTHAKGFIQLRFWLSLEFDMCQYD 180  
 QY 181 YVEYRDGDNRDQIIRKVCNERNAPPTOSIGSSJLVLPHSGSKXNFDGFAIYEEITKCS 240

Db 181 YVEVRDGDNRDGGIIRKVCNGNERPAPIQISGLSLHVLHSDGSKNFDGFHAIYEIETACS 240  
 Qy 241 SSPFHGTGTYLDKAGSYKACACLAGYTGRCENLLEERNSSDGGPANGYQKITGGPGLI 300  
 Db 241 SSPFHGTGTYLDKAGSYKACACLAGYTGRCENLLEERNSSDGGPANGYQKITGGPGLI 300  
 Qy 301 NGRRAKIGTVVSPFCNNSSYVLGNEKRTCOONGEMSGKOPICIKACREPTISLVRRLV 360  
 Db 301 NGRRAKIGTVVSPFCNNSSYVLGNEKRTCOONGEMSGKOPICIKACREPTISLVRRLV 360  
 Qy 361 PMQVSEHETPLHQLYSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSA 420  
 Db 361 PMQVSEHETPLHQLYSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSAFSA 420  
 Qy 421 RLGSRRRTCLRTGWSGRAPSCIPICGKIENITAPKQGLRMPQALYRTSGVHDSGL 480  
 Db 421 RLGSRRRTCLRTGWSGRAPSCIPICGKIENITAPKQGLRMPQALYRTSGVHDSGL 480  
 Qy 481 HKGAMFLVCGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKFEYRDDDEKTIQS 540  
 Db 481 HKGAMFLVCGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKFEYRDDDEKTIQS 540  
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 Db 541 LQISAILHPNYDPIILDADIAIKLIDKARISTRVOPICIASRDLSTSFQESHITVAG 600  
 Qy 601 MNVLADVRSPGKNDTLRSQGVSVVDSILCEQHEHDGIPVSDNMFCSWERTAPSDI 660  
 Db 601 MNVLADVRSPGKNDTLRSQGVSVVDSILCEQHEHDGIPVSDNMFCSWERTAPSDI 660  
 Qy 661 CTAETGGIAVSPFGRAPEPRMHLMGIVSYDKTCSHRLSTAFTVLPFKMIEHNMK 720  
 Db 661 CTAETGGIAVSPFGRAPEPRMHLMGIVSYDKTCSHRLSTAFTVLPFKMIEHNMK 720

## RESULT 13

ABUS9111  
 ID ABUS9111 standard; protein; 720 AA.

XX ABUS9111;

XX 28-APR-2003 (first entry)

XX Novel human secreted or transmembrane protein PRO1344.

Km Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 Km cardiac insufficiency disorder; cancer; tumour; immune response;  
 Km adrenal cortical capillary endothelial growth; c-fos induction;  
 Km vascular endothelial growth factor inhibition; VEGF inhibition;  
 Km endothelial cell growth inhibitor; T-lymphocytes stimulation;  
 Km retinal neurons cell survival; rod photoreceptor cell survival;  
 Km retinal disorder; retinitis pigmentosa; kidney disorder;  
 Km mammalian kidney mesangial cell proliferation; Berger disease;  
 Km dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
 Km chondrocyte redifferentiation; sports injury; arthritis.

XX Homo sapiens.

XX US2002132252-A1.

XX 19-SEP-2002.

XX 14-NOV-2001; 2001US-00990442.

XX 16-JUN-1997; 97US-0049787P.

XX 17-OCT-1997; 97US-0062230P.

XX 05-NOV-1997; 97WO-US020069.

XX 12-NOV-1997; 97US-0065186P.

XX 13-NOV-1997; 97US-0065311P.

XX 24-NOV-1997; 97US-0066770P.

XX 25-FEB-1998; 98US-0075945P.

XX 28-APR-1998; 98US-0078910P.

PR 07-MAY-1998; 98US-0084600P.  
 PR 28-MAY-1998; 98US-0087106P.  
 PR 02-JUN-1998; 98US-0087607P.  
 PR 02-JUN-1998; 98US-0087609P.  
 PR 02-JUN-1998; 98US-0087759P.  
 PR 03-JUN-1998; 98US-0087827P.  
 PR 04-JUN-1998; 98US-0088021P.  
 PR 04-JUN-1998; 98US-0088025P.  
 PR 04-JUN-1998; 98US-0088026P.  
 PR 04-JUN-1998; 98US-0088028P.  
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 PR 04-JUN-1998; 98US-0088033P.  
 PR 04-JUN-1998; 98US-0088326P.  
 PR 05-JUN-1998; 98US-0088167P.  
 PR 05-JUN-1998; 98US-0088202P.  
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 PR 09-JUN-1998; 98US-0088655P.  
 PR 10-JUN-1998; 98US-0088734P.  
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 PR 10-JUN-1998; 98US-0088742P.  
 PR 10-JUN-1998; 98US-0088810P.  
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 PR 11-JUN-1998; 98US-0088858P.  
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 PR 11-JUN-1998; 98US-0088876P.  
 PR 12-JUN-1998; 98US-0089105P.  
 PR 16-JUN-1998; 98US-0089440P.  
 PR 16-JUN-1998; 98US-0089512P.  
 PR 16-JUN-1998; 98US-0089514P.  
 PR 17-JUN-1998; 98US-0089532P.  
 PR 17-JUN-1998; 98US-0089538P.  
 PR 17-JUN-1998; 98US-0089598P.  
 PR 17-JUN-1998; 98US-0089599P.  
 PR 17-JUN-1998; 98US-0089600P.  
 PR 17-JUN-1998; 98US-0089653P.  
 PR 18-JUN-1998; 98US-0089801P.  
 PR 18-JUN-1998; 98US-0089807P.  
 PR 18-JUN-1998; 98US-0089908P.  
 PR 16-SEP-1998; 98WO-US013330.  
 PR 17-SEP-1998; 98WO-US019437.  
 PR 07-OCT-1998; 98WO-US021141.  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 05-JAN-1999; 99WO-US000106.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 02-JUN-1999; 99WO-US01252.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 06-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 02-MAR-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 15-MAY-2000; 2000WO-US013358.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.



PR 11-AUG-2000; 2000MO-US022031.  
 PR 23-AUG-2000; 2000MO-US023522.  
 PR 24-AUG-2000; 2000MO-US023328.  
 PR 08-NOV-2000; 2000MO-US030952.  
 PR 01-DEC-2000; 2000MO-US032678.  
 PR 28-FEB-2001; 2001MO-US006520.  
 PR 01-JUN-2001; 2001MO-US017800.  
 PR 20-JUN-2001; 2001MO-US019692.  
 PR 29-JUN-2001; 2001MO-US021066.  
 PR 09-JUL-2001; 2001MO-US021735.  
 PR 28-AUG-2001; 2001US-00941992.

(GENTH ) GENTECH INC.

XX Askenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Geisler H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gunney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;

XX WPI: 2003-247083/24.  
 DR N-PSDB: ABX80270.

XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 PT are therapeutically useful for enhancing immune response and in cancer  
 PT treatments.

XX Claim 12; Fig 159; 648bp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO  
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 CC in modulating at least one biological activity of a cell expressing a PRO  
 CC polypeptide. PRO1312 stimulates hypertrophy or neonatal heart and is thus  
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
 CC stimulate adrenal cortical insufficiency disorders. PRO1536,  
 CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
 CC PRO1366 and PRO1387 induce c-fos in endothelial cells, and are thus  
 CC useful for treating conditions or disorders where angiogenesis would be  
 CC beneficial, e.g. wound healing and antagonists of this polypeptide are  
 CC useful for treating cancerous tumors. PRO812 inhibits vascular  
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 CC cells and is thus useful for inhibiting endothelial cell growth in  
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
 CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
 CC rod photoreceptor cells) and therefore are useful for treating retinal  
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
 CC and therefore are useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger disease or other  
 CC nephropathies associated with dermatitis, herpetic forms or Crohn's  
 CC disease. PRO110, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
 CC proliferation and/or redifferentiation of chondrocytes in culture and are  
 CC thus useful for treating sports injuries, and arthritis. This is the  
 CC amino acid sequence of a novel human PRO protein

XX Sequence 720 AA;

Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGCTOLGTLTLLLSIPREYVINEACPAENINMRECCERDQIEVCPRGRE 60  
 DB 1 MELGCTOLGTLTLLLSIPREYVINEACPAENINMRECCERDQIEVCPRGRE 60  
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 DB 61 VVGATIPCCRNENECDSCLIRPGCTIFENCKSCRNNGSGTLDLFYVYKGFACACRAGW 120

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 DB 121 YGDCNRGCGVLRAPKQIILLESYPLNACSWTIHAPGVILQRFVYMLSEPDYMCQYD 180  
 QY 181 YVEVRDNDNDGQITIKRVCGNERPAPIQSIGSSLHVLPHSDGSKNPFQFHAIEEITACS 240  
 DB 181 YVEVRDNDNDGQITIKRVCGNERPAPIQSIGSSLHVLPHSDGSKNPFQFHAIEEITACS 240  
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 DB 241 SSPCFHGTCTVLKAGSYKACLAGYGRCEMLLEBRNCSDDGPGPNVGYOKITGPGQLI 300  
 QY 301 NGRHAKIGTVSFEFCNNYSVLSGNEKRTCCONGEWSGKQPICIKACREPKISDLVRRVL 360  
 DB 301 NGRHAKIGTVSFEFCNNYSVLSGNEKRTCCONGEWSGKQPICIKACREPKISDLVRRVL 360  
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 DB 361 PMOVQSRREPLHQLYSAAFSKOKLQSAFTKPKPALPFEDLPMGYOHLTOLQYECISPFYR 420  
 QY 421 RLSSRRRTCLRTGKSGRASCIPIGKIENTITAPKTQGLRMPQOAIYRRTSGVHGSGL 480  
 DB 421 RLSSRRRTCLRTGKSGRASCIPIGKIENTITAPKTQGLRMPQOAIYRRTSGVHGSGL 480  
 QY 481 HKGAMFLVCSGALVNERTVVAAHCVTDLGRVTWIKTADLRVYLGKFRYRDDREKTIQS 540  
 DB 481 HKGAMFLVCSGALVNERTVVAAHCVTDLGRVTWIKTADLRVYLGKFRYRDDREKTIQS 540  
 QY 541 LQSAIILHNPYDPLDADIAIILKLDKARISFRVOPICLAASRDISTFOESHITVAG 600  
 DB 541 LQSAIILHNPYDPLDADIAIILKLDKARISFRVOPICLAASRDISTFOESHITVAG 600  
 QY 601 MNVLADRSFGFKNDLRSQVSVDSLLCEQHEHDGIPVSYVDNMFCAWEPAPSIDI 660  
 DB 601 MNVLADRSFGFKNDLRSQVSVDSLLCEQHEHDGIPVSYVDNMFCAWEPAPSIDI 660  
 QY 661 CTATGGAIVSFEGRASPEPRHMLMGLVMSYDKTCSHRLSTAFTVLPFKMIEENMK 720  
 DB 661 CTATGGAIVSFEGRASPEPRHMLMGLVMSYDKTCSHRLSTAFTVLPFKMIEENMK 720

RESULT 14  
 ABU82623  
 ID ABU82623 standard; protein; 720 AA.  
 AC ABU82623;  
 DT 26-JUN-2003 (first entry)  
 DE Human secreted/transmembrane protein PRO1344.  
 KW Human; PRO; secreted protein; transmembrane protein;  
 KW cardiac insufficiency disorders; angiogenesis; wound healing;  
 KW cancerous tumour; immune response; retinal disorder; sight loss;  
 KW retinitis pigmentosa; age-related macular degeneration; AMD;  
 KW kidney disorder; Berger disease; nephropathy; dermatitis; herpetic forms;  
 KW Crohn's disease; sports injury; arthritis.  
 OS Homo sapiens.  
 PN US2003032023-A1.  
 PD 13-FEB-2003.  
 PF 14-NOV-2001; 2001US-00990711.  
 PR 16-JUN-1997; 97US-0049787P.  
 PR 17-OCT-1997; 97US-0062250P.  
 PR 05-NOV-1997; 97MO-US020069.  
 PR 12-NOV-1997; 97US-0065186P.  
 PR 13-NOV-1997; 97US-0065311P.  
 PR 24-NOV-1997; 97US-0066770P.



PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US000356.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-JUN-2000; 2000US-0213637P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.

Query Match 100.0%; Score 720; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;

Matches 720; Conservative 0; Mismatches 0;

QY 1 MELGCTTOLGTLTFLQLLISLPLETYVINEACPGAEWNIMCECEYDOIECVCPGKRE 60  
DB 1 MELGCTTOLGTLTFLQLLISLPLETYVINEACPGAEWNIMCECEYDOIECVCPGKRE 60  
QY 61 VVGYYTTPCCRNENECDCSLIHGCTTIFENCKSCRNKSGWGTDDYVYKGFYCAEGRAM 120  
DB 61 VVGYYTTPCCRNENECDCSLIHGCTTIFENCKSCRNKSGWGTDDYVYKGFYCAEGRAM 120  
QY 121 YGSDCKRCGCVLAPKQOILLESYPLNACCEWTHKPGVYIOLRVMLSLEPDYCOYD 180  
DB 121 YGSDCKRCGCVLAPKQOILLESYPLNACCEWTHKPGVYIOLRVMLSLEPDYCOYD 180  
QY 181 YVEVRDGNRDGQIIKRVCGNERPAPIQISGSLHYLFHSDGSKNDFPHAIYEETIACS 240  
DB 181 YVEVRDGNRDGQIIKRVCGNERPAPIQISGSLHYLFHSDGSKNDFPHAIYEETIACS 240  
QY 241 SSPCFHDGTCTVLDAKAGSYKACLAGTTCQRCENULBERNCSDDGCVNGYQKTTGPGDI 300  
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AC AB082790;  
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KW chromosome mapping; gene mapping; cytosolic.  
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Search completed: August 18, 2004, 16:32:15  
Job time : 74 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:20:53 ; Search time 42 Seconds  
(without alignments)  
5408.883 Million cell updates/sec

Title: US-10-063-546-38  
Perfect score: 3945  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues  
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 700 summaries

- Database :
- 1: SP archaea:\*
  - 2: SP bacteria:\*
  - 3: SP fungi:\*
  - 4: SP human:\*
  - 5: SP\_invertebrate:\*
  - 6: SP\_mammal:\*
  - 7: SP\_mhc:\*
  - 8: SP\_organelle:\*
  - 9: SP\_phage:\*
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  - 11: SP\_rodent:\*
  - 12: SP\_virus:\*
  - 13: SP\_vertebrate:\*
  - 14: SP\_unclassified:\*
  - 15: SP\_virus:\*
  - 16: SP\_bacteriap:\*
  - 17: SP\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	3612	91.6	720	11	O8B0Z5
4	949	24.1	181	4	O9Y432
5	678	17.2	1019	5	O8T961
6	665	16.9	1083	5	O26423
7	608.5	15.4	680	5	O868H7
8	604	15.3	680	5	O868H5
9	597	15.1	688	5	O868H6
10	576.5	14.6	688	5	O868H4
11	489.5	12.4	698	13	O9PU71
12	483	12.2	701	11	O9JUS9
13	482.5	12.2	703	11	O8CHN8
14	482	12.2	717	13	O8AXR1
15	468	11.9	728	4	O96RS4
16	467	11.8	697	11	O8CG43

17	466	11.8	717	13	O8AXR0	O8axr0 xenopus lae
18	459	11.6	733	11	O8CD27	O8cd27 mus musculu
19	457	11.6	719	13	O9PVY2	O9pvY2 triakis acy
20	452	11.5	733	11	O920S0	O920s0 mus musculu
21	448	11.4	745	13	O9PVY3	O9pvY3 cyprinus ca
22	436.5	11.1	681	13	O7ZT70	O7zt70 lampetra ja
23	429	10.9	707	11	O9ET60	O9et60 mus musculu
24	428	10.8	707	11	O99K16	O99k16 mus musculu
25	428	10.8	707	11	O8CG16	O8cg16 mus musculu
26	424	10.7	678	11	O9JUS8	O9jUs8 rattus norv
27	421.5	10.7	688	13	O9PVY4	O9pvY4 xenopus lae
28	420	10.6	643	11	O9QX84	O9qx84 rattus norv
29	417	10.6	685	11	O91WPO	O91wP0 mus musculu
30	416.5	10.6	706	11	O8CFP9	O8cfP9 mus musculu
31	412	10.4	685	11	O92338	O92338 mus musculu
32	401.5	10.2	746	11	O8CHP7	O8chP7 cavia porce
33	401.5	10.2	746	5	O81AD8	O81ad8 halocynthia
34	400.5	10.2	746	5	O01654	O01654 halocynthia
35	398.5	10.1	686	13	O9DGC2	O9dgc2 cyprinus ca
36	395	10.0	721	13	O7ZTF69	O7ztF69 lampetra ja
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38	382.5	9.7	752	5	O01655	O01655 halocynthia
39	382	9.7	722	13	O8AW90	O8aw90 lampetra ja
40	381	9.7	722	13	O9PSZ5	O9psZ5 lampetra ja
41	376	9.5	623	11	O9JJP3	O9jJp3 rattus norv
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50	354	9.0	1524	13	O91674	O91674 xenopus lae
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52	340.5	8.6	449	4	O8U012	O8u012 homo sapien
53	340.5	8.6	694	11	O70542	O70542 rattus norv
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55	329.5	8.4	3389	4	O96QY9	O96qY9 homo sapien
56	329.5	8.4	3566	4	O96RM4	O96rm4 homo sapien
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58	318	8.1	3487	4	O7Z408	O7z408 homo sapien
59	316.5	8.0	460	11	O99PC6	O99pc6 mus musculu
60	316.5	8.0	460	11	O91WN8	O91wn8 mus musculu
61	313	7.9	855	11	O9JUT7	O9jUt7 rattus norv
62	311	7.9	446	11	O8K3U6	O8k3U6 rattus norv
63	310.5	7.9	434	13	O7R3B6	O7r3b6 brachydanio
64	305	7.7	456	6	O9TTR0	O9ttr0 canis famli
65	301.5	7.6	433	13	O8JHD0	O8jhd0 brachydanio
66	300.5	7.6	446	11	O61109	O61109 mus musculu
67	299	7.6	1111	11	O80YN4	O80yn4 rattus norv
68	298.5	7.6	433	13	O8CANY	O8cany mus musculu
69	297.5	7.5	777	11	O8CIR9	O8cIr9 mus musculu
70	295.5	7.5	336	11	O8CIR9	O8cIr9 mus musculu
71	295.5	7.5	441	13	O804X2	O804x2 fugu rubrip
72	295	7.5	425	13	O804X7	O804x7 gallus gall
73	293	7.4	430	13	O804X0	O804x0 fugu rubrip
74	291.5	7.4	516	4	O9B0Y9	O9b0Y9 homo sapien
75	291	7.4	475	13	O804W9	O804w9 fugu rubrip
76	284	7.2	974	13	O90WMD	O90wM8 buteo japoni
77	283.5	7.2	482	11	O63207	O63207 rattus norv
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79	282	7.1	469	6	O9GMD9	O9gmd9 ornithorhyn
80	282	7.1	1466	13	O7Z241	O7z241 brachydanio
81	281	7.1	481	11	O99L32	O99l32 mus musculu
82	281	7.1	481	11	O8B947	O8b947 mus musculu
83	280.5	7.1	269	4	O81WMO	O81wM0 homo sapien
84	280	7.1	562	4	O86YK8	O86yK8 homo sapien
85	278	7.0	408	5	O9VW19	O9vw19 drosophiila
86	278	7.0	433	13	O804X5	O804x5 gallus gall
87	276.5	7.0	679	4	O96P08	O96p08 homo sapien
88	276	7.0	481	11	O54740	O54740 mus musculu
89	274.5	7.0	3501	4	O7Z407	O7z407 homo sapien

90	273.5	6.9	443	13	Q8H9C9	Q8H9C9 brachydanio
91	273.5	6.9	517	11	Q8K0D2	Q8K0D2 mus musculus
92	273	6.9	366	11	Q9OXB5	Q9OXB5 rattus norv
93	273	6.9	560	4	Q14520	Q14520 homo sapien
94	273	6.9	2796	11	Q80T79	Q80T79 mus musculus
95	271	6.9	433	6	Q8M1L0	Q8M1L0 oryctolagus
96	271	6.9	433	6	Q8MHW7	Q8MHW7 oryctolagus
97	269	6.8	643	6	Q97506	Q97506 sus scrofa
98	269	6.8	833	5	Q96442	Q96442 strongyloce
99	267	6.8	339	11	Q9QX91	Q9QX91 rattus norv
100	267	6.8	435	11	Q7SY86	Q7SY86 xenopus lae
101	267	6.8	868	5	Q9Y1V3	Q9Y1V3 polyandroca
102	265.5	6.7	250	5	Q9V514	Q9V514 dirosophila
103	263.5	6.7	263	13	Q7SX97	Q7SX97 brachydanio
104	263	6.7	653	11	Q8VCS4	Q8VCS4 mus musculus
105	262.5	6.7	300	5	Q819P4	Q819P4 aurelia aur
106	262.5	6.7	461	6	Q9SND7	Q9SND7 pan troglod
107	261.5	6.6	284	13	Q8AX08	Q8AX08 xenopus lae
108	260.5	6.6	264	11	Q9EQZ8	Q9EQZ8 rattus norv
109	260.5	6.6	456	11	Q7TT43	Q7TT43 mus musculus
110	259	6.6	474	13	Q8THC8	Q8THC8 brachydanio
111	259	6.6	581	5	Q9XZM7	Q9XZM7 strongyloce
112	258.5	6.6	683	5	Q8MRH5	Q8MRH5 dirosophila
113	258.5	6.6	787	5	Q9VEY6	Q9VEY6 dirosophila
114	258	6.5	263	13	Q9PMQ6	Q9PMQ6 gadus morhu
115	258	6.5	612	13	Q804W7	Q804W7 fugu rubrip
116	257.5	6.5	1004	13	P79953	P79953 xenopus lae
117	256.5	6.5	264	11	Q9D7P8	Q9D7P8 mus musculus
118	256.5	6.5	264	11	Q9ER05	Q9ER05 mus musculus
119	255.5	6.5	763	7	Q31430	Q31430 lampetra ja
120	255	6.5	325	5	O15944	O15944 sarcophaga
121	254.5	6.5	315	11	Q7TT44	Q7TT44 mus musculus
122	254.5	6.5	461	6	Q9SND6	Q9SND6 pan troglod
123	254	6.4	314	4	Q9VR15	Q9VR15 dirosophila
124	253.5	6.4	487	4	Q9N2P8	Q9N2P8 homo sapien
125	253.5	6.4	1468	4	Q9VER6	Q9VER6 dirosophila
126	253.5	6.4	1048	4	Q96PZ7	Q96PZ7 homo sapien
127	253	6.4	471	13	Q804X6	Q804X6 gallus gall
128	253	6.4	616	6	Q97507	Q97507 sus scrofa
129	253	6.4	1070	5	P91972	P91972 aplysia cal
130	251	6.4	295	11	Q8C1P7	Q8C1P7 rattus norv
131	251	6.4	537	13	Q804W8	Q804W8 fugu rubrip
132	250	6.3	562	6	Q8EQ23	Q8EQ23 sus scrofa
133	250	6.3	1379	5	Q9VAN6	Q9VAN6 dirosophila
134	249.5	6.3	400	5	Q27081	Q27081 tachyleus
135	249	6.3	263	11	Q9CR35	Q9CR35 mus musculus
136	248	6.3	261	13	Q9W7Q4	Q9W7Q4 paratichthy
137	248	6.3	540	13	Q800Y7	Q800Y7 melagris g
138	248	6.3	764	6	Q864W0	Q864W0 pan troglod
139	247.5	6.3	307	11	Q7TML0	Q7TML0 mus musculus
140	247.5	6.3	311	5	Q9W2C2	Q9W2C2 dirosophila
141	247	6.3	235	6	Q28731	Q28731 oryctolagus
142	247	6.3	366	5	Q917V4	Q917V4 dirosophila
143	247	6.3	386	5	Q81924	Q81924 bombix mori
144	246.5	6.2	235	13	Q9O387	Q9O387 cyrops pyrr
145	246.5	6.2	264	11	Q9D960	Q9D960 mus musculus
146	246.5	6.2	297	11	Q88781	Q88781 rattus rati
147	246.5	6.2	323	4	Q96Q64	Q96Q64 homo sapien
148	246.5	6.2	622	4	Q7Z7P3	Q7Z7P3 homo sapien
149	246	6.2	263	11	Q9D8X8	Q9D8X8 mus musculus
150	246	6.2	764	6	Q864V9	Q864V9 gorilla gor
151	245.5	6.2	265	13	Q804G1	Q804G1 brachydanio
152	245.5	6.2	467	5	Q967X8	Q967X8 panulirus a
153	245	6.2	638	11	Q8R0P5	Q8R0P5 mus musculus
154	244.5	6.2	608	13	Q9PTW7	Q9PTW7 struthio ca
155	244	6.2	263	11	Q9DC86	Q9DC86 mus musculus
156	244	6.2	322	11	Q920S2	Q920S2 mus musculus
157	243.5	6.2	285	11	Q8CG42	Q8CG42 rattus norv
158	243.5	6.2	435	5	Q9VFZ7	Q9VFZ7 pongo pygma
159	243	6.2	764	6	Q864W1	Q864W1 mus musculus
160	243	6.2	282	11	Q9D413	Q9D413 fugu rubrip
161	243	6.1	442	13	Q804X1	Q804X1 oryctolagus
162	242.5	6.1	564	6	Q8MKB1	Q8MKB1 oryctolagus
163	242.5	6.1	574	5	Q86RL8	Q86RL8 liyanasea o
164	242.5	6.1	691	13	O57658	O57658 gallus gall
165	242.5	6.1	1019	13	O57382	O57382 xenopus lae
166	241.5	6.1	279	11	Q9NMS4	Q9NMS4 mus musculus
167	241.5	6.1	416	4	Q86T26	Q86T26 homo sapien
168	241	6.1	1415	6	Q8MJ16	Q8MJ16 bos taurus
169	240.5	6.1	238	13	Q8W7Q6	Q8W7Q6 paratichthy
170	240.5	6.1	422	4	Q8MVC1	Q8MVC1 homo sapien
171	240	6.1	242	13	Q92099	Q92099 paratichthe
172	240	6.1	1059	4	Q7Z411	Q7Z411 homo sapien
173	239.5	6.1	240	13	Q98TH0	Q98TH0 engraulis j
174	239.5	6.1	926	14	Q9UQ00	Q9UQ00 homo sapien
175	239.5	6.1	1015	4	Q9Y6L7	Q9Y6L7 homo sapien
176	239.5	6.1	3567	11	Q9SE77	Q9SE77 mus musculus
177	239	6.1	977	13	Q91925	Q91925 xenopus lae
178	238.5	6.0	268	5	Q66151	Q66151 pacifastacu
179	238.5	6.0	946	4	Q96Q03	Q96Q03 homo sapien
180	238	6.0	435	5	Q9NFX2	Q9NFX2 anopheles g
181	238	6.0	767	13	Q9DGR2	Q9DGR2 xenopus lae
182	237.5	6.0	735	13	O57381	O57381 xenopus lae
183	237	6.0	237	13	Q91515	Q91515 fugu rubrip
184	236.5	6.0	761	11	Q93YC8	Q93YC8 rattus norv
185	236.5	6.0	1013	11	Q62381	Q62381 mus musculus
186	235.5	6.0	260	13	Q9W7Q3	Q9W7Q3 paratichthy
187	235.5	6.0	453	11	Q812A6	Q812A6 mus musculus
188	235	6.0	345	6	Q28800	Q28800 pan troglod
189	235	6.0	524	13	Q7SXH8	Q7SXH8 brachydanio
190	235	6.0	812	11	Q9R0W3	Q9R0W3 rattus norv
191	234.5	5.9	395	4	Q9BZW1	Q9BZW1 homo sapien
192	234.5	5.9	624	11	Q9D4T3	Q9D4T3 mus musculus
193	234	5.9	575	5	O81R88	O81R88 dirosophila
194	233.5	5.9	267	13	Q7SZ51	Q7SZ51 brachydanio
195	233.5	5.9	420	13	Q90504	Q90504 eplatretus
196	233	5.9	273	6	Q9XSM1	Q9XSM1 ovis aries
197	233	5.9	445	11	Q8CJ17	Q8CJ17 rattus norv
198	232.5	5.9	483	5	Q8TRX4	Q8TRX4 crassostrea
199	232.5	5.9	1013	4	Q9NQG4	Q9NQG4 homo sapien
200	232.5	5.9	1033	4	Q43897	Q43897 homo sapien
201	231.5	5.9	270	13	Q91039	Q91039 gadus morhu
202	231.5	5.9	371	11	O8CJ16	O8CJ16 rattus norv
203	231.5	5.9	483	5	Q8TRX4	O8TRX4 dirosophila
204	231.5	5.9	483	5	Q9VK10	Q9VK10 dirosophila
205	231.5	5.9	624	6	Q95ME7	Q95ME7 oryctolagus
206	231	5.9	242	13	Q93266	Q93266 pseudopleur
207	231	5.9	1008	11	Q9DER7	Q9DER7 gallus gall
208	231	5.9	1012	11	Q9WM6	Q9WM6 mus musculus
209	230	5.8	244	13	O8QGW3	O8QGW3 anguilla ja
210	230	5.8	265	5	Q9VVT3	Q9VVT3 dirosophila
211	230	5.8	372	5	Q9Y1K6	Q9Y1K6 anopheles g
212	230	5.8	607	13	Q91001	Q91001 gallus gall
213	229.5	5.8	374	5	Q9VU02	Q9VU02 dirosophila
214	229.5	5.8	624	11	Q91Y47	Q91Y47 mus musculus
215	229	5.8	267	5	Q9BK47	Q9BK47 liddia foli
216	229	5.8	274	11	Q924N9	Q924N9 mus musculus
217	229	5.8	733	5	Q9VTX9	Q9VTX9 dirosophila
218	229	5.8	845	13	Q9DCR1	Q9DCR1 xenopus lae
219	228.5	5.8	347	11	Q63927	Q63927 mus sp. hap
220	228.5	5.8	600	5	O17490	O17490 anopheles g
221	228.5	5.8	1084	5	Q9BP40	Q9BP40 halocynthia
222	228.5	5.8	2516	11	Q7TQ52	Q7TQ52 mus musculus
223	228.5	5.8	2526	11	Q7TQ51	Q7TQ51 mus musculus
224	228.5	5.8	2531	11	Q8K428	Q8K428 mus musculus
225	228.5	5.8	2531	11	Q7TQ50	Q7TQ50 mus musculus
226	228	5.8	3687	5	Q9WJ32	Q9WJ32 dirosophila
227	227.5	5.8	235	13	Q91004	Q91004 gecko gecko
228	227.5	5.8	349	6	Q28802	Q28802 pan troglod
229	227.5	5.8	385	4	Q92659	Q92659 homo sapien
230	227	5.8	263	13	Q7S954	Q7S954 xenopus lae
231	227	5.8	275	6	Q7Y562	Q7Y562 equus cabal
232	227	5.8	336	11	O80YD8	O80YD8 mus musculus
233	227	5.8	417	11	O8BZ10	O8BZ10 mus musculus
234	227	5.8	488	5	Q9TYH4	Q9TYH4 echisocoma
235	227	5.8	1464	5	Q23995	Q23995 dirosophila

236	227	5.8	1464	5	Q9VC47	Q9VC47 drosophila	309	215	5.4	116	11	Q7RP05	Q7RP05 rattus norv
237	227	5.8	1464	5	Q24132	Q24132 drosophila	310	214.5	5.4	195	5	Q819P3	Q819P3 aurelia aur
238	226.5	5.7	257	11	Q8B204	Q8B204 mus musculus	311	214.5	5.4	366	11	Q70170	Q70170 mus musculus
239	226.5	5.7	371	5	Q8MS52	Q8MS52 drosophila	312	214.5	5.4	505	5	Q966V4	Q966V4 halocynthia
240	226.5	5.7	855	4	Q72410	Q72410 homo sapien	313	214.5	5.4	1322	5	Q9NAT0	Q9NAT0 anopheles g
241	226.5	5.7	405	4	Q96E86	Q96E86 homo sapien	314	214	5.4	810	4	Q15146	Q15146 homo sapien
242	225.5	5.7	418	5	Q8SZK2	Q8SZK2 drosophila	315	213.5	5.4	241	13	Q98TG9	Q98TG9 engraulis j
243	225.5	5.7	429	5	Q9VAB7	Q9VAB7 drosophila	316	213.5	5.4	248	5	Q9V0T8	Q9V0T8 drosophila
244	225.5	5.7	438	5	Q8AVB0	Q8AVB0 brachydanto	317	213.5	5.4	423	11	Q8BM10	Q8BM10 mus musculus
245	225.5	5.7	328	11	Q80Z40	Q80Z40 rattus norv	318	213.5	5.4	2352	5	Q61240	Q61240 halocynthia
246	225	5.7	387	5	Q9XV57	Q9XV57 ctenocephal	319	213	5.4	355	5	Q9NFU1	Q9NFU1 anopheles g
247	225	5.7	455	11	Q8CDR0	Q8CDR0 mus musculus	320	213	5.4	394	5	P91817	P91817 tachyples
248	225	5.7	490	11	Q920X3	Q920X3 rattus norv	321	213	5.4	615	4	Q81Z25	Q81Z25 homo sapien
249	225	5.7	490	11	Q7TN04	Q7TN04 mus musculus	322	212.5	5.4	327	4	Q8N171	Q8N171 homo sapien
250	224.5	5.7	246	11	Q8B301	Q8B301 mus musculus	323	212.5	5.4	339	11	Q99L44	Q99L44 mus musculus
251	224.5	5.7	251	11	Q54854	Q54854 rattus norv	324	212.5	5.4	778	5	Q9V519	Q9V519 drosophila
252	224.5	5.7	143	11	Q91Y82	Q91Y82 mus musculus	325	212	5.4	340	11	Q8BVT6	Q8BVT6 mus musculus
253	224.5	5.7	127	11	Q91Y82	Q91Y82 mus musculus	326	212	5.4	1322	5	Q9NUS5	Q9NUS5 anopheles g
254	224	5.7	222	13	Q8AV11	Q8AV11 oncorhynch	327	211	5.3	237	6	Q29464	Q29464 bos taurus
255	224	5.7	242	13	Q7TIR8	Q7TIR8 pangasius h	328	211	5.3	2447	13	Q13149	Q13149 fugu rubrip
256	224	5.7	248	5	Q16126	Q16126 bolitaeon vl	329	210.5	5.3	360	5	Q9M1X6	Q9M1X6 drosophila
257	224	5.7	174	5	Q9VTR4	Q9VTR4 drosophila	330	210.5	5.3	505	4	Q8N963	Q8N963 homo sapien
258	223.5	5.7	234	13	Q90244	Q90244 acipenser c	331	210.5	5.3	754	6	Q28290	Q28290 canis faml
259	223.5	5.7	266	13	Q9W7Q0	Q9W7Q0 parailichth	332	209.5	5.3	313	5	Q81N51	Q81N51 drosophila
260	223.5	5.7	159	5	Q9V513	Q9V513 drosophila	333	209.5	5.3	321	4	Q96RZ8	Q96RZ8 homo sapien
261	223.5	5.7	1674	5	Q8SY35	Q8SY35 drosophila	334	209.5	5.3	1441	4	Q723G3	Q723G3 homo sapien
262	223.5	5.7	422	13	Q9W7Q7	Q9W7Q7 parailichth	335	209	5.3	384	13	Q9W630	Q9W630 cyprinus ca
263	222.5	5.6	411	5	Q9VUP0	Q9VUP0 drosophila	336	208.5	5.3	236	5	Q9YTH3	Q9YTH3 schistosoma
264	222	5.6	267	5	Q9V940	Q9V940 drosophila	337	208.5	5.3	258	6	Q28B03	Q28B03 pan troglod
265	222	5.6	273	11	Q921N4	Q921N4 mus musculus	338	208.5	5.3	279	11	Q7TNX3	Q7TNX3 mus musculus
266	222	5.6	275	4	Q86TM8	Q86TM8 homo sapien	339	208.5	5.3	311	11	Q80XZ3	Q80XZ3 rattus norv
267	222	5.6	276	4	Q86UM5	Q86UM5 homo sapien	340	208.5	5.3	417	11	Q80VD1	Q80VD1 mus musculus
268	221.5	5.6	271	13	Q803Z4	Q803Z4 brachydanto	341	208.5	5.3	417	11	Q8VHK8	Q8VHK8 mus musculus
269	221.5	5.6	3620	6	Q9TUS3	Q9TUS3 canis faml	342	208.5	5.3	444	5	Q9V4M6	Q9V4M6 mus musculus
270	221	5.6	258	5	Q97J39	Q97J39 phaeton coc	343	208.5	5.3	471	11	Q8CPR0	Q8CPR0 mus musculus
271	221	5.6	974	5	P91658	P91658 drosophila	344	208	5.3	256	5	Q25082	Q25082 heliothis z
272	220.5	5.6	242	11	Q80V54	Q80V54 mus musculus	345	208	5.3	271	6	Q8H1J2	Q8H1J2 bos taurus
273	220.5	5.6	250	11	Q8CGM5	Q8CGM5 mus musculus	346	208	5.3	275	4	Q81XD7	Q81XD7 homo sapien
274	220.5	5.6	277	11	Q80CM7	Q80CM7 mus musculus	347	208	5.3	558	4	Q86YX4	Q86YX4 homo sapien
275	220.5	5.6	360	5	Q17489	Q17489 anopheles g	348	207.5	5.3	195	4	Q8U006	Q8U006 homo sapien
276	220.5	5.6	408	5	Q9UDG3	Q9UDG3 pacifastacu	349	207.5	5.3	233	13	Q91218	Q91218 oncorhynch
277	220.5	5.6	488	5	Q7YU36	Q7YU36 drosophila	350	207.5	5.3	266	13	Q20277	Q20277 gadus morhu
278	220	5.6	260	13	Q9W7P9	Q9W7P9 parailichth	351	207.5	5.3	1282	5	Q9NH06	Q9NH06 heliothis z
279	220	5.6	261	5	Q962G7	Q962G7 culx pipie	352	207.5	5.3	298	4	Q8TER0	Q8TER0 homo sapien
280	220	5.6	331	11	Q8B1A6	Q8B1A6 mus musculus	353	207	5.2	240	13	Q7SY08	Q7SY08 mus musculus
281	220	5.6	331	11	Q80X17	Q80X17 mus musculus	354	206.5	5.2	269	4	Q96C0V5	Q96C0V5 homo sapien
282	219.5	5.6	255	5	Q7S2T1	Q7S2T1 xenopus lae	355	206.5	5.2	269	5	Q9Y929	Q9Y929 drosophila
283	219.5	5.6	318	11	Q80UR4	Q80UR4 galleria me	356	206.5	5.2	284	4	Q27824	Q27824 uca pugilic
284	219	5.6	365	5	Q97366	Q97366 mus musculus	357	206.5	5.2	284	4	Q8NFM6	Q8NFM6 homo sapien
285	219	5.5	374	5	Q81862	Q81862 holotrichia	358	206.5	5.2	467	4	Q86WX2	Q86WX2 homo sapien
286	218.5	5.5	375	5	Q817W8	Q817W8 dermacentor	359	206.5	5.2	573	5	Q9V516	Q9V516 drosophila
287	218.5	5.5	1007	13	Q8U128	Q8U128 xenopus lae	360	206	5.2	1065	11	Q810H2	Q810H2 mus musculus
288	218	5.5	242	13	Q7SX90	Q7SX90 brachydanto	361	206	5.2	293	5	Q9NB92	Q9NB92 agrotis ips
289	218	5.5	271	2	Q54213	Q54213 streptomyc	362	206	5.2	492	5	Q72155	Q72155 chironomus
290	218	5.5	275	4	Q96R26	Q96R26 homo sapien	363	205.5	5.2	316	11	Q8BZ30	Q8BZ30 mus musculus
291	217	5.5	597	11	Q35727	Q35727 mus musculus	364	205.5	5.2	416	11	Q8BZ13	Q8BZ13 mus musculus
292	217	5.5	277	5	Q96899	Q96899 scolopendra	365	205	5.2	264	5	Q02569	Q02569 culx quinq
293	216.5	5.5	346	6	Q28801	Q28801 pan troglod	366	205	5.2	492	4	Q96T73	Q96T73 homo sapien
294	216.5	5.5	2528	13	Q8AXP0	Q8AXP0 cynops pyrr	367	205	5.2	814	5	Q810G6	Q810G6 drosophila
295	216.5	5.5	255	11	Q7NTI0	Q7NTI0 mus musculus	368	205	5.2	216	11	Q9Q0X3	Q9Q0X3 rattus norv
296	216.5	5.5	269	11	Q9D7E9	Q9D7E9 mus musculus	369	204.5	5.2	247	11	Q9DPN7	Q9DPN7 mus musculus
297	216	5.5	269	11	Q9C052	Q9C052 mus musculus	370	204.5	5.2	247	11	Q9CPN9	Q9CPN9 mus musculus
298	216	5.5	269	11	Q9C052	Q9C052 mus musculus	371	204.5	5.2	281	5	Q46137	Q46137 lumbricus r
299	215.5	5.5	243	5	Q9TXD8	Q9TXD8 agelenopsis	372	204.5	5.2	367	11	Q70169	Q70169 mus musculus
300	215.5	5.5	254	11	Q8CGR4	Q8CGR4 mus musculus	373	204.5	5.2	449	5	Q9SRA3	Q9SRA3 drosophila
301	215.5	5.5	326	11	Q80X38	Q80X38 mus musculus	374	204.5	5.2	510	4	Q9H4V1	Q9H4V1 homo sapien
302	215.5	5.5	326	11	Q9D9M0	Q9D9M0 mus musculus	375	204.5	5.2	752	6	Q8SQV5	Q8SQV5 pongo pygma
303	215.5	5.5	256	5	Q25081	Q25081 hypodermis 1	376	204.5	5.2	1497	4	Q8NBT9	Q8NBT9 homo sapien
304	215	5.4	609	13	Q9PVX7	Q9PVX7 xenopus lae	377	204	5.2	367	11	Q9QXD2	Q9QXD2 mus musculus
305	215	5.4	609	11	Q80YC5	Q80YC5 mus musculus	378	204	5.2	417	11	Q8VHU4	Q8VHU4 rattus norv
306	215	5.4	749	13	Q9YGE8	Q9YGE8 oncorhynch	379	203.5	5.2	195	4	Q81XB4	Q81XB4 homo sapien
307	215	5.4	760	13	Q8UG08	Q8UG08 tetraodon n	380	203.5	5.2	261	4	Q725F3	Q725F3 homo sapien
308	215	5.4					381	203.5	5.2				



382	203.5	5.2	309	5	Q27083	Q27083 tachyleus	455	195.5	5.0	752	6	Q8S074	Q8eq74 pan troglod
383	203.5	5.2	335	11	Q8VIF2	Q8vif2 mus musculu	456	195	4.9	262	5	Q7Z0G3	Q7z0g3 phlebotomus
384	203.5	5.2	664	13	Q8IAT6	Q8iat6 brachydanio	457	195	4.9	276	4	Q9BRJ3	Q9brj3 homo sapien
385	203.5	5.2	750	13	Q9W633	Q9w633 cyprinus ca	458	194.5	4.9	246	11	Q9ROT7	Q9rot7 mus musculu
386	203.5	5.2	1232	4	Q7Z387	Q7z387 homo sapien	459	194.5	4.9	261	4	Q7Z5F4	Q7z5f4 homo sapien
387	203.5	5.2	1323	11	Q9J986	Q9j986 rattus norv	460	194.5	4.9	283	5	Q9S5V2	Q9s5v2 lumbricue b
388	203.5	5.2	3623	4	Q6O494	Q6o494 homo sapien	461	194.5	4.9	1374	5	Q9VSU0	Q9vsu0 drosophila
389	203	5.1	177	11	Q9OX66	Q9ox66 rattus norv	462	194.5	4.9	1449	5	Q9U1I2	Q9u1i2 drosophila
390	203	5.1	185	11	Q9OX88	Q9ox88 rattus norv	463	194.5	4.9	1450	5	Q8IOQ8	Q8ioq8 drosophila
391	203	5.1	185	11	Q9OX88	Q9ox88 rattus norv	464	194.5	4.9	1462	5	Q9B1I3	Q9b1i3 drosophila
392	203	5.1	186	11	Q9OX88	Q9ox88 rattus norv	465	194.5	4.9	2382	5	Q9B1I3	Q9b1i3 drosophila
393	203	5.1	370	5	Q9VA44	Q9va44 drosophila	466	194.5	4.9	2409	5	Q9B0G6	Q9b0g6 drosophila
394	203	5.1	403	16	Q9XS06	Q9xs06 vibrio chol	467	194.5	4.9	2428	5	Q8I6X6	Q8i6x6 boophilus m
395	203	5.1	537	4	Q9BYE1	Q9bye1 homo sapien	468	194.5	4.9	2786	5	Q9VSU2	Q9vsu2 drosophila
396	203	5.1	581	4	Q9BYE2	Q9bye2 homo sapien	469	194	4.9	245	13	Q42160	Q42160 petromyzon
397	203	5.1	833	13	Q9YIC5	Q9yic5 cyprinus ca	470	194	4.9	253	5	Q9VAG3	Q9vag3 drosophila
398	202.5	5.1	239	4	Q8N1C9	Q8n1c9 homo sapien	471	194	4.9	514	4	Q9FPZ3	Q9fpz3 homo sapien
399	202.5	5.1	274	5	Q16133	Q16133 anopheles s	472	194	4.9	556	13	Q8Q3D5	Q8q3d5 brachydanio
400	202.5	5.1	372	5	Q9W2C8	Q9w2c8 drosophila	473	194	4.9	806	6	Q18783	Q18783 macropus eu
401	202	5.1	190	11	Q9QXDS	Q9qxd5 mus musculu	474	193.5	4.9	246	11	Q9OUK9	Q9ouk9 mus musculu
402	202	5.1	488	13	Q8IUV8	Q8iuv8 homo sapien	475	193.5	4.9	247	13	Q9W7O5	Q9w7o5 paralicthy
403	202	5.1	743	13	Q9YGE7	Q9yge7 oncorhynch	476	193.5	4.9	256	5	Q27540	Q27540 drosophila
404	201.5	5.1	195	4	Q8J008	Q8j008 homo sapien	477	193.5	4.9	267	5	Q9V5X7	Q9v5x7 drosophila
405	201.5	5.1	195	4	Q8J007	Q8j007 homo sapien	478	193.5	4.9	317	13	Q9DGR3	Q9dgr3 xenopus lae
406	201.5	5.1	320	13	Q7T0X2	Q7t0x2 xenopus lae	479	193.5	4.9	790	4	Q8IYD1	Q8iyd1 homo sapien
407	201	5.1	247	13	Q42608	Q42608 petromyzon	480	193.5	4.9	830	4	Q8T3A0	Q8t3a0 clona infes
408	201	5.1	260	4	Q8IM69	Q8im69 homo sapien	481	193.5	4.9	1089	5	Q867B0	Q867b0 canis famli
409	201	5.1	351	5	Q8I6K0	Q8i6k0 holotrichia	482	193	4.9	258	6	Q867B0	Q867b0 canis famli
410	201	5.1	392	5	Q9VMZ3	Q9vmz3 drosophila	483	193	4.9	268	5	Q9X1S6	Q9x1s6 ctenocephal
411	200.5	5.1	175	4	Q9UMV3	Q9umv3 homo sapien	484	193	4.9	269	6	Q9SKW7	Q9skw7 bos taurus
412	200.5	5.1	249	13	Q9W7Q1	Q9w7q1 paralicthy	485	193	4.9	423	13	Q57433	Q57433 figu rubrip
413	200.5	5.1	358	13	Q57434	Q57434 figu rubrip	486	193	4.9	481	4	Q9H284	Q9h284 homo sapien
414	200.5	5.1	451	5	Q9UKZ9	Q9ukz9 homo sapien	487	193	4.9	962	11	Q8CA20	Q8ca20 mus musculu
415	200.5	5.1	951	5	Q20176	Q20176 caenorhabdi	488	192.5	4.9	178	13	Q93594	Q93594 dicentrarch
416	200	5.1	247	13	Q42158	Q42158 petromyzon	489	192.5	4.9	232	5	Q94508	Q94508 dermatopnag
417	200	5.1	504	6	Q46506	Q46506 papio hamad	490	192.5	4.9	246	11	Q9Z1R9	Q9z1r9 mus musculu
418	199.5	5.1	545	5	Q9VFM0	Q9vfm0 drosophila	491	192.5	4.9	247	4	Q8NHM4	Q8nhm4 homo sapien
419	199.5	5.1	223	5	Q9VBY4	Q9vby4 drosophila	492	192.5	4.9	249	11	Q9OYN4	Q9oyn4 drosophila
420	199.5	5.1	258	6	Q28508	Q28508 macaca mula	493	192.5	4.9	276	11	Q9OYN3	Q9oyn3 m hippocaa
421	199.5	5.1	348	4	Q8KMS5	Q8kms5 homo sapien	494	192.5	4.9	381	5	Q8MOY4	Q8moy4 drosophila
422	199.5	5.1	378	13	Q9OWP0	Q9owp0 trachemys s	495	192.5	4.9	438	4	Q8H804	Q8h804 homo sapien
423	199.5	5.1	1193	13	Q20819	Q20819 gallus gall	496	192.5	4.9	754	13	F79816	F79816 oryzias lat
424	199.5	5.1	1175	11	Q99PM0	Q99pm0 rattus norv	497	192	4.9	244	13	Q42159	Q42159 petromyzon
425	199.5	5.1	253	5	Q25253	Q25253 lucilia cup	498	192	4.9	246	5	Q9B1I7	Q9b1i7 lumbricue r
426	199	5.0	263	5	Q6Z562	Q6z562 penaeus van	499	192	4.9	254	5	Q9XYX0	Q9xyx0 rhyzopercha
427	199	5.0	264	13	Q8QGF6	Q8qgf6 xenopus lae	500	192	4.9	380	5	Q9YIK5	Q9yik5 anopheles g
428	199	5.0	441	5	Q9XXV0	Q9xxv0 bombyx mori	501	192	4.9	383	5	Q77102	Q77102 manduca rex
429	198.5	5.0	181	4	Q9IUL7	Q9iul7 homo sapien	502	191.5	4.9	247	5	Q77039	Q77039 anopheles g
430	198.5	5.0	237	5	Q17035	Q17035 anopheles g	503	191.5	4.9	281	5	Q76898	Q76898 drosophila
431	198.5	5.0	260	13	Q7SZC3	Q7szc3 gallus gall	504	191.5	4.9	284	5	Q8IRX5	Q8irx5 drosophila
432	198.5	5.0	279	11	Q9QZ74	Q9qz74 rattus norv	505	191.5	4.9	360	5	Q8SX54	Q8sx54 drosophila
433	198.5	5.0	364	5	Q9NAN9	Q9nan9 anopheles g	506	191.5	4.9	385	5	Q8SX54	Q8sx54 drosophila
434	198.5	5.0	388	5	Q44330	Q44330 manduca sex	507	191.5	4.9	579	4	Q96DQ9	Q96dq9 homo sapien
435	198.5	5.0	461	5	Q8T4N2	Q8t4n2 rhipicephal	508	191.5	4.9	713	11	Q80TF0	Q80tf0 mus musculu
436	198.5	5.0	752	6	Q863A0	Q863a0 xenopus lae	509	191.5	4.9	2468	13	Q8MOE4	Q8moe4 brachydanio
437	198.5	5.0	1214	13	Q90YD2	Q90ydz xenopus lae	510	191.5	4.9	3396	5	Q9VM55	Q9vm55 drosophila
438	197.5	5.0	255	4	Q96R00	Q96rg0 homo sapien	511	191	4.8	255	5	Q25227	Q25227 lucilia cup
439	197.5	5.0	258	6	Q28805	Q28805 pan troglod	512	191	4.8	256	5	Q818B5	Q818b5 ochlerotatu
440	197	5.0	222	11	Q91WZ0	Q91wz0 rattus norv	513	191	4.8	277	5	Q810J0	Q810j0 drosophila
441	197	5.0	236	4	Q9H4V7	Q9h4v7 homo sapien	514	191	4.8	317	11	Q8K4D1	Q8k4d1 mus musculu
442	197	5.0	261	5	Q9VXC7	Q9vxc7 drosophila	515	191	4.8	317	11	Q8K4I7	Q8k4i7 mus musculu
443	197	5.0	421	5	Q9SR86	Q9s8r6 drosophila	516	191	4.8	415	5	Q9GRW0	Q9grw0 holotrichia
444	197	5.0	585	5	Q9U0E2	Q9u0e2 ciribolium c	517	191	4.8	646	6	Q29097	Q29097 sus scrofa
445	197	5.0	745	13	Q91701	Q91701 xenopus lae	518	190.5	4.8	579	4	Q818B3	Q818b3 aedes polyn
446	197	5.0	760	11	Q70350	Q70350 mus musculu	519	190.5	4.8	579	4	Q9BY79	Q9by79 homo sapien
447	196.5	5.0	219	13	Q91036	Q91036 gadus morhu	520	190.5	4.8	762	13	Q9YIC6	Q9yic6 cyprinus ca
448	196.5	5.0	259	5	Q8IRB0	Q8irb0 drosophila	521	190	4.8	243	4	Q86VU5	Q86v55 homo sapien
449	196.5	5.0	298	5	Q8T4N4	Q8t4n4 rhipicephal	522	190	4.8	253	4	Q8WZB4	Q8wzb4 homo sapien
450	196	5.0	400	5	Q9GRG2	Q9grg2 tenebrio mo	523	190	4.8	277	6	Q8SQ44	Q8sq44 sus scrofa
451	196	5.0	3623	11	Q70244	Q70244 rattus norv	524	190	4.8	282	5	Q25395	Q25395 lumbricue r
452	195.5	5.0	267	5	Q9GP27	Q9gp27 drosophila	525	190	4.8	334	6	Q46507	Q46507 papio hamad
453	195.5	5.0	274	5	Q17086	Q17086 anopheles s	526	190	4.8	378	5	Q8S5Y0	Q8s5y0 drosophila
454	195.5	5.0	276	5	Q18443	Q18443 helicoverpa	527	190	4.8	414	11	Q8R4W6	Q8r4w6 mus musculu

528	189.5	4.8	241	11	Q92135	Q92135 rattus norv	601	182.5	4.6	257	5	Q81883	Q81883 aedes albop
529	189.5	4.8	255	3	Q9Y7A9	Q9Y7A9 metarhizium	602	182.5	4.6	274	5	Q9Y8S7	Q9Y8S7 drosophila
530	189.5	4.8	257	5	Q27440	Q27440 aedes aegypt	603	182.5	4.6	295	5	Q9N6C6	Q9N6C6 heliothis z
531	189.5	4.8	258	6	Q28804	Q28804 pan troglod	604	182.5	4.6	297	5	Q86M89	Q86M89 spodoptera
532	189.5	4.8	263	5	Q9Y116	Q9Y116 penaeus van	605	182.5	4.6	310	11	Q9QY29	Q9QY29 mus musculu
533	189.5	4.8	263	5	Q02570	Q02570 culicx quing	606	182.5	4.6	327	5	Q8MS77	Q8MS77 drosophila
534	189.5	4.8	266	5	Q27761	Q27761 penaeus van	607	182.5	4.6	371	5	Q8MRX3	Q8MRX3 drosophila
535	189.5	4.8	271	5	Q9VRS6	Q9VRS6 drosophila	608	182.5	4.6	482	6	Q28982	Q28982 sus scrofa
536	189.5	4.8	281	5	Q8YB55	Q8YB55 drosophila	609	182.5	4.6	520	5	Q81NG0	Q81NG0 drosophila
537	189.5	4.8	381	5	Q9V866	Q9V866 drosophila	610	182.5	4.6	1551	5	Q9NGV4	Q9NGV4 drosophila
538	189.5	4.8	385	13	Q90MS2	Q90MS2 elaphie sp.	611	182.5	4.6	2531	5	Q16004	Q16004 lytechinus
539	189.5	4.8	470	5	Q8T3A1	Q8T3A1 cioma intes	612	182	4.6	240	5	Q96C00	Q96C00 biophalari
540	189.5	4.8	572	11	Q8B1K6	Q8B1K6 mus musculu	613	182	4.6	241	5	Q917L2	Q917L2 drosophila
541	189.5	4.8	649	6	Q28657	Q28657 oryctolagus	614	182	4.6	254	5	Q18434	Q18434 heliocoverpa
542	189.5	4.8	1737	4	Q75097	Q75097 homo sapien	615	182	4.6	280	5	Q9V5X8	Q9V5X8 drosophila
543	189.5	4.8	2386	4	Q727M0	Q727M0 homo sapien	616	182	4.6	391	5	Q9V3Z2	Q9V3Z2 drosophila
544	189	4.8	181	5	Q9GSM5	Q9GSM5 chrysomya b	617	182	4.6	836	13	Q8AM87	Q8AM87 cymops pyrr
545	189	4.8	245	5	Q9BL18	Q9BL18 lumbricus r	618	181.5	4.6	284	5	Q96089	Q96089 haemaphysal
546	189	4.8	246	11	Q7TT42	Q7TT42 mus musculu	619	181.5	4.6	295	5	Q9NH07	Q9NH07 heliothis z
547	189	4.8	414	11	Q9CX06	Q9CX06 mus musculu	620	181.5	4.6	450	13	Q7SY99	Q7SY99 xenopus lae
548	189	4.8	758	11	Q8C1P8	Q8C1P8 paratithode	621	181.5	4.6	487	13	Q7ZMR8	Q7ZMR8 xenopus lae
549	188.5	4.8	382	13	Q90MT4	Q90MT4 crocodylus	622	181.5	4.6	754	13	Q98U16	Q98U16 cyprinus ca
550	188.5	4.8	713	5	Q962M9	Q962M9 podocoryne	623	181	4.6	254	5	Q18436	Q18436 heliocoverpa
551	188	4.8	235	4	Q8N4E0	Q8N4E0 homo sapien	624	181	4.6	254	5	Q76934	Q76934 lacnobia o
552	188	4.8	253	4	Q8N5N9	Q8N5N9 homo sapien	625	181	4.6	255	13	Q34289	Q34289 salvelinus
553	188	4.8	266	5	Q8MR10	Q8MR10 paratithode	626	181	4.6	270	5	Q819P2	Q819P2 aplysina fl
554	188	4.8	271	5	Q18487	Q18487 penaeus van	627	181	4.6	405	5	Q8MQS8	Q8MQS8 apis mellif
555	188	4.8	276	5	Q9VXP8	Q9VXP8 drosophila	628	181	4.6	412	13	Q7SYT3	Q7SYT3 xenopus lae
556	187.5	4.8	250	5	Q17036	Q17036 anopheles g	629	181	4.6	840	4	Q9VUD7	Q9VUD7 drosophila
557	187.5	4.8	251	4	Q8N2U3	Q8N2U3 homo sapien	630	181	4.6	840	4	Q9UD45	Q9UD45 homo sapien
558	187.5	4.8	257	5	Q9N849	Q9N849 aedes aegypt	631	180.5	4.6	1229	5	Q9EMB0	Q9EMB0 caenorhabd1
559	187.5	4.8	283	5	Q25394	Q25394 lumbricus r	632	180.5	4.6	264	5	Q62561	Q62561 penaeus van
560	187.5	4.8	283	5	Q81TU7	Q81TU7 lumbricus r	633	180.5	4.6	266	5	Q81916	Q81916 blomla trop
561	187.5	4.8	1216	13	Q90Y55	Q90Y55 brachydantio	634	180.5	4.6	293	4	Q725A4	Q725A4 homo sapien
562	187	4.7	256	5	Q18439	Q18439 heliocoverpa	635	180.5	4.6	390	5	Q8MP08	Q8MP08 bombyx mori
563	187	4.7	261	6	Q29474	Q29474 canis famli	636	180.5	4.6	520	5	Q8S193	Q8S193 drosophila
564	187	4.7	261	6	Q25510	Q25510 manduca sex	637	180.5	4.6	717	13	P70006	Q9N076 xenopus lae
565	186.5	4.7	235	5	Q9GTX7	Q9GTX7 aedes albop	638	180	4.6	203	5	Q9N877	Q9N877 heliothis z
566	186.5	4.7	250	13	Q93265	Q93265 pseudopleur	639	180	4.6	234	11	Q9CV76	Q9CV76 mus musculu
567	186.5	4.7	257	5	Q81BE2	Q81BE2 aedes trise	640	180	4.6	254	3	Q01136	Q01136 metarhizium
568	186.5	4.7	287	5	Q9VWY2	Q9VWY2 drosophila	641	180	4.6	256	3	Q9Y842	Q9Y842 drosophila
569	186.5	4.7	397	5	Q9W314	Q9W314 drosophila	642	180	4.6	511	5	Q9VZM5	Q9VZM5 drosophila
570	186	4.7	181	5	Q9G5N1	Q9G5N1 chrysomya b	643	180	4.6	546	5	Q8SXG6	Q8SXG6 drosophila
571	186	4.7	249	13	Q92046	Q92046 disosotichu	644	179.5	4.6	354	5	Q9U611	Q9U611 drosophila
572	186	4.7	449	6	Q9VDU8	Q9VDU8 oryctolagus	645	179.5	4.6	581	5	Q96015	Q96015 drosophila
573	185	4.7	1594	6	Q95218	Q95218 oryctolagus	646	179.5	4.6	728	13	Q90656	Q90656 gallus gall
574	185.5	4.7	211	4	Q8U009	Q8U009 homo sapien	647	179.5	4.6	1047	5	Q9VZH2	Q9VZH2 drosophila
575	185.5	4.7	256	5	Q9XYS1	Q9XYS1 ctenocephal	648	179.5	4.6	1047	5	Q9VZH2	Q9VZH2 drosophila
576	185.5	4.7	292	5	Q18438	Q18438 heliocoverpa	649	179	4.5	270	5	Q8WR11	Q8WR11 paratithode
577	185.5	4.7	310	11	Q91XC4	Q91XC4 mus musculu	650	179	4.5	282	5	Q18655	Q18655 plodia inte
578	185.5	4.7	439	11	Q8BHM9	Q8BHM9 mus musculu	651	179	4.5	384	5	Q9XY63	Q9XY63 drosophila
579	185.5	4.7	1254	13	Q90YU2	Q90YU2 brachydantio	652	179	4.5	440	5	Q8MRF6	Q8MRF6 drosophila
580	185.5	4.7	1254	13	Q90YU5	Q90YU5 brachydantio	653	179	4.5	606	11	P70412	P70412 mus musculu
581	185	4.7	287	5	Q9NH10	Q9NH10 agrotis ips	654	179	4.5	675	13	Q9M6U8	Q9M6U8 disosotichu
582	185	4.7	508	16	Q8DA23	Q8DA23 vibrio vuln	655	179	4.5	905	13	Q8U0L4	Q8U0L4 gallus gall
583	185	4.7	709	13	Q7ZTN9	Q7ZTN9 xenopus lae	656	179	4.5	919	13	Q8UVR0	Q8UVR0 gallus gall
584	184.5	4.7	295	5	Q18445	Q18445 heliocoverpa	657	179	4.5	936	13	Q8UVC9	Q8UVC9 gallus gall
585	184.5	4.7	295	5	Q18450	Q18450 heliocoverpa	658	179	4.5	2898	5	Q9VLT6	Q9VLT6 drosophila
586	184.5	4.7	427	11	Q8BQH6	Q8BQH6 mus musculu	659	178.5	4.5	292	13	Q7S206	Q7S206 xenopus lae
587	184	4.7	246	5	Q817P0	Q817P0 lumbricus b	660	178.5	4.5	300	5	Q9NH08	Q9NH08 agrotis ips
588	184	4.7	381	11	Q7TP23	Q7TP23 rattus norv	661	178.5	4.5	300	5	Q9NVCJ8	Q9NVCJ8 drosophila
589	184	4.7	405	5	Q8S260	Q8S260 drosophila	662	178.5	4.5	400	5	Q09020	Q09020 rattus norv
590	184	4.7	745	13	Q90WF9	Q90WF9 triakiia ecy	663	178	4.5	212	11	Q09020	Q09020 rattus norv
591	184	4.7	988	4	Q81WY4	Q81WY4 homo sapien	664	178	4.5	256	5	Q18599	Q18599 drosophila
592	183.5	4.7	247	11	Q9C9N7	Q9C9N7 mus musculu	665	178	4.5	289	5	Q8MR67	Q8MR67 drosophila
593	183.5	4.7	257	5	Q86P18	Q86P18 aedes aegypt	666	178	4.5	290	5	Q9VRT2	Q9VRT2 drosophila
594	183.5	4.7	329	13	Q42272	Q42272 xenopus lae	667	178	4.5	434	5	Q9V7S7	Q9V7S7 drosophila
595	183.5	4.7	1372	6	P91526	P91526 caenorthabdt	668	178	4.5	996	4	Q8TD25	Q8TD25 homo sapien
596	183	4.6	257	6	Q19023	Q19023 macaca mula	669	177.5	4.5	1212	13	Q42347	Q42347 gallus gall
597	183	4.6	267	6	Q720B3	Q720B3 stomoxys ca	670	177.5	4.5	261	3	Q00344	Q00344 cochliobolu
598	183	4.6	267	6	Q9MZ26	Q9MZ26 macaca fasc	671	177.5	4.5	267	5	Q9VLP5	Q9VLP5 drosophila
599	183	4.6	272	5	Q9V5X6	Q9V5X6 drosophila	672	177.5	4.5	2524	5	Q9GP45	Q9GP45 branchiostoc
600	183	4.6	752	13	Q42374	Q42374 brachydantio	673	177	4.5	233	4	Q96R27	Q96R27 homo sapien

674	177	4.5	258	5	Q9WSU8	Q9WSU8 drosophila
675	177	4.5	328	11	Q9BUB6	Q9BUB6 mus musculus
676	177	4.5	385	5	Q2S101	Q2S101 herdamia m
677	177	4.5	425	5	Q9W1Q9	Q9W1Q9 drosophila
678	177	4.5	737	13	Q90422	Q90422 brachydanio
679	177	4.5	747	13	Q91900	Q91900 xenopus lae
680	176.5	4.5	267	5	Q9VRU0	Q9VRU0 drosophila
681	176.5	4.5	413	13	Q7S25	Q7S25 brachydanio
682	176.5	4.5	716	13	Q91691	Q91691 xenopus lae
683	176.5	4.5	926	11	Q9Q2Y7	Q9Q2Y7 mus musculus
684	176	4.5	243	13	Q8AV83	Q8AV83 brachydanio
685	176	4.5	260	5	Q8T4P5	Q8T4P5 leopobthel
686	176	4.5	270	4	Q96QL8	Q96QL8 homo sapien
687	176	4.5	389	5	Q9V517	Q9V517 drosophila
688	176	4.5	575	5	Q22328	Q22328 caenorhabdi
689	176	4.5	584	11	Q8K480	Q8K480 mus musculus
690	176	4.5	891	5	Q9V338	Q9V338 drosophila
691	175.5	4.4	257	5	Q818B4	Q818B4 ochlerotatu
692	175.5	4.4	272	5	Q9VRS3	Q9VRS3 drosophila
693	175.5	4.4	459	5	Q9V4W7	Q9V4W7 drosophila
694	175.5	4.4	522	5	Q8MQM9	Q8MQM9 drosophila
695	175.5	4.4	617	13	Q8J1S1	Q8J1S1 triakis scy
696	175.5	4.4	677	5	Q9VYC7	Q9VYC7 drosophila
697	175.5	4.4	921	11	Q9QX38	Q9QX38 rattus norv
698	175.5	4.4	1316	4	Q96JU7	Q96JU7 homo sapien
699	175	4.4	260	5	Q8T4P6	Q8T4P6 leopobthel
700	175	4.4	261	5	Q62598	Q62598 plodia inte

## ALIGNMENTS

PRELIMINARY; PRT; 737 AA.

RESULT 1

Q96JW2 ID Q96JW2 PRELIMINARY; PRT; 737 AA.

AC 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Hypothetical protein FLJ14935.

OC Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_Taxid=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shitatori A., Sudo H., Wagaetsuna M., Hosoki T., Kaku Y., Kodaira H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Matenabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto U., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y., Niimiya K., Iwayanagi T.,

RT "NEO human cDNA sequencing project."

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

EMBL AK027841, BAB55404.1, -

GO GO:0004263, F:chymotrypsin activity, IEA.

GO GO:0008233, F:peptidase activity, IEA.

GO GO:0004295, F:trypsin activity, IEA.

GO GO:0006508, P:proteolysis and peptidolysis, IEA.

InterPro: IPR000859, CUB.

InterPro: IPR009003, Cys\_Ser\_tryptin.

InterPro: IPR000742, EGF\_2.

InterPro: IPR006209, EGF-like.

InterPro: IPR006210, IEGF.

InterPro: IPR001254, Peptidase\_S1.

InterPro: IPR001314, Peptidase\_S1A.

InterPro: IPR000436, Sushi\_SCR\_CCP.

Pfam: PF00431, CUB; 1.

Pfam: PF00008, EGF; 1.

DR Pfam: PF00084; sushi; 2.

DR Pfam: PF00089; trypsin; 1.

DR PRINTS; PRO0722; CHYMOTRYPSIN.

DR SMART; SM00032; CCP; 2.

DR SMART; SM00042; CUB; 1.

DR SMART; SM00181; EGF; 2.

DR SMART; SM00020; Tryp\_Spe; 1.

DR PROSITE; PS01180; CUB; 1.

DR PROSITE; PS00022; EGF; 1.

DR PROSITE; PS01186; EGF\_2; 1.

DR PROSITE; PS02440; TRYPSIN\_DOM; 1.

KW Hypothetical protein; EGF-like domain; Hydrolase; Protease;

KW Serine protease.

SEQUENCE 737 AA; 81952 MW; 4F51689C5EB32B44 CAC64;

Query Match 99.4%; Score 3921.5; DB 4; Length 737;

Best Local Similarity 97.6%; Pred. No. 0;

Matches 719; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

QY 1 MELGCTQLGLTFPLQLLISLSPRETYINACPGAEWNIMCECEYDOIECVCPGARE 60

DB 1 MELGCTQLGLTFPLQLLISLSPRETYINACPGAEWNIMCECEYDOIECVCPGARE 60

QY 61 VGYTIPCCRNENECDSCLIPGCTIFENCKSCRNMGGLTDFYKGFYCAECRAAG 120

DB 61 VGYTIPCCRNENECDSCLIPGCTIFENCKSCRNMGGLTDFYKGFYCAECRAAG 120

QY 121 YGDCMRCGQVLRAKQGLLESTPLNACWTHAKGPIQLRFNWLSTLEFDWQCYD 180

DB 121 YGDCMRCGQVLRAKQGLLESTPLNACWTHAKGPIQLRFNWLSTLEFDWQCYD 180

QY 181 YVEVADGNRDGQIIKRVCGNERPAPISISSLHVLPHSDGSKNFDFAHAYEITACS 240

DB 181 YVEVADGNRDGQIIKRVCGNERPAPISISSLHVLPHSDGSKNFDFAHAYEITACS 240

QY 241 SSPCFHDTGCVLDKAGSYKCACLAGYTGRCENT-----LEERNCSDP 283

DB 241 SSPCFHDTGCVLDKAGSYKCACLAGYTGRCENTLEAGSKYIKASEDELSTVLEERNCSDP 300

QY 284 GPPNVGYKTIQGPGLINGRAKIGTVVSPFCNNSYVLSGNEKTPCOQNGMSGKOPICI 343

DB 301 GPPNVGYKTIQGPGLINGRAKIGTVVSPFCNNSYVLSGNEKTPCOQNGMSGKOPICI 360

QY 344 KACREPKISDLVRRLVPMQVSRETPLHQVYSAFQKQASAPTKKPAIPFGDLPNGY 403

DB 361 KACREPKISDLVRRLVPMQVSRETPLHQVYSAFQKQASAPTKKPAIPFGDLPNGY 420

QY 404 QHLHTQLQYECISPPYRRLSSRRCTLTGKWSGAPSCIPICGKIENITAPKTOGLRMP 463

DB 421 QHLHTQLQYECISPPYRRLSSRRCTLTGKWSGAPSCIPICGKIENITAPKTOGLRMP 480

QY 464 WQALVRRFTSGVHSGSLHKGMFLVCSGALVNERVVVAACVTDLGVTMKTADLVV 523

DB 481 WQALVRRFTSGVHSGSLHKGMFLVCSGALVNERVVVAACVTDLGVTMKTADLVV 540

QY 524 LKGFRRDDRDDEKTIQSLSAIIHPYDPIILDADIAIKLADKARISTRVOPICLAA 583

DB 541 LKGFRRDDRDDEKTIQSLSAIIHPYDPIILDADIAIKLADKARISTRVOPICLAA 600

QY 584 SRDLSTSGQESHITVAGNNVLADVASPFGKNDTLRSQVSVYVDSLLCEQHEHDGIPSV 643

DB 601 SRDLSTSGQESHITVAGNNVLADVASPFGKNDTLRSQVSVYVDSLLCEQHEHDGIPSV 660

QY 644 TDNMFCASEPAPSDICTAETGGLAASFGPARSPERPMILMGLVSVSYKTCSHRLST 703

DB 661 TDNMFCASEPAPSDICTAETGGLAASFGPARSPERPMILMGLVSVSYKTCSHRLST 720

QY 704 AFTKVLPPKDWIERNMK 720

DB 721 AFTKVLPPKDWIERNMK 737

RESULT 2

Q8K2B8  
ID O8K2B8 PRELIMINARY; PRT; 720 AA.  
AC O8K2B8;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Similar to DKFZP586H2123 protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN  
RP  
SEQUENCE FROM N.A.  
RA Strauberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
DR EMBL; BC031841; AAH31841.1; -  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR009003; Cys\_ser\_trypsin.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR001254; IEGF.  
DR InterPro; IPR001314; Peptidase\_S1.  
DR InterPro; IPR000436; Sush1\_SCR\_CCP.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00084; Sush1; 2.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00032; CCP; 2.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00181; EGF; 2.  
DR SMART; SM00020; TRYP\_SPC; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR EGF-like domain; Hydrolase; Protease; Serine protease.  
KW EGF-like domain; Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 720 AA; 80377 MW; 717287F1E69FDD8 CRC64;  
Query Match 91.6%; Score 3612; DB 11; Length 720;  
Best Local Similarity 90.1%; Pred. No. 0;  
Matches 649; Conservative 33; Mismatches 38; Indels 0; Gaps 0;  
QY 1 MELGCTQLGLTFQQLLLISLPREYVINEACPGAMNIMCECEYDQIECVCPGKRE 60  
DB 1 MELDRMQLGLVIFQQLLLISLPREYVINEACPGAMNIMCECEYDQIECVCPGKRE 60  
QY 61 VGGYTIICCRNEENECSCLIHPGCTI FENCKSCRNCSWGGLTDDFYKGFYCAECGAG 120  
DB 61 VGGYTIICCRNEENECSCLIHPGCTI FENCKSCRNCSWGGLTDDFYKGFYCAECGAG 120  
QY 121 YGGGCMACCGVLRAPKQIILLESYPLNAHCWTHARPGVIOURFMLSLEPYMCOYD 180  
DB 121 YGGGCMACCGVLRAPKQIILLESYPLNAHCWTHARPGVIOURFMLSLEPYMCOYD 180  
QY 181 YVEVRDGDNDGQIIRKVCNGNERAPFIOSSIGSLAHVLFHSDGSGNFQGFHAYEIRFACS 240  
DB 181 YVEVRDGDNDGQIIRKVCNGNERAPFIOSSIGSLAHVLFHSDGSGNFQGFHAYEIRFACS 240  
QY 241 SSPCFHDTGTVLDVAGSYKCACTAGYTGORCENILLEERNCSGPGPVNGYOKITGFGLI 300  
DB 241 SSPCFHDTGTVLDVAGSYKCACTAGYTGORCENILLEERNCSGPGPVNGYOKITGFGLI 300  
QY 301 NGRAXKIGTVVSPFNNSYVLSGNEKRTCOONGEMSGKOPICIKACREPKISDVRBRVL 360  
DB 301 NGRAXKIGTVVSPFNNSYVLSGNEKRTCOONGEMSGKOPICIKACREPKISDVRBRVL 360

QY 361 PMQVQSRFETPLHQLISAAFSKQKLGAPTKKRALPPGDI PMGYQHHTLOLYECISPFYR 420  
DB 361 SMQVQSRFETPLHQLISAAFSKQKLGAPTKKRALPPGDI PMGYQHHTLOLYECISPFYR 420  
QY 421 RIGSSRRTCLRTKSGRASPSCIPICGKIENITAPTOGLRMPWQAAYIRRTSGVYDGS 480  
DB 421 RIGSSRRTCLRTKSGRASPSCIPICGKIENITAPTOGLRMPWQAAYIRRTSGVYDGS 480  
QY 481 HKGAMFLVCSGLVNERTVVAACHCTVDGKVTMIKTADLKVLGKPYRDDDEKTIQS 540  
DB 481 HKGAMFLVCSGLVNERTVVAACHCTVDGKVTMIKTADLKVLGKPYRDDDEKTIQS 540  
QY 541 LQISAIILHPNDPIILDDADIALKLDKARISTRVQPICLAASRLSTSFQSHITVAG 600  
DB 541 LQISAIILHPNDPIILDDADIALKLDKARISTRVQPICLAASRLSTSFQSHITVAG 600  
QY 601 KVVVLADVRSPGPNQDLRSGVSVYDSSLCEQHEHGGIPVSTVDMPFCSMPPTAPSDI 660  
DB 601 KVVVLADVRSPGPNQDLRSGVSVYDSSLCEQHEHGGIPVSTVDMPFCSMPPTAPSDI 660  
QY 661 CTAETGGIAVSPGRASPEPRMHLMLGLVSWSYDKTCSHRLSTAFKVLPEFKDMIRNNK 720  
DB 661 CTAETGGIAVSPGRASPEPRMHLMLGLVSWSYDKTCSHRLSTAFKVLPEFKDMIRNNK 720

## RESULT 3

O8BU25  
ID O8BU25 PRELIMINARY; PRT; 720 AA.  
AC O8BU25;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical EGF-like domain.  
GN E430002G05SRK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN  
RP  
SEQUENCE FROM N.A.  
RA STRAIN=NOD; TISSUE=Thymus;  
RX MEDLINE=22354683; PubMed=12466851;  
RA THE RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs."  
RT MATURE 420-563-573(2002).  
RL EMBL; AK088017; BAC40098.1; -  
DR MGD; MGI:2445082; E430002G05SRK.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR009003; Cys\_ser\_trypsin.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR001254; IEGF.  
DR InterPro; IPR001314; Peptidase\_S1.  
DR InterPro; IPR000436; Sush1\_SCR\_CCP.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00084; Sush1; 2.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00032; CCP; 2.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00181; EGF; 2.  
DR SMART; SM00179; EGF\_Ca; 1.  
DR SMART; SM00020; TRYP\_SPC; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS00022; EGF\_1; 1.

DR PROSITE: PS01186; EGF\_2; 1.  
 DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
 DR Hypothetical protein.  
 KW Hypothetical protein.  
 SQ SEQUENCE 720 AA; 80300 MW; C098E076D903A5A0 CRC64;

Query Match 91.6%; Score 3612; DB 11; Length 720;  
 Best Local Similarity 90.1%; Pred. No. 0;  
 Matches 649; Conservative 33; Mismatches 38; Indels 0; Gaps 0;

1 MEAGCWTQGLTFLQLLISLPREYTVNKAQPGAEWIMRECEQYDQICVPGKRE 60  
 1 MELDRMAQGLVFLQLLISLPREYTVNKAQPGAEWIMRECEQYDQICVPGKRE 60  
 61 VVGYTIPCCRNENECDSCLIHPGCTIFENCKSCRNNGWGLTDPFYVGYCAECRAW 120  
 61 VVGYTIPCCRNENECDSCLIHPGCTIFENCKSCRNNGWGLTDPFYVGYCAECRAW 120  
 61 VVGYTIPCCRNENECDSCLIHPGCTIFENCKSCRNNGWGLTDPFYVGYCAECRAW 120  
 121 YGGDCRCGQVYRAPGQILLESYPLNACWNTIHAKEPVYQLAFWMLSEFDYMCQYD 180  
 121 YGGDCRCGQVYRAPGQILLESYPLNACWNTIHAKEPVYQLAFWMLSEFDYMCQYD 180  
 121 YGGDCRCGQVYRAPGQILLESYPLNACWNTIHAKEPVYQLAFWMLSEFDYMCQYD 180  
 181 YVEVDGDRDQGIIRKVCGERPAPIOIGSSLHVLFFSDSKKIPDGFHAYEETIACS 240  
 181 YVEVDGDRDQGIIRKVCGERPAPIOIGSSLHVLFFSDSKKIPDGFHAYEETIACS 240  
 181 YVEVDGDRDQGIIRKVCGERPAPIOIGSSLHVLFFSDSKKIPDGFHAYEETIACS 240  
 241 SSPCFHDGTCLVLDKAGSYKACLAGYTGRCENLLEERNCSDPGPPVNGYOKITGAPGLI 300  
 241 SSPCFHDGTCLVLDKAGSYKACLAGYTGRCENLLEERNCSDPGPPVNGYOKITGAPGLI 300  
 241 SSPCFHDGTCLVLDKAGSYKACLAGYTGRCENLLEERNCSDPGPPVNGYOKITGAPGLI 300  
 301 NGRBAKIGVVSFFCNSVYLSGNEKRTQONENSGKQPCITAKCREKISDLYRRRLV 360  
 301 NGRBAKIGVVSFFCNSVYLSGNEKRTQONENSGKQPCITAKCREKISDLYRRRLV 360  
 301 NGRBAKIGVVSFFCNSVYLSGNEKRTQONENSGKQPCITAKCREKISDLYRRRLV 360  
 361 PMOVOSRETPQLQVLSAFAKOKLAGAPTKKAPALPFGDLPMGQYHATLOQYECISPFYR 420  
 361 PMOVOSRETPQLQVLSAFAKOKLAGAPTKKAPALPFGDLPMGQYHATLOQYECISPFYR 420  
 361 PMOVOSRETPQLQVLSAFAKOKLAGAPTKKAPALPFGDLPMGQYHATLOQYECISPFYR 420  
 421 RLGSRRRTCLRTGKSGRAPSCIPICGKIENITAPKTOGLRMPWQAAIYRRTSGVHDSGL 480  
 421 RLGSRRRTCLRTGKSGRAPSCIPICGKIENITAPKTOGLRMPWQAAIYRRTSGVHDSGL 480  
 421 RLGSRRRTCLRTGKSGRAPSCIPICGKIENITAPKTOGLRMPWQAAIYRRTSGVHDSGL 480  
 481 HKGAWFLVSSGALVNERTVVAACHCTDYGKTMITADLKLVLLGKPYDDDRDEKTIOS 540  
 481 HKGAWFLVSSGALVNERTVVAACHCTDYGKTMITADLKLVLLGKPYDDDRDEKTIOS 540  
 481 HKGAWFLVSSGALVNERTVVAACHCTDYGKTMITADLKLVLLGKPYDDDRDEKTIOS 540  
 541 LQISATILHPNDPILLDADIALIKLIDKARISTRVQPICLAASRDLSFQESHITVAG 600  
 541 LQISATILHPNDPILLDADIALIKLIDKARISTRVQPICLAASRDLSFQESHITVAG 600  
 541 LQISATILHPNDPILLDADIALIKLIDKARISTRVQPICLAASRDLSFQESHITVAG 600  
 541 LQISATILHPNDPILLDADIALIKLIDKARISTRVQPICLAASRDLSFQESHITVAG 600  
 601 NNVLADVRSPPGKNDTLRSVSVVDSLLCEQHEDHGI PVSVDNMFCAWEPAPSIDI 660  
 601 NNVLADVRSPPGKNDTLRSVSVVDSLLCEQHEDHGI PVSVDNMFCAWEPAPSIDI 660  
 601 NNVLADVRSPPGKNDTLRSVSVVDSLLCEQHEDHGI PVSVDNMFCAWEPAPSIDI 660  
 601 NNVLADVRSPPGKNDTLRSVSVVDSLLCEQHEDHGI PVSVDNMFCAWEPAPSIDI 660  
 661 CTAETGGIAAIVSPGRASPEPRWHLGLVSWSYDKTCSHRLSTAFYKVLFPKMIERNM 720  
 661 CTAETGGIAAIVSPGRASPEPRWHLGLVSWSYDKTCSHRLSTAFYKVLFPKMIERNM 720  
 661 CTAETGGIAAIVSPGRASPEPRWHLGLVSWSYDKTCSHRLSTAFYKVLFPKMIERNM 720  
 661 CTAETGGIAAIVSPGRASPEPRWHLGLVSWSYDKTCSHRLSTAFYKVLFPKMIERNM 720

RESULT 4  
 ID Q9Y432 PRELIMINARY; PRT; 181 AA.

AC Q9Y432; PRELIMINARY; PRT; 181 AA.  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN DKFZP586H2123.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC Tissue-Uterus;  
 RA Anorga W., Winkler U., Mewes H.W., Gassenhuber J., Wiemann S.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL050214; CAB43317.1; -.  
 DR PIR: T08805; T08805.  
 DR HSSP: P00742; IHCG.
 DR MEROPS: S01.998; -.
 DR GO: GO:0008233; F:peptidase activity; IEA.
 DR GO: GO:0004295; F:trypsin activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR009003; Cys Ser trypsin.
 DR InterPro: IPR001254; peptidase\_S1.
 DR Pfam: PF00089; trypsin\_1.
 DR SMART: SM00020; Tryp\_Spc; 1.
 DR PROSITE: PS50240; TRYPSIN\_DOM; 1.
 KW Hypothetical protein; Hydrolase; Protease; Serine protease.
 FT NON TER 1  
 SQ SEQUENCE 181 AA; 19962 MW; ABC793BB682D439 CRC64;

Query Match 24.1%; Score 949; DB 4; Length 181;  
 Best Local Similarity 99.4%; Pred. No. 3,5e-80;  
 Matches 180; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

540 SLQISATILHPNDPILLDADIALIKLIDKARISTRVQPICLAASRDLSFQESHITVA 599  
 1 SLRISATILHPNDPILLDADIALIKLIDKARISTRVQPICLAASRDLSFQESHITVA 60  
 600 GNNVLADVRSPPGKNDTLRSVSVVDSLLCEQHEDHGI PVSVDNMFCAWEPAPSIDI 659  
 61 GNNVLADVRSPPGKNDTLRSVSVVDSLLCEQHEDHGI PVSVDNMFCAWEPAPSIDI 120  
 61 GNNVLADVRSPPGKNDTLRSVSVVDSLLCEQHEDHGI PVSVDNMFCAWEPAPSIDI 120  
 61 GNNVLADVRSPPGKNDTLRSVSVVDSLLCEQHEDHGI PVSVDNMFCAWEPAPSIDI 120  
 660 ICTAETGGIAAIVSPGRASPEPRWHLGLVSWSYDKTCSHRLSTAFYKVLFPKMIERNM 719  
 121 ICTAETGGIAAIVSPGRASPEPRWHLGLVSWSYDKTCSHRLSTAFYKVLFPKMIERNM 180  
 720 K 720  
 181 K 181

RESULT 5

ID Q8T9S1 PRELIMINARY; PRT; 1019 AA.

AC Q8T9S1; PRELIMINARY; PRT; 1019 AA.  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Factor C precursor.  
 OS Tachypneus tridentatus (Japanese horseshoe crab).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;  
 OC Limulidae; Tachypneus.  
 OX NCBI\_TaxID=6653;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=21955715; PubMed=11958140;  
 RA Wang D., Liu J., Chen L., Wang L., Yang G., Wu X., Zhang W.;  
 RL "Cloning and Expression of Tachypneus tridentatus Factor C";  
 RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 34:77-82 (2002).  
 DR EMBL: AF467804; AAL75577.1; -.  
 DR HSSP: P00761; JAN1.  
 DR GO: GO:0004265; F:chymotrypsin activity; IEA.  
 DR GO: GO:0008233; F:peptidase activity; IEA.  
 DR GO: GO:0005229; F:sugar binding; IEA.  
 DR GO: GO:0004295; F:trypsin activity; IEA.  
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro: IPR009003; Cys Ser trypsin.  
 DR InterPro: IPR006209; BGF-like.  
 DR InterPro: IPR006210; IBGF.  
 DR InterPro: IPR003006; 19\_MHC.  
 DR InterPro: IPR004043; LCC1\_dom.  
 DR InterPro: IPR001304; Lectin C.  
 DR InterPro: IPR001254; peptidase\_S1.  
 DR InterPro: IPR001314; peptidase\_S1A.

DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
 DR Pfam; PF03815; LCCU; 1.  
 DR Pfam; PF00059; Lectin\_C; 1.  
 DR Pfam; PF00084; Sushi\_5.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00032; CCP; 5.  
 DR SMART; SM00034; CLECT; 1.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00603; LCCU; 1.  
 DR SMART; SM00020; tryp\_spc; 1.  
 DR PROSITE; PS50041; C-TYPE\_LECTIN\_2; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR PROSITE; PS50820; LCCU; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR Hydrolase; Protease; Serine protease; Signal.  
 PT SIGNAL 1 25 POTENTIAL.  
 FT CHAIN 26 1019 FACTOR C.  
 SQ SEQUENCE 1019 AA; 112248 MW; B8E51730A559593 CRC64;

Query Match 17.2%; Score 678; DB 5; Length 1019;  
 Best Local Similarity 25.6%; Pred. No. 8,1e-54;  
 Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;

QY 34 PGAWNMIM---CRECCYDIF--CYCPKREVVGTITCCNENECSCILHIGCT 86  
 DB 184 PNGWMSSEPPKICRECAKVSPEHGKVTAPSGNMIEGATL-----RFSCHS-----PHYLT 233  
 QY 87 IFENCKSCR-NGSGKGLT----- 103  
 DB 234 IGGITLTGSGNGSGGQIPCKKLVFCDDLPVNAHEHGVKIGVCKGQPGQTEVYTT 293  
 QY 104 --DDPYKGFYCAECR--AGNYG--DCMR-----CGQVLR--APKG 137  
 DB 294 CSGNYFLMGFTLCKNLDSWSGSPSCVVAADREVDCSKAVDFLDVGEFVHICPAG 353  
 QY 138 QILLES-----YPLNAHEMTIHA---KPGFV-----Q 163  
 DB 354 CSLTAGVTGTAIYHELSVCRAAHAGKLPNSGGAHVNNNGPDSFLSGDLIKSEE 413  
 QY 164 LRFVWLSLEPYM-----CQDYVEVAD-----GDRDGOITIKVCGN--ERRAP 206  
 DB 414 LKSLARSRFPYVSSSTAGSGCDGMEVEVENCVVYTSKRAERAGVCTMAALAV 473  
 QY 207 IQS--IGSSLHLVLFHSDG-SKNPFGF-----AIYEITACSSPCF 245  
 DB 474 LDKDVIPBSLLEALRGKGLTTWTLGHLDAEKPFVWELMDRSVVVINDNLTFWASGEPG 533  
 QY 246 HDGTCV-LDKAGS---YKCACLAGYTCQRENLEERN---CSDPGPNVGYKTIQGP 297  
 DB 534 NETNCVYLDIRDLOQPVWKTKSCFOPSSFAQMDLSDNNKAKCDPSSLGHAHTLHGQS 593  
 QY 298 GLINGRAKTIQVAFPCNNNSVYLSGNEKRTCCQNGSGEKOPICIK--ACREPKISDLV 355  
 DB 594 --IDGFYA--GSSIRYSCVLAHYLSGTETVCTTNGTMSAKPRCIVKTCQNPVSYG 649  
 QY 356 RRRVLPVMOVSGREPLHOLYSAAPSOKLOQ--SAPYKPLPFGD-----LP 400  
 DB 650 SVEIKP--PRTMTSISRVGSPFLRLPLPLRLAARAPPKPRSSQPSYVDLASKVLP 706  
 QY 401 MGVOHLHTOLOYECISPFYRLGSSRRCTCLATGMSGAPSCITCKIENITAP----- 455  
 DB 707 EGHRTVSGRAIYTESRYELLSQGRCDNSNGMSGPACIVCGSDSPRSPFWNG 766  
 QY 456 -KTGELMPWQAAIYRRTSGVHDSLHGAMFLVCSGALVNERTVVAHAACVTDLGHVTM 514  
 DB 767 NSTEIGMPWQAGISRWLA-----DHNMFLLCGGSLNEKVIYVAHAACVTVSATAEI 819  
 QY 515 IKTADLVKVLGKFRDDDRDEKTIQSLQISAIILHPNYDPLLDADIAIKLDAKARIST 574

DB 820 IDPSQFIYLGKYYRDSRDDYQVREALEIHVNNENYDNGNINFDIALIQLKTPVTLTT 879  
 QY 575 RVQPICLAASRDISTFQESH-----TYAGNNVLADVRSPFGKNDTLRSGVSVVDSL 628  
 DB 880 RVQPICLPT--DIT--REHLEGLAVTNG---LNNNTYSEMTQOAVLPVVAAS 930  
 QY 629 LCEEHEDHGIPIVVDNMFCAWEPASDICTAETGGINAVSPGRASPEPRMLMGL 688  
 DB 931 TCEGKREKDLPLVTEHMFCAQYK-KGRYDACSQSGG--PLVPADDSRTERRWLEGI 987  
 QY 689 VSWSYDTCGH-RLSTAFYKVLDPFKQWIER 717  
 DB 988 VSWSGSPGCGKANQYGFYKVNFLSMIRQ 1017

RESULT 6  
 Q26423  
 ID Q26423 PRELIMINARY; PRT; 1083 AA.

AC Q26423; 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Factor C.  
 GN FACTOR C.  
 OS Carthoscorpius rotundicauda (Southeast Asian horseshoe crab).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;  
 OC Limulidae; Carthoscorpius.  
 OX NCBI\_TaxId=6848;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95268506; PubMed=7536401;  
 RA Ding J.L., Navas M.A.3rd, Ho B.;  
 RT "Molecular cloning and sequence analysis of factor C cDNA from the  
 RL Singapore horseshoe crab, Carthoscorpius rotundicauda.";  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 DR EMBL; S77064; AAB34362.1; -.  
 DR HSP; P00763; IDPO.

DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0005529; F:sugar binding; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR009003; Cys Ser trypsin.  
 DR InterPro; IPR006209; EGF\_like.

DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR004043; LCCU\_dom.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR000436; Sushi\_SCR\_CCP.

DR Pfam; PF03815; LCCU; 1.  
 DR Pfam; PF00059; Lectin\_C; 1.  
 DR Pfam; PF00084; Sushi; 5.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00032; CCP; 5.  
 DR SMART; SM00034; CLECT; 1.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00603; LCCU; 1.  
 DR SMART; SM00020; tryp\_spc; 1.

DR PROSITE; PS50041; C-TYPE\_LECTIN\_2; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR PROSITE; PS50820; LCCU; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolase; Protease; Serine protease.

SEQUENCE 1083 AA; 120228 MW; C82CC45A5C9FCB7 CRC64;

Query Match 16.9%; Score 665; DB 5; Length 1083;



Best Local Similarity 25.4%; Pred. No. 1.5e-52;  
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

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QY 34 PGAEINIMRECEYQIEVCCEKRE-----VGYTIPCCNNEECDSCLIH 82
DB 248 PNGQWSNFPKICR-----SCAMVSPENKVNALSGDMLEGATL-----RPSCDG----- 293
QY 83 PGCTIENKCKSR-NGSWGTL----- 103
DB 294 FYLLIGETLTCQNGQNGQIPQCKNLVFCEDLDEVNNAHKVKIGVEQKYGQPPQGT 353
QY 104 -----DFFVKGFCACR--AGWYG--DCMR-----CGQVLR-- 133
DB 354 VVYTGSGNFMFGFDLTKCNPDGSGGSPSCYKVAADREVDGSKAVDFLDVGEVRLH 413
QY 134 ARKQQLLES-----YPLNACWTHA-----KPGVVI----- 162
DB 414 CPAGCSLTAGTWTGTAIYHLSVCRPAALHAGKLPNSGGAHVNNNGPYSDFLGSDLNGI 473
QY 163 -----QLRFVWLSLEFDY-----CQDYVEVRD-----GDNRDQIIRKVCN--E 202
DB 474 KSEELKSLARSPFDVSSSTAGKSGCPDGMFEVDENCYVTSKQAMERAGVCTNMAA 533
QY 203 RPAPIQS--IGSLHVLHSDG-SKNFDGF-----AIYEITACSS 241
DB 534 RLAVLDKDVLPNSLTETLKGGLTTWIGLHRLDAEKPTWELMDRSNVVLDNLTWMS 593
QY 242 SCCHFDGTCL-----DKAGS--YKACIAGTGORCNLEERN--CSPGPGVNGYQKI 293
DB 594 GEPGETNCVVDIDIQQLQSVKTKSCFOPSPBACMMDDSDRKAACDDPGSLENGHATL 653
QY 294 TSGPGLINGRAKIGTVSPFCNNSVLSGNEKRTQONGEMSGKOPICK--ACREPKI 351
DB 654 HGOSS--IDGFYA--GSSIRYCEVLAHLEGTETVCTTNGTMSAPRRCIKYITCONPV 709
QY 352 SOLVRRRLVPMOVQSEETPLHOLYSAF8KQKIQ--SAPTKKPALPGD----- 398
DB 710 PSYGVVIEKP--PSRTNISRYGSPFLRLPLRLPLABAKPPKPRSSQSTVDLASK 766
QY 399 --LPMQYOLHLOQYECTSPFYRLGSSRRCTLRGKSKSGAPGICPICGKINENTAP- 455
DB 767 VKLPBEGHYVVGSAIYTCESRYELLGSGRCDSNGNSGSPASTIPVCGSDSPRSF 826
QY 456 -----KTQGLRFPWQAIYRTSGVHDGSLHKGAWFLVSGALVNERTVVAHCVTDLG 510
DB 827 INNGNSTELGQWPMQGISRWLA-----DINMWLQCGSLINKEKIVTAAHCVTYSA 879
QY 511 KVTMIKTADLVKVLGKFRDDDEKTIQSLQISALIIHPNYDPILLADIALKLIDKA 570
DB 880 TAEIIPNOFKVYLGKYRDDSDDDYQVREALIHNVPNYPDGNLFDIALIQKTFV 939
QY 571 RSTRVOPICLASRPLSTSPQESH-----TVAGMNLAVRSRFGKNDLRSGVSV 624
DB 940 TLTTRQOPICLPT--DIT--REHKEGTLAVVWGM--LNENNYSETTIOQAVLPV 990
QY 625 VDSLCEQEDHGLPVSTYDNMFCAWEPAPSDICTAETGIAAASPAGASPEPRWA 684
DB 991 VAASTEEBYKADLPLVTBNMFCAGYK-KGRYDSCGSDSG--PLVYADDSRTERRNV 1047
QY 685 LMGVWSYDKTCSH-RLSTAFTKVLPRKWIET 717
DB 1048 LEGIVSWGSPSGCGKANQYGFVKVAVFWLWIRQ 1081

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RESULT 7

Q868H7 PRELIMINARY; PRT; 680 AA.  
AC Q868H7;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Mannose-binding lectin associated serine protease-1.  
GN MASP-1.

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OS Branchiostoma belcheri (Amphioxus).
OC Euteleostomi; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma
OK NCBI_TaxID=7741;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Notochord;
RX MEDLINE=22593355; PubMed=12707349;
RA Endo Y., Nonaka M., Saiga H., Kakimura Y., Matsushita A., Takahashi M.,
  Matsushita M., Fujita T.;
RT "Origin of Mannose-Binding Lectin-Associated Serine Protease (MASP)-1
  and MASP-3 involved in the Lectin Complement Pathway Traced Back to
  the Invertebrate, Amphioxus."
RL J. Immunol. 170:4701-4707(2003).
DR EMBL: AB089267; BAC75886.1;
DR GO:0005509; F:calcium ion binding; IEA.
DR GO:0004263; F:chymotrypsin activity; IEA.
DR GO:0008233; F:peptidase activity; IEA.
DR GO:0005529; F:sugar binding; IEA.
DR GO:0004295; F:trypsin activity; IEA.
DR GO:0007157; P:heterophilic cell adhesion; IEA.
DR GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR00152; Asx_Hydroxyl_S.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR009003; Cys_Ser_Trypsin.
DR InterPro: IPR006209; EGF_Like.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR001254; peptidase_S1.
DR InterPro: IPR001314; peptidase_S1A.
DR InterPro: IPR000436; Subst_SCR_CCP.
DR Pfam: PF00431; CUB; 2.
DR Pfam: PF00084; subst_1.
DR Pfam: PF00089; trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00032; CCP; 2.
DR SMART: SM00042; CUB; 2.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS01180; CUB; 2.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS02040; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Lectin; Protease.
SQ SEQUENCE 680 AA; 75871 MW; 496985A94A728318 CRC64;

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Query Match

Best Local Similarity 15.4%; Score 608.5; DB 5; Length 680;  
Matches 195; Conservative 92; Mismatches 239; Indels 215; Gaps 35;

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QY 46 CEYDQIECV-----CPGKREV-----VGYT 65
DB 84 CEYDVYKMEBQKLVGLFCGTEDTQTEKVPDGVLESTGQLSEFKSDFSNVRHKGFV 143
QY 66 IPCNENEDSCLIHFGCTIFENKSCGRNGSGTLDYVYKGFYAEGRAG-WYSGD 124
DB 144 VHYRVVDEDC--AVDNGCHFP-----CHN-----YISGYCS-CRAGYMIKD 185
QY 125 ---C-MRGC-OVLAPKQQLLES-----YPLNACWTHAHPGVQLRFVWLSLEFD- 174
DB 186 RETCKFGCGRQVLVQLSTISPEYPRLYPRVLDCKMIGVBPVVTLQF---DDDDV 242
QY 175 ---YMCQDYVEVRDNGDQIIRKVCNERPAPIQSIGSLHVLHSDGSKNFDGF 229
DB 243 EQHBEVSCPYDHLKQAGADEKYG--YCGKTVPTTSTDHKNVYFHSDDSGENKGF 298
QY 230 HAIYEIRACSSPCHFGTCLVDAKSGYKACIAGTYGQNCENLBERNCSGPGPVNG 289
DB 299 RATYFT-----TARPEAL-----SAP----- 315

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QY 290 YOKITGPGILNGHAKIGTVSPFCNNSVYLSGNEKRTCOONGEMSGKOPICIKACREP 349  
DB 316 -----AYGMEGNSFTYSQKVPACBEGYLLDPPHRCVQADSGMSGVQPTC----- 362  
QY 350 KISDLVRRVYLPKQVQRETPPLHOLYSAASKOKLQSAPTKRPALPPGDLPMGYOHLATQ 409  
DB 363 ---ELVNCGPPL-NISNGEIEVDGNFS-----YADIAL----- 391  
QY 410 LQYECISPEFRRLGSSRRTCLRTKMGSRAPSCIPICGKIENITAPKTQGLR-----WP 463  
DB 392 --YRC-QQFYEMAGEGRFCFCEADCKMTGNBSCPTGCKEFYTRGLVGRPRAMGAMP 448  
QY 464 WQALVYRTSGSVHGSJLHKGMFLVCSGALVNERTVVAACVTDLKVMTIKADLKV 523  
DB 449 WMAALHRTPRGP-----FCGGTLGDDWVLTAAHCLVSPVTSPIKDSFSVI 496  
QY 524 LGKF-YRDDREDEKTIQSLQISAILHPNYDPIILDADIALKLDKARISTRVQPICLA 582  
DB 497 LGKHKARDKOTEGTV---QVAQIVHAPAFNFTFLADILKLKESPARLNPYTPICLL 553  
QY 583 ASRDLSTSP---QESHITVAGMNLADVRSPGKNDILRSQVSVVDSLLCEQHEHDGI 639  
DB 554 SEERATATLVGRBAAYT--GWC---HSDGFIANELREVFLPLVDITCNKTYD---- 603  
QY 640 PVSTLDMPCASWEPTAPSDICTAETGGAIVSPFGASPEPRHMLGLVMSYDXTCSH 699  
DB 604 -FTTSDMTCAGFO-EGKDKACRGDSG--PLAFPERTA--EKVQGVVTTMGWG--CGR 655  
QY 700 RLS-TAFTKVLFPKQWIERNM 719  
DB 656 KMKGYVTVNTVIOYLPWIDEM 676

RESULT 8

ID Q068H5 PRELIMINARY; PRT; 680 AA.  
AC Q068H5;  
DT 01-JUN-2003 (Tremblrel. 24, Created)  
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Manose-binding lectin associated serine protease-1.  
GN MASP1/3.  
OS Branchiostoma belcheri (Amphioxus).  
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;  
OC Branchiostoma.  
CX NCBI\_TaxID=7741;  
RN  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22593355; PubMed=12707349;  
RA Endo Y, Nonaka M, Saiga H, Kakimura Y, Matsushita A, Takahashi M, Matsushita M, Fujita T,  
"Origin of Manose-binding Lectin-Associated Serine Protease (MASP)-1 the Invertebrate, Amphioxus."  
RT J. Immunol. 170:4701-4707(2003).  
RL EMBL; AB089507; BAC75888.1;  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0005529; F:sugar binding; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR009003; Cys\_ser\_trypsin.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1.  
DR InterPro; IPR000436; Subtil\_SCR\_CCP.

DR Pfam; PF00431; CUB; 2.  
DR Pfam; PF00084; subtil; 2.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PRO0722; CHYMOTRYPSIN.  
DR SMART; SM00032; CCP; 2.  
DR SMART; SM00042; CUB; 2.  
DR SMART; SM00181; EGF; 1.  
DR SMART; SM00179; EGF\_Ca; 1.  
DR SMART; SM00020; Tryp\_SPC; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS01180; CUB; 2.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS01187; EGF\_Ca; 1.  
DR PROSITE; PS02440; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
DR KEGG; K06840; MASP1; 1.  
DR KEGG; K06841; MASP2; 1.  
DR KEGG; K06842; MASP3; 1.  
DR KEGG; K06843; MASP4; 1.  
DR KEGG; K06844; MASP5; 1.  
DR KEGG; K06845; MASP6; 1.  
DR KEGG; K06846; MASP7; 1.  
DR KEGG; K06847; MASP8; 1.  
DR KEGG; K06848; MASP9; 1.  
DR KEGG; K06849; MASP10; 1.  
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DR KEGG; K06851; MASP12; 1.  
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DR KEGG; K06855; MASP16; 1.  
DR KEGG; K06856; MASP17; 1.  
DR KEGG; K06857; MASP18; 1.  
DR KEGG; K06858; MASP19; 1.  
DR KEGG; K06859; MASP20; 1.  
DR KEGG; K06860; MASP21; 1.  
DR KEGG; K06861; MASP22; 1.  
DR KEGG; K06862; MASP23; 1.  
DR KEGG; K06863; MASP24; 1.  
DR KEGG; K06864; MASP25; 1.  
DR KEGG; K06865; MASP26; 1.  
DR KEGG; K06866; MASP27; 1.  
DR KEGG; K06867; MASP28; 1.  
DR KEGG; K06868; MASP29; 1.  
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DR KEGG; K06870; MASP31; 1.  
DR KEGG; K06871; MASP32; 1.  
DR KEGG; K06872; MASP33; 1.  
DR KEGG; K06873; MASP34; 1.  
DR KEGG; K06874; MASP35; 1.  
DR KEGG; K06875; MASP36; 1.  
DR KEGG; K06876; MASP37; 1.  
DR KEGG; K06877; MASP38; 1.  
DR KEGG; K06878; MASP39; 1.  
DR KEGG; K06879; MASP40; 1.  
DR KEGG; K06880; MASP41; 1.  
DR KEGG; K06881; MASP42; 1.  
DR KEGG; K06882; MASP43; 1.  
DR KEGG; K06883; MASP44; 1.  
DR KEGG; K06884; MASP45; 1.  
DR KEGG; K06885; MASP46; 1.  
DR KEGG; K06886; MASP47; 1.  
DR KEGG; K06887; MASP48; 1.  
DR KEGG; K06888; MASP49; 1.  
DR KEGG; K06889; MASP50; 1.  
DR KEGG; K06890; MASP51; 1.  
DR KEGG; K06891; MASP52; 1.  
DR KEGG; K06892; MASP53; 1.  
DR KEGG; K06893; MASP54; 1.  
DR KEGG; K06894; MASP55; 1.  
DR KEGG; K06895; MASP56; 1.  
DR KEGG; K06896; MASP57; 1.  
DR KEGG; K06897; MASP58; 1.  
DR KEGG; K06898; MASP59; 1.  
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DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
DE	Mannose-binding lectin associated serine protease-3.			
GN	MASP-3.			
OS	Branchiostoma belcheri (Amphioxus).			
OC	Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;			
OC	Branchiostoma.			
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RC	TISSUE=Notochord;			
RX	MEDLINE=22593355; PubMed=12707349;			
RA	Endo Y., Nonaka M., Saita H., Kakimura Y., Matsumita A., Takahashi M.,			
RA	Matsumita M., Fujita T.,			
RT	"Origin of Mannose-Binding Lectin-Associated Serine Protease (MASP)-1			
RT	and MASP-3 involved in the lectin Complement Pathway Traced Back to			
RT	the Invertebrate, Amphioxus."			
RL	J. Immunol. 170:4701-4707(2003).			
DR	EMBL: AB089268; BAC75887.1; -			
DR	GO:GO:0005509; F:calcium ion binding; IEA.			
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DR	GO:GO:0004295; F:trypsin activity; IEA.			
DR	GO:GO:0007157; P:heterophilic cell adhesion; IEA.			
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QY</				

Qy	17	-----YMCQYDVEVRDGNNDGQILIKRVCGNERPAPIQSIGSSHLVLFHSDGKNFDG	22
Db	243	EQHPEVSCSYDHLKTKAAGEKGP---YCGKTPPTITSDHMYAFPHSDSGENKGF	238
Qy	230	HAIIYEITACSSPCPFHDGTCVLDKAGSYKCACTAGYTGRCENTLLEBRNCSPDFGVNG	289
Db	299	RATYFR-----TARFCEAL-----SAP-----	315
Qy	290	YQKITTGPELIIIGRRRAKIGTVSPFCNNSTYLSGNEKRTCCQNEMSGKQPICIKAREP	349
Db	316	-----AYETMGESNFTYSQKVSFPCGEGYLLDGDHRCQADSMGSGVPTC-----	362
Qy	350	KISDLVRRVVLPMQVQSRBETPLHQYSAFAFKOKLQSAFTKCPALPGDLPNGYQHLHQ	409
Db	363	---ELVNGCEPL-NISNGEIVDNGFS-----YADIAL-----	391
Qy	410	LOYECISPPYRRLGSSRRTCLNTGKWSGRAPSCIPICGKI---ENIT--APPTQGLRW	462
Db	392	--YRC--DQEVEMAGGRTFCPCAGCKMTGNBPSCKPICGSPSPDRRIVGGGPEKKG-AW	447
Qy	463	PMQAAIYRRTSGVHDSGLHKGMFL---VCGSLVNBETVVAAHACTDGLKVMITAD	519
Db	448	PMQAMV-----IHQGAPRRKPPCGALWDKKMILTAAHC---GENDILTGY	495
Qy	520	LKVLGKFRDDDRDEKTIQSLQISAILHPHYDPILADIALIKLIDKARISTRVQPI	579
Db	494	FNVLGLHKRKEPDDNVVFP--EVERVIRRHDPMDKNDSDIALLELKEBVDLTDYIRPV	555
Qy	580	CIAAS--RDLSTSPQESH-I-TVAGNNVLADYRSPGKNDILRSGVSVSDSLCEQHEH	636
Db	552	CIQRSGRQSAQDVQGRAGVVTGKRTSNLF--GSEANTIQEVEVPPVDQEECVSAYEG	609
Qy	637	HGIPTSVTNMCAENEPAPSPDICTAETGCIANVSPFGRRSPPRMHLGVSWSYDKT	696
Db	610	--DYPTVGSNLCAGLR-IGKQSCDQSGDGGPLLFPDDTT---KFLVAGLVSNGEPPSE	661
Qy	697	CSH-RLSTAFYKLPFKMWIE	716
Db	662	CGRAKCYAVARVENVCMWIK	682
RESULT 10			
Q068H4		PRELIMINARY;	PRT; 688 AA.
Q068H4			
AC	068H4		
DT	01-JUN-2003	(TEMBLurel. 24, Created)	
DT	01-JUN-2003	(TEMBLurel. 24, Last sequence update)	
DT	01-OCT-2003	(TEMBLurel. 25, Last annotation update)	
DE	Mannose-binding lectin associated serine protease-3.		
GN	MASP1/3.		
OC	Branchiostoma belcheri (Amphioxus).		
OC	Eukaryote; Metazoa; Chordata; Cephalochordata; Branchiostomidae;		
CC	Branchiostoma.		
CC	NCBI_TaxID=7741;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22593355; PubMed=12707349;		
RA	Endo Y., Nonaka M., Saiga H., Kakimura Y., Matsushita A., Takahashi M.,		
RA	Matsushita M., Fujita T.		
RT	"Origin of Mannose-Binding Lectin-Associated Serine Protease (MASP)-1		
RT	and MASP-3 involved in the Lectin Complement Pathway Traced Back to		
RT	the Invertebrate, Amphioxus."		
RL	J. Immunol. 170:4701-4707(2003).		
DR	EMBL: AB089507; BAC75889.1; -		
DR	GO: GO:0005509; F:calcium ion binding; IEA.		
DR	GO: GO:0004263; F:chymotrypsin activity; IEA.		
DR	GO: GO:0008233; F:peptidase activity; IEA.		
DR	GO: GO:0005529; F:sugar binding; IEA.		
DR	GO: GO:0004295; F:trypsin activity; IEA.		
DR	GO: GO:0007157; P:phagocytosis and phagocytosis; IEA.		
DR	GO: GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro: IPR000152; Asx_hydroxyl_5.		

DR InterPro; IPR000859; CUB.  
 DR InterPro; IPR003003; Cys\_ser\_trypsin.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR000436; Sush1\_SCR\_CCP.  
 DR Pfam; PF00431; CUB; 2.  
 DR Pfam; PF00084; sush1; 2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00032; CCP; 2.  
 DR SMART; SM00042; CUB; 2.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00020; TRYD\_SPE; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS01180; CUB; 2.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS0240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR Lectin; Protease.  
 SQ SEQUENCE 688 AA; 76890 MW; 39D62C0C38A78EB CRC64;

Query Match 14.6%; Score 576.5; DB 5; Length 688;  
 Best Local Similarity 27.4%; Pred. No. 1.4e-44;

Matches 185; Conservative 79; Mismatches 231; Indels 181; Gaps 34;

DR 77 DSCLI-HBGTCTIFENCKSCRNAGSGTLDYVKGFGYCAECRAG-WYGGD--C-MRGC-129  
 DB 152 DECAVNDNGCHNF-----CHN-----YISGYCS-CRAGYIMKDETKCFGGR 195  
 QY 130 QVLPAKQQLLES---YPLNAHCWTIAKPGFVIQLRFVMSLEFD-----YWCQY 179  
 DB 196 QVLQLSGTISSEYPRLYPKVLCDWKI QVEPGVYVTLQ---DDPDVQHEVSCPY 252  
 QY 180 DYVAVRODNDGQIKRVCGNERPAPIQSIGSLHVL FHSDSKSNFPGFAIYEITAC 239  
 DB 253 DILKIQADEXKGP---CCGKTVPPITTSIDNNRVRFFSHDDSGENKGFATYFT--- 304  
 QY 240 SSSPCFHDGTCVLDAKAGSKACLAGYTGRCENILEERNCSDDPGPVNGQXITGGPGL 299  
 DB 305 -----TARCEAL-----SAP-----AYGT 319  
 QY 300 INGRHAKIGTVSPFCNNSYVLSGNEKRTCOQNGMSGKQPI-C-IKACREPKISDLVARR 358  
 DB 320 MEGSNFTSQKVSFACGEGYLDGPDHRVCOADGWSGVQPTCELVNGCPP----- 370  
 QY 359 VLPNOVQRETFPHOLVLAASKQQLGSAPIKKPLPFGDLPKYGQHLHTLO-Q-YECISP 417  
 DB 371 -----PVISNGELEVDGNFSEYADIAIYRC-DQ 396  
 QY 418 FYRRLGSSRRCTCLRTGKMSGRAPSCIPICGKI-----ENIT--APKTQGLRPMQAIYR 470  
 DB 397 FYENAGESTRCLEADGKMTGNEPCKP/CGSSSPFSRRITVGGPSKKG-AMPQANV-- 453  
 QY 471 RTSGVHDSLHKA-----WFLVCSGALVNERVVAHAACVTLDGKVTMIKTADLKKVL 524  
 DB 454 -----HQGAPRIKKPF---GGLVLDKMWILTAHVC---GENDILPTGVFNVL 498  
 QY 525 GKTFYRDDREKTIQSLQISAILHPNYDPIILLADNILLKDKARISTVQPICLAAS 584  
 DB 499 GLHKRKEPDDVVPF--QVERVIRHPDWKDNFSDILLLKEKEVDLTDIRPVCQRS 556  
 QY 585 --RDLSTGFQESH-TVAGMVLADVRSPGFKNDFLRGGVSVVDSLLCECHEDHGIVP 641  
 DB 557 GRQSAQOVQDGRAGVTVGKRTSLF--GSEANTLQVENVYVVDQECVAYE--DY 611  
 QY 642 SYTDNMFCASEPIAASDICTAETGIIAASVFGPGRASPEPMHMLGLVMSYDKTQSH-R 700

DB 612 PYTGNNLCAGLR-IGGKSCDSDSGGPELLFQDDPTT---RFYVAGLVSGEPESECGRAR 666  
 QY 701 LSTAFTKVLFPKDMIE 716  
 DB 667 KGVYARVENFVQMIK 682

RESULT 11

09PU71 ID 09PU71 PRELIMINARY; PRT; 698 AA.  
 AC 09PU71; ID 09PU71; PRT; 698 AA.  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Mannose-binding protein-associated serine protease (Masp)  
 DE precursor.  
 GN MASP.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_Taxid=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=99008558; PubMed=9794427;  
 RA Endo Y., Takahashi M., Nakao M., Saiga H., Sekine H., Matsushita M.,  
 RA Nomaka M., Fujita T.;  
 RT "Two lineages of mannose-binding lectin-associated serine protease  
 (Masp) in vertebrates.";  
 RL J. Immunol. 161:4924-4930(1998).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.  
 DR EMBL; D83276; BAA86669.1; -.  
 DR HSP; P00763; IDPO.  
 DR MEROPS; S01.198; -.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000152; Asx\_hydroxyl\_5.  
 DR InterPro; IPR000181; CUB.  
 DR InterPro; IPR009003; Cys\_ser\_trypsin.  
 DR InterPro; IPR000859; CUB.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR000436; Sush1\_SCR\_CCP.  
 DR Pfam; PF00431; CUB; 2.  
 DR Pfam; PF00084; sush1; 2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00032; CCP; 2.  
 DR SMART; SM00042; CUB; 2.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00020; TRYD\_SPE; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS01180; CUB; 2.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS0240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR EGF-like domain; Hydroxylase; Protease; Serine protease; Signal.  
 FT SIGNAL 1 17  
 SQ SEQUENCE 698 AA; 79414 MW; 79CE2FA4B77A6BB CRC64;

Query Match 12.4%; Score 489.5; DB 13; Length 698;  
 Best Local Similarity 25.0%; Pred. No. 1.9e-36;  
 Matches 183; Conservative 96; Mismatches 219; Indels 233; Gaps 36;

QY 142 ESYPLNAHCWTIAKPGFVIQLRFVMSLEFDYMCQYDYVAVRDGNNRQGIIRKVCN 201

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Db      36 DSVPSBSVTWNTVTRGFSKLYFNGHFDLBSYLCEYDAKVESD-----QVIANFGCK 91
      202 E-----RPA-----IQIGSSHLVLFHSDS--KNPGFAIY-----EITACSSPCRH 246
      92 ESTDTQAFGRQITTPSPNFLTFFSDPSNEERFGFAHSAIDIDICTEKSDBLVC 151
      247 DGTGVLDDKSGYKACLAGY---TGQR-----CENILEERN--CSDPG-----284
      152 DHHC-HNYIGGFGCSGFGVLTHTDRTCKVECSDDLFGKGLISPPYSPYAKSSDC 210
      285 -----GPNVGY-----QKITG 296
      211 RYRIELBEGFVILNHDNFDVDEHPEVCPYDLKIKTGKNEFGPLCEKSPGRKETS 270
      297 -----PGV-----INGR-----HAKITGVSPFCN 316
      271 NTVOQLIFHRNGENGENGRSLYSVTGMPCPNLTAPPNGKLEPPQSEYTRKQDVLS--CN 328
      317 NSY-VLSGNEKR-----TCQNGEMSGK-QPICIKAREPKISDLVRRRLPMVOVSRET 369
      329 QGVRVLKDNVEMSLQIECKRGTGWNQIPVQIVDCKPK-----EIEHG--374
      370 PLHQLYSAFSSKQKLOSAPTKKALPFGDLPMGYQHLATQLOECISPFYRLGSR--R 427
      375 ---FITYSTAENRTFQSS-----FNVSCREPYMMVVPNTLVY 410
      428 TGLRTGKWS-----GRAPSCIPICG-----KIENITAPKT--QGLRPMQOAIYRRTS 473
      411 TCDASEMTSGEIGAKIPTCPVCYPRPSRSLAIAIGAKTRAKRIS-PWIMF-----464
      474 GVHDSLHGKAMELVSCGALVNERVVAACHV-----TDLGKVTMIKTADLVKLVG 525
      465 --SDSQNNQP-----FCGALISNKWIVTAAHCLHEDLTEDDNLNKLKFELESFVILG 518
      526 KFYRDDDRREKTIQSIQIAIILHPYVDPLDADIAIKLIDKAISTRVQICLAAR 585
      519 K-HRTLKQD-TEQTOQANKLILHPYKPTFRFDIALVELSLDKAPALNDYVMPICPEKO 576
      586 DLSTSPQSHITVAGNVLADVRSPPFKNDTLRSGVVSDSLCEQHEHGIPIVSTD 645
      577 ---VQDDEHVIVSGMKFKRLP-----DSLMEVPIPVGOLCTIVQT--LELLVTD 626
      646 NMFCAWSEPTAPSDICTAETGTIAVSPGARSPERPMHLMGLVSNYDKTCSHRLSTA- 704
      627 EMICAGFK-EGGKDACSGDSGGMVT-----KNELKGMVLAGTVSGVG--CGKIRYGM 679
      705 FTKVLPFKMIER 717
      680 YSDVYNKLDWIKK 692

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## RESULT 12

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ID      09JUS9      PRELIMINARY;      PRT;      701 AA.
AC      09JUS9;
DT      01-OCT-2000 (Tremblrel. 15, Created)
DT      01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT      01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE      Mannose-binding protein associated serine protease-1 precursor
      (Fragment).
GN      MASP-1.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      (1)
RP      SOURCE FROM N.A.
RC      TISSUE=Liver;
RX      MEDLINE=20469449; PubMed=10913141;
RA      Wallis R., Dodd R.B.;
RT      "Interaction of mannose-binding protein with associated serine
      proteases: Effects of naturally occurring mutations.";

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RL      J. Biol. Chem. 275:30962-30969 (2000).
CC      -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
DR      EMBL: AJ277423; CAB86935.1; --
DR      HSSP: P00736; IARQ.
DR      MEROPS: S01.198; --
DR      GO: GO:0005509; F:calcium ion binding; IEA.
DR      GO: GO:0004263; F:chymotrypsin activity; IEA.
DR      GO: GO:0008233; F:peptidase activity; IEA.
DR      GO: GO:0004295; F:trypsin activity; IEA.
DR      GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR      InterPro: IPR000152; Asx_hydroxyl_S.
DR      InterPro: IPR000859; CUB.
DR      InterPro: IPR009003; Cys_ser_trypsin.
DR      InterPro: IPR001881; EGF_Ca.
DR      InterPro: IPR006209; EGF_like.
DR      InterPro: IPR001254; Peptidase_S1.
DR      InterPro: IPR001314; Peptidase_S1A.
DR      InterPro: IPR000436; Sush1_SCR_CCP.
DR      Pfam: PF00431; CUB; 2.
DR      Pfam: PF00084; Sush1; 2.
DR      PRINTS: PR00722; CHYMOTRYPSIN.
DR      SMART: SM00032; CCP; 2.
DR      SMART: SM00042; CUB; 2.
DR      SMART: SM00179; EGF_CA; 1.
DR      SMART: SM00020; Tryp_Spc; 1.
DR      PROSITE: PS00010; ASX_HYDROXYL; 1.
DR      PROSITE: PS01180; CUB; 2.
DR      PROSITE: PS01186; EGF_2; 1.
DR      PROSITE: PS01187; EGF_CA; 1.
DR      PROSITE: PS00240; TRYPsin_DOM; 1.
DR      PROSITE: PS00134; TRYPSIN_HIS; 1.
DR      PROSITE: PS00135; TRYPSIN_SER; 1.
KW      EGF-like domain; Hydrolase; Protease; Serine protease; signal.
FT      NON TER 1
FT      SIGNAL <1 21
FT      CHAIN 22 701
SQ      SEQUENCE 701 AA; 79663 MW; B5CFD619D63CE3DD CRC64;
      QUERY MATCH 12.2%; Score 483; DB 11; Length 701;
      Best Local Similarity 22.9%; Pred. No. 7,66-36;
      Matches 193; Conservative 109; Mismatches 256; Indels 282; Gaps 44;
      11 LTFQLLL-----ISSLPRETVINE-----ACPG-----AEINIMCRE-----44
      1 LSFRLLLVHVLCTLTVESAHVTELMEMFGQIOSPGYDPSSEVTWNTVTRGFSRV 60
      45 -----CCEYQIR-----CVC-----PGKREV-----61
      61 QLYFMHFLSSYLCEYDVYKVEDQVLATFCGRETTDTEQTPQGEVVLSPGSMVTF 120
      62 -----VGYTIPCCRNENECDSCLIHFGCTIFENCKSCRNGSWGTLTD 104
      121 RSDFSNEERFTGFDHNVAVDVDECKERDEBELSDNH-----CIN-----161
      105 DFTYKGFYCAECRAGWY-----GGDC-MFC-GQVLRAPGQILL-----ESYPLAHCEWTI 154
      162 --YIGGYCS-CRFYIATDNRKTRVCSGNTLFTORTGITSPDPYPNYPSPSSCSYTI 218
      155 HAKPGFVQLRFVMSLEFD-----WMOYDYVVRDGDNRDGOIIRKVCNERNPAPIQ 208
      219 DLBEGFMVTLQPEDI--FDIEDHPEVCPDYDIYIKAGSKMGPF-----CGEKSPFIS 271
      209 SIGSLHLVLFHSDGSKNDFGFAIYEITACSSSPCFHDTGVLDDKAGSYKACLAGYTG 268
      272 TQSHSIQLIFRSNDNGENRGMRL-----SYRA-----G 300
      269 QRCENULEERNCSDDGGPYNGQKITGPGGLNGHAKIGTVSFFCNVSY-VLSGNE--325
      301 NECPFL-----QP--PV--YGKIEPSQAVYSFQDQ-----VLISCTGYKVLKDNVEM 344
      326 ---KTCQNGEMSGKQPTIC-IKACREPKISDLVRRRLPMVOVSRETPLHQLYSAFSSK 381

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Db      345 DTQIELKDGAMSNKIPCTKIVDCGP-----AVLK 376
QY      382 OKLQSAFTKKRALPFGDLPNGYOHHTOLOECISPEYRLGSSR--RTCLRTGKMSGRA 439
Db      377 HGLVTFSTRNNLTYY-----KSEIRYSCQOPFYKMLHNTTGVYTCSAHGTWNEV 426
QY      440 -----PSCIPICG-----KIENITAPKTOGLRMPOQALYRTSGVHDSLHKGA 484
Db      427 LKSLPFLCLPVCGLPKFSRKHISIFN-GRPAQKGT-PIIAML-----SOLNGP 474
QY      485 WFLVSGALVNERVVAHAACVTD-----LGKVTMIKADLKVVLGKPY-RDDDRDE 535
Db      475 PF--CGSLLSGSNVNLAAHCLHNPDRPEPILHNSLSPDFKIMGMRRRSDDE 532
QY      536 KTQSLQISAIIHFNYPDILLADIALILKLDKARISTVOPTCLAASDLSTFQESH 595
Db      533 ---QHLYVKHIMLHPLNPFSTFENDLGLVELSESPLINDFVMPCLPE---HPSTEGTW 585
QY      596 ITVAGMNVLDVSPGKNDLRSQVSVVSDLLCEQHEDHGIPIVSTDNMFCAWEP 655
Db      586 VIVSGMKQFLQRLP---ENLMEIEIPIVYHTCOEAYPLG--KKTVDIMICAG-EKE 638
QY      656 APSDICTAETGIAAVSPGRASPEPRMLMGLVMSYDTKCSHRLSTAFKVLFPKDWI 715
Db      639 GGDACAGDSGSPVNT---KDAERDQWLVGVVSWEDGCKKDRYG-VYSIYIPNDWI 693
QY      716 ER 717
Db      694 QR 695

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## RESULT 13

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Q8CHNB PRELIMINARY; PRT; 703 AA.
AC Q8CHNB;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Mannose-binding protein associated serine protease-1.
GN MASP-1/3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague Dawley;
RA Slevier C.M., Lynch N.J., Dahl M.R., Hanson S., Frankenberger M.,
RA Ziegler-Heitbrock L., Thiel S., Schwaeble W.J.;
RT "the rat homologues of MASP-1 and MASP-3, components of the lectin
RT activation pathway of Complement.";
RL Submlited (ABR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ457084; CAD29746.1;
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004235; F:peptidase activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR00152; Aex_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00084; sushi; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00424; CUB; 2.

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DR SMART; SM00179; EGF CA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM PROTEASE.
SQ SEQUENCE 703 AA; 80049 MW; 8E4CFA6413020F18 CRC64;

Query Match 12.2%; Score 482.5; DB 11; Length 703;
Best Local Similarity 22.9%; Pred. No. 8,5e-36;
Matches 193; Conservative 108; Mismatches 259; Indels 281; Gaps 44;

QY 11 LTFLOLL-----ISSLPREYVINE-----ACPG-----AEWIMCRE---- 44
Db 4 LSFRRLLVHVLCLTLEVSAAHVELNEMFGQIQSGYDPSYSDSEVTNITVPEFRVQ 63
QY 45 -----CCEYDOIE-----CVC-----PGKREV----- 61
Db 64 LYFMHFNLSSTLCEDYDVKETEDEVLTATFCGRTTTEQTPGQEVLSPSGFSVTR 123
QY 62 -----VGYTIPCCNENECDCULHPGCTIFENCKSGRSGWGTLTD 105
Db 124 SDFSNERTFGPDANMAVDVDECKERDELSCHY-----CHN----- 163
QY 106 FYVKGFFYCAECRAGY---GGDC-MRC-GQVLRAPKQIIL---ESYPLNHCWTH 155
Db 164 -YIGGYCS-CRFGYILHTDNRTRCVKESGNLFTQRTGTPSPDYPNPKSECSYITD 221
QY 156 AKRGFVIOIRFVWLSEFD-----YMCQDYVEVDGNNRQGIKRGNGRPAPIOS 209
Db 222 LSEGFVWLHFDI---FDIEDPEVPCPYDIKIKAGSKWGP---CGEKSPPIST 274
QY 210 ISSSLVLFHSDGSKNFDGFAHIEBITACSSPCEHDTGCVLDKAGSYKACLAGYTQ 269
Db 275 QSHSITILFRSDNSGNRMRL-----SYRAA-----GN 303
QY 270 RCENLLEBKNCSDPGPVNGYOKITGGPGLNGRAKIGTVVSFFCNISY-VLSGNE--- 325
Db 304 EEPKL-----QP--PV--YKIEPSQAVSFQKQ---VLISCDTYKVLKQNEVND 347
QY 326 --KRTQNGEMSGKQIC-IKACREPKISDLVRRRLVPMQVSRETPHOLYSAFASK 382
Db 348 TFOIELKDGAMSNKIPCTKIVDCGP-----AVLK 379
QY 383 KLOSAFTKKRALPFGDLPNGYOHHTOLOECISPEYRLGSSR--RTCLRTGKMSGRA 439
Db 380 GLVTFSTRNNLTYY-----KSEIRYSCQOPFYKMLHNTTGVYTCSAHGTWNEV 429
QY 440 -----PSCIPICG-----KIENITAPKTOGLRMPOQALYRTSGVHDSLHKGA 485
Db 430 KSLPFLCLPVCGLPKFSRKHISIFN-GRPAQKGT-PIIAML-----SOLNGP 477
QY 486 FLVCSGALVNERVVAHAACVTD-----LGKVTMIKADLKVVLGKPY-RDDDRDE 536
Db 478 F--CGSLLSGSNVNLAAHCLHNPDRPEPILHNSLSPDFKIMGMRRRSDDE- 534
QY 537 KTQSLQISAIIHFNYPDILLADIALILKLDKARISTVOPTCLAASDLSTFQESH 596
Db 535 ---QHLYVKHIMLHPLNPFSTFENDLGLVELSESPLINDFVMPCLPE---HPSTEGTW 588
QY 597 TVAGMNVLDVSPGKNDLRSQVSVVSDLLCEQHEDHGIPIVSTDNMFCAWEP 655
Db 589 IYSGMKQFLQRLP---ENLMEIEIPIVYHTCOEAYPLG--KKTVDIMICAG-EKEG 641
QY 657 PSDICTAETGIAAVSPGRASPEPRMLMGLVMSYDTKCSHRLSTAFKVLFPKDWI 716
Db 642 GGDACAGDSGSPVNT---KDAERDQWLVGVVSWEDGCKKDRYG-VYSIYIPNDWI 696
QY 717 R 717

```

Db 697 R 697

## RESULT 14

Q8AXR1 PRELIMINARY; PRT; 717 AA.

AC Q8AXR1; 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 GN Mammose-binding lectin-associated serine protease-3a.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 NCBI\_TaxID=8355;  
 (1)  
 SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Takahashi M.,  
 Matsumita M., Fujita T.  
 RT "Ancient origin and extensive distribution of mannose-binding lectin-  
 associated serine protease-3 in vertebrate lineage."  
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AB076636; BAC41339.1; -.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:000529; F:sugar binding; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro: IPR000152; Asx\_hydroxyl\_S.  
 DR InterPro: IPR000859; CUB.  
 DR InterPro: IPR009003; Cys\_ser\_trypsin.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR006209; EGF\_Like.  
 DR InterPro: IPR006210; IEGF.  
 DR InterPro: IPR001254; Peptidase\_S1.  
 DR InterPro: IPR001314; Peptidase\_S1A.  
 DR InterPro: IPR000436; Sushi\_SCR\_CCP.  
 DR Pfam: PF00431; CUB; 2.  
 DR Pfam: PF00084; sushi; 2.  
 DR Pfam: PF00089; trypsin; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SM00032; CCP; 2.  
 DR SMART: SM00042; CUB; 2.  
 DR SMART: SM00181; EGF; 1.  
 DR SMART: SM00179; EGF\_Ca; 1.  
 DR SMART: SM00020; TRYD\_SPC; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS01180; CUB; 2.  
 DR PROSITE: PS01186; EGF\_2; 1.  
 DR PROSITE: PS01187; EGF\_Ca; 1.  
 DR PROSITE: PS02040; TRYPsin DOM; 1.  
 DR PROSITE: PS00135; TRYPsin\_SER; 1.  
 KW lectin; Protease.  
 SQ SEQUENCE 717 AA; 80959 MW; 513CFAF3CBEBBA0 CRC64;

Query Match 12.2%; Score 482; DB 13; Length 717;  
 Best Local Similarity 25.4%; Pred. No. 9, 7e-36;  
 Matches 180; Conservative 100; Mismatches 240; Indels 188; Gaps 36;

QY 69 CRNEBNCBCLHPPGCTIENCKSRNGSWGTLDDFYVKGFCACRCAGWY---GGD 124  
 Db 141 CTKSEBDLVCDH-----CHN-----YIGGYCS-CFPGYLLHMDNRT 178  
 QY 125 C-MRGOVLAAPK-GQILLESYP-----LNAHCMTIHAKEGVYQIRF--VMSLEPDY 175  
 Db 179 CKVECSDNLFTRSGSLISPDYGPVAKSSDCRYRIQLBEGFVYNLHFDNFVVEHPEV 238

QY 176 MCOYDYVEVRDNDRDQIIRKVCNERNPAPFIOGSISSLHYLFHSDSKNFDGFAHYEE 235  
 Db 239 KCPYDYLIKTKTKKEFGPL-----CGEKSPGRIETGNSVQILFHSNDSNGENGRISTY-- 292

QY 236 ITACSSPCHFDGTCLDKAGSYKACLAGYTGRCENLEBRNCSPDGCVNG-----Y 290  
 Db 293 -----SVTGNPCPRL-----HPPNCKLEBPQ 314

QY 291 QKITGPELNGRAHAKIGTVSPFCNNNSY-VLGSNERK-----TCOONGESGKPTC-I 343  
 Db 315 SEYV-----FKQVVIS--CNOGIRYKKNVEMESIQICRDKDTGINSNOIPQOI 362

QY 344 KACREPKISDLVRRRVLPVQVSRREPLHQLYSAFSAFSAFSAFSAFSAFSAFSAFSAF 403  
 Db 363 VDCKKPK-----EIENG-----FIYSTAEKRTYQSS----- 390

QY 404 QHMTQLOLEYCISPPYRLGSSR--RTCLRKGKS-----GRASCLPICGK----- 448  
 Db 391 -----FNYSCEPEYMMVNPITLVYTCDSAGEWTSOEIGAKIPTCPVCGKPARPLPGI 444

QY 449 IENITAPKT--QGLRMPQALVYRTSGVHDGS-LHKGMFLVCSGALVNERTVVAANC 505  
 Db 445 VKRIIGGNAPGP-FPQVULIV-----VEDLSKVPMMKWF--GGGALISDQWVLTAAHN 496

QY 506 VTDLGK--VTMIKTADLKVVLGKFRYRDDDEKTTOSLOISAILLHPNVDPIILLADIA 562  
 Db 497 LRSQRDNTVMPVAKHEVTYLG--LHDVASKTDAVVRITKILILHMFDPESVYNDIA 553

QY 553 ILKLDKRISTRQPIQL-AAARDLSTSPESHITVAGNV-----LADVRPGRFND 615  
 Db 554 LVKNKRYKIQVMPVCLPFLHELEGPQNTGLVAGWISDPNITVDVSISSGKTH 613

QY 616 T--LRSQVSVVSDLSCEQHEHDGIPVSVTDNMFCSAMEBTASDICTAETGIAVASP 673  
 Db 614 SAILQVVLPLYVAHVACSEYSSRGVSVTEENFCAGYV-EGGKDTLGLSGG---AF 668

QY 674 PGRASPEPRMELMGLVSWSYKTC-SHRLTAFTKVLFPKQWIERANK 720  
 Db 669 IMODTTRKVAAGLVSGPEEGSGKQVGVYTKVSNFVMDNLK 716

## RESULT 15

ID Q96RS4 PRELIMINARY; PRT; 728 AA.

AC Q96RS4; 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Complement factor MASP-3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_TaxID=9606;

SEQUENCE FROM N.A.

RP MEDLINE=21378425; PubMed=11485744;  
 RA Dahl M.R., Thiel S., Matsushita M., Fujita T., Willie A.C.,  
 Christensen T., Vorup-Jensen T., Jensenius J.C.;  
 RT "MasP-3 and its association with distinct complexes of the mannan-  
 binding lectin complement activation pathway";  
 RL Immunity 15:127-135(2001).

CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

CC -1 SIMILARITY: CONTAINS 2 CUB DOMAINS.

DR EMBL: AF284421; AAK84071.1; -.  
 DR HSBP; P00761; IAN1.

DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.

DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro: IPR000152; Asx\_hydroxyl\_S.  
 DR InterPro: IPR000859; CUB.  
 DR InterPro: IPR009003; Cys\_ser\_trypsin.

Search completed: August 18, 2004, 16:25:01  
Job time : 49 secs

DR InterPro; IPR001861; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_Like.  
DR InterPro; IPR01254; Peptidase\_S1.  
DR InterPro; IPR01314; Peptidase\_S1A.  
DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
DR Pfam; PF00431; CUB; 2.  
DR Pfam; PF00064; Sushi; 2.  
DR Pfam; PF00069; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00032; CCP; 2.  
DR SMART; SM00042; CUB; 2.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS01180; CUB; 2.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS0240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
DR EGF-like domain; Hydrolyase; Protease; Serine protease.  
SC SEQUENCE 728 AA; 81860 MW; 09B5297A6C14283A CRC64;

Query Match 11.9%; Score 468; DB 4; Length 728;

Best Local Similarity 25.0%; Pred. No. 2e-34;

Matches 180; Conservative 97; Mismatches 228; Indels 214; Gaps 39;

QY 69 CRNEBNECDCLIPHCCTIFENCKSCRNQSWGTLDDFYVKGFCACGRAGWY----CGD 124  
DB 143 CKEREDEBELSCDHY-----CHN-----YIGYYCS-CRFGYIATDNR 180  
QY 125 C-MRGGQVLRAPKQGIIL-----ESYPLNAHCWETIHAKPGFVIOLEFVMSLEFD--- 174  
DB 181 CRVECSDNLFQRTGVITSPDPFNPYKSSCLYTIIEBEGFMVNLQFEDI---FDIEDH 237  
QY 175 --YMQQDYVEVRGDNDGQIIRKVCGERPAPQISGSSLAHVLPHSDGSKNDFGFHAI 232  
DB 238 PEVPCPYDIKIKVGP-----KVLGPFCEKAPETISTQSHVILIFHSDNNGENRGWRL- 292  
QY 233 YEBITACSSPCFHDGTVDLKAQSYKACACLAGTGCENLLEBRNCSDPGQVNGYQK 292  
DB 293 -----SYRAA-----GNECPPL-----QP-FVH----- 309  
QY 293 ITGGPGLINGRAKIGTVVSFF-----CNNSY-VLSGNEK-----TCQONGEMSKQ 339  
DB 310 -----GKIEBSQAKT-----FFKQVVLVSCDTGYKVLKDNVEMDTFOIECLAKDTGWSNKI 359  
QY 340 PIC-IKACREPKISDLVRRVLPQVQSRETPLHQLYSAFSSKQLOAPTKKPLPFGD 398  
DB 360 FTCKIVDCRAP-----GE 372  
QY 399 LPMGYQHHT-----QIQYECISPFYRLGSSR--RTCLRTGKWS---GRA--PSC 442  
DB 373 LEHGILTFSTNNLTTYKSEIKYSCQEPYKMLNNTGIYTCAGVMMNKVLRSLPTC 432  
QY 443 IPIGK-----IENITAPKT--QGLRWPQOAIYRTSGVHDS--LHKGAWFLVCSG 491  
DB 433 LPECCQPSRSLPVKRIIGGRNAPGL--FPMQALIV-----VEDTSRVNDKWF--CSG 484  
QY 492 ALVNERVVAACHVTDIGKVTMIKTADLVKLVGKPYRDDDRDEKTIQSLQISAILHPN 551  
DB 485 ALLSASWILTAHVRSQRDITVIVSGKEHTVYVGLAHVDKSGAVNSAARVVLHPD 544  
QY 552 YDPIILDADIALIKLDAKISTRVQPCICLASRLDSTSPESH--TVAGW-----NYL 604  
DB 545 FNIQNTNHDIALVQIQEPVPLGPHWPCVCLPR--LEPEGPAFHLGLVAGMGISNPVT 601  
QY 605 AD-VASPGFK--NDTLRSGVSVVDSLLCEBQEDHGIPVSTDMFCASWEPTAPSDIC 661  
DB 602 VDEIISSTRTLSIDLQVYKLPVPHABCKTSYBSRSGNYSVTENMFCAGY--EGKQDTC 660  
QY 662 TAETGGIAVSPFGASPEPRMHLMLGLVSWSYDKTC-SHRLSTAFTKVLPFKDWIERNM 719  
DB 661 LGDSGG-AFVIFDDLSQ--RNVVQGLVSWGPEBCGSKQYGVYTKVSNYVDWVMEQM 715

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:29:15 ; Search time 44 Seconds  
(without alignments)  
5163.025 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 720

Sequence: 1 MBLGCTGTLGTLFLQLLLIS.....LSTAFKVLPEKDWIRBNK 720

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 700 summaries

Database :

SPREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_plant:\*  
10: sp\_rodent:\*  
11: sp\_virus:\*  
12: sp\_vertebrate:\*  
13: sp\_unclassified:\*  
14: sp\_rv1rus:\*  
15: sp\_bacteriap:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	446	61.9	737	4 Q96JW2	Q96JW2 homo sapien
2	178	24.7	181	4 Q9Y432	Q9Y432 homo sapien
3	61	8.5	720	11 Q8BU25	Q8BU25 mus musculu
4	41	5.7	720	11 Q8K2B8	Q8K2B8 mus musculu
5	9	1.2	222	11 Q91W20	Q91W20 rattus norv
6	9	1.2	276	16 Q86553	Q86553 streptomyce
7	9	1.2	691	13 Q57658	Q57658 gallus gall
8	9	1.2	923	13 Q8QFX6	Q8QFX6 brachydanto
9	9	1.2	923	13 Q8AXP1	Q8AXP1 brachydanto
10	9	1.2	926	4 Q9U000	Q9U000 homo sapien
11	9	1.2	1015	4 Q9Y6L7	Q9Y6L7 homo sapien
12	9	1.2	1464	5 Q23995	Q23995 drosophila
13	9	1.2	1464	5 Q9VC47	Q9VC47 drosophila
14	9	1.2	1464	5 Q24132	Q24132 drosophila
15	9	1.2	2531	5 Q16004	Q16004 lytechinus
16	8	1.1	81	15 Q79204	Q79204 human immun

17	8	1.1	136	11 Q8CEX5	Q8CEX5 mus musculu
18	8	1.1	152	11 Q924X1	Q924X1 mus musculu
19	8	1.1	234	13 Q90244	Q90244 actinomer t
20	8	1.1	235	6 Q28731	Q28731 oryctolagus
21	8	1.1	240	16 Q8D223	Q8D223 yersinia pe
22	8	1.1	242	16 Q8D079	Q8D079 yersinia pe
23	8	1.1	302	5 Q9XUN6	Q9XUN6 caenorhabd
24	8	1.1	385	13 Q90WS2	Q90WS2 elaphes sp.
25	8	1.1	413	2 Q7X370	Q7X370 uncultured
26	8	1.1	556	16 Q7UX12	Q7UX12 rhodospirell
27	8	1.1	607	13 Q91001	Q91001 gallus gall
28	8	1.1	608	13 Q9PTW7	Q9PTW7 struthio ca
29	8	1.1	611	10 Q94HU9	Q94HU9 oryza sativ
30	8	1.1	611	10 Q7XG00	Q7XG00 oryza sativ
31	8	1.1	719	13 Q9PYV2	Q9PYV2 triakis bcy
32	8	1.1	737	16 Q8YTB7	Q8YTB7 anabaena sp
33	8	1.1	752	13 Q42374	Q42374 brachydanto
34	8	1.1	764	16 Q8XTM0	Q8XTM0 raietonia s
35	8	1.1	963	5 Q44393	Q44393 plasator oc
36	8	1.1	1019	5 Q8T9S1	Q8T9S1 tachyleus
37	8	1.1	1070	5 P91972	P91972 aplysia cal
38	8	1.1	1083	5 Q26423	Q26423 carcinocor
39	8	1.1	1238	5 Q9VCD8	Q9VCD8 drosophila
40	8	1.1	1238	5 Q9N614	Q9N614 drosophila
41	8	1.1	1316	4 Q96JU7	Q96JU7 homo sapien
42	7	1.0	36	16 Q7UL51	Q7UL51 rhodospirell
43	7	1.0	37	16 Q8F0D5	Q8F0D5 leptopiriz
44	7	1.0	54	16 Q8N087	Q8N087 corynebact
45	7	1.0	59	16 Q99SV1	Q99SV1 staphylococ
46	7	1.0	59	16 Q931M9	Q931M9 staphylococ
47	7	1.0	61	10 Q8GZP9	Q8GZP9 arabidopsis
48	7	1.0	61	10 Q8GZP8	Q8GZP8 arabidopsis
49	7	1.0	61	10 Q8GZP7	Q8GZP7 arabidopsis
50	7	1.0	61	10 Q8GZP6	Q8GZP6 arabidopsis
51	7	1.0	61	10 Q8GZP5	Q8GZP5 arabidopsis
52	7	1.0	61	10 Q8GZP4	Q8GZP4 arabidopsis
53	7	1.0	61	10 Q8GZP3	Q8GZP3 arabidopsis
54	7	1.0	61	10 Q8GZP2	Q8GZP2 arabidopsis
55	7	1.0	61	10 Q8GZP1	Q8GZP1 arabidopsis
56	7	1.0	71	9 Q855B3	Q855B3 mycobacteri
57	7	1.0	75	10 Q9C8F3	Q9C8F3 arabidopsis
58	7	1.0	81	12 Q9EMT8	Q9EMT8 amebaeta moo
59	7	1.0	81	15 Q79303	Q79303 human immun
60	7	1.0	81	15 Q79209	Q79209 human immun
61	7	1.0	82	15 Q90D16	Q90D16 human immun
62	7	1.0	86	2 Q7X3H3	Q7X3H3 thlocapra r
63	7	1.0	91	10 Q9M9B7	Q9M9B7 arabidopsis
64	7	1.0	106	12 Q87074	Q87074 suid herpes
65	7	1.0	109	5 Q966A7	Q966A7 caenorhabd
66	7	1.0	112	5 P91967	P91967 trichinella
67	7	1.0	114	17 Q9YCI9	Q9YCI9 aeropyrum p
68	7	1.0	120	5 Q8T6A0	Q8T6A0 aplysia cal
69	7	1.0	124	16 Q8G3X3	Q8G3X3 bifidobacte
70	7	1.0	124	16 Q81G20	Q81G20 bacillus ce
71	7	1.0	124	16 Q7WC39	Q7WC39 bordetella
72	7	1.0	129	16 Q87F53	Q87F53 vibrio para
73	7	1.0	132	8 Q8W697	Q8W697 apatania zo
74	7	1.0	132	16 Q9L158	Q9L158 streptomyce
75	7	1.0	143	10 Q9S9X5	Q9S9X5 arabidopsis
76	7	1.0	144	8 Q8WG98	Q8WG98 morosyche
77	7	1.0	154	2 Q50211	Q50211 mycobacteri
78	7	1.0	156	16 Q8PFF6	Q8PFF6 xanthomonas
79	7	1.0	157	5 Q95W21	Q95W21 anthomomus
80	7	1.0	158	10 Q9AV48	Q9AV48 oryza sativ
81	7	1.0	158	10 Q7XDB3	Q7XDB3 oryza sativ
82	7	1.0	164	4 Q96QK6	Q96QK6 homo sapien
83	7	1.0	168	16 Q8DUF0	Q8DUF0 synchococ
84	7	1.0	168	16 Q928J3	Q928J3 chlamydia p
85	7	1.0	169	16 Q87NK8	Q87NK8 vibrio para
86	7	1.0	170	10 Q84SG4	Q84SG4 chlamydom
87	7	1.0	170	10 Q84RT8	Q84RT8 chlamydom
88	7	1.0	171	2 Q9R0P0	Q9R0P0 vibrio chol
89	7	1.0	171	16 Q9K279	Q9K279 chlamydia p



90	172	13	Q9DFD1	Q9d41 oncorhynch	163	7	1.0	286	4	Q9H7G9	Q9H799 homo sapien
91	172	16	Q9CYV6	Q9c16 psateurella	164	7	1.0	291	2	Q9R9T0	Q9r9c0 pseudomonas
92	176	13	Q9PUC7	Q9puc7 gallus gall	165	7	1.0	291	16	Q9BN41	Q9bn41 pseudomonas
93	178	10	Q9IMH2	Q9imh2 arabidopsis	166	7	1.0	299	5	Q9TRD9	Q9trd9 trypanosoma
94	181	16	Q97N26	Q97n26 vibrio para	167	7	1.0	300	5	Q81N70	Q81n70 drosophila
95	185	2	Q9KWV2	Q9kwv2 salmonella	168	7	1.0	301	13	Q7ZSK7	Q7zsk7 fugu rubrip
96	187	10	Q84SJ0	Q84sj0 matricaria	169	7	1.0	304	16	Q8XKF6	Q8xkf6 ralsontia s
97	189	10	Q84SJ1	Q84sj1 matricaria	170	7	1.0	306	10	Q8LSB0	Q8lsb0 oryza sativ
98	191	16	Q9R8A2	Q9raa2 deinooccus	171	7	1.0	307	17	Q9KV69	Q9kv69 vibrio chol
99	191	16	Q8ILD6	Q8ild6 bacillus an	172	7	1.0	312	3	Q12125	Q12125 saccharomyc
100	198	16	Q8XR75	Q8xr75 ralsontia s	173	7	1.0	315	2	Q55220	Q55220 streptomyce
101	204	13	Q8JIS7	Q8jis7 xenopus lae	174	7	1.0	317	2	Q9KWA7	Q9kwa7 agrobacteri
102	208	13	Q9Z315	Q9z315 bradyrhizob	175	7	1.0	324	13	Q90Z55	Q90z55 scophthalmu
103	211	16	Q8ZEH2	Q8zeh2 yersinia pe	176	7	1.0	329	16	Q89MG1	Q89mg1 bradyrhizob
104	212	16	Q8XCB6	Q8xcb6 escherichia	177	7	1.0	329	17	Q8ZM31	Q8zmg1 pyrococcus
105	213	16	Q9CE55	Q9ce55 lactococcus	178	7	1.0	330	2	Q30523	Q30523 vibrio shil
106	214	16	Q87K02	Q87k02 streptomyce	179	7	1.0	332	16	Q8NKT9	Q8nkt9 strephlococ
107	215	16	Q9RKP8	Q9rkp8 streptomyce	180	7	1.0	333	16	Q9K7W7	Q9k7w7 bacillus ha
108	215	16	Q8DOJ8	Q8doj8 yersinia pe	181	7	1.0	336	16	Q8PR42	Q8pr42 xanthomonas
109	221	5	Q95S24	Q95s24 drosophila	182	7	1.0	336	16	Q69510	Q69510 mycobacteri
110	221	5	Q9VWV7	Q9vwv7 drosophila	183	7	1.0	337	17	Q7ML07	Q7ml07 bordetella
111	222	5	Q8KOM4	Q8km4 saccharopol	184	7	1.0	337	17	Q9YDH3	Q9ydh3 aeropyrum p
112	222	3	Q871A9	Q871a9 neutrospora	185	7	1.0	338	16	Q8PE85	Q8pe85 xanthomonas
113	223	3	Q7Z724	Q7z724 inocybe sie	186	7	1.0	342	10	Q7XK33	Q7xk33 oryza sativ
114	225	8	Q8M0X1	Q8mox1 gynodiactyl	187	7	1.0	343	16	Q8D7G2	Q8d7g2 vibrio vuln
115	225	10	Q8W5L0	Q8w5l0 oryza sativ	188	7	1.0	344	16	Q7VVL3	Q7vv13 bordetella
116	225	10	Q7XH60	Q7xh60 oryza sativ	189	7	1.0	344	10	Q84QA9	Q84qa9 oryza sativ
117	226	16	Q81KCS	Q81kcs bacillus an	190	7	1.0	344	16	Q9ZM18	Q9zml8 rhizobium m
118	226	16	Q816L1	Q816l1 bacillus ce	191	7	1.0	345	16	Q7W718	Q7w718 bordetella
119	227	3	Q7Z8D8	Q7z8d8 inocybe ada	192	7	1.0	349	17	Q9YBV1	Q9ybv1 aeropyrum p
120	227	16	Q88Q18	Q88q18 pseudomonas	193	7	1.0	350	5	Q18122	Q18122 caenorhabdi
121	227	17	Q29875	Q29875 archaeoglob	194	7	1.0	352	11	Q8C9H0	Q8c9h0 mus musculu
122	228	3	Q7Z8Z5	Q7z8z5 inocybe che	195	7	1.0	354	16	Q9Q0E0	Q9q0e0 bradyrhizob
123	228	16	Q889S0	Q889s0 pseudomonas	196	7	1.0	354	16	Q99Q08	Q99q08 bradyrhizob
124	231	16	Q9Z795	Q9z795 chlamydia p	197	7	1.0	355	2	Q99Z86	Q99z86 bradyrhizob
125	232	16	Q9HWM1	Q9hwm1 pseudomonas	198	7	1.0	355	8	Q37446	Q37446 carabus bla
126	233	3	Q7Z8Z4	Q7z8z4 inocybe che	199	7	1.0	355	8	Q99052	Q99052 carabus por
127	233	10	Q8YV63	Q8yv63 arabidopsis	200	7	1.0	355	8	Q9PM04	Q9pm04 carabus van
128	235	10	Q8LD25	Q8ld25 arabidopsis	201	7	1.0	355	8	Q9TE94	Q9te94 carabus bla
129	235	13	Q91004	Q91004 gecko gecko	202	7	1.0	355	8	Q9GBL3	Q9gb13 carabus poc
130	236	17	Q9HGG1	Q9hgg1 halobacteri	203	7	1.0	355	8	Q9B9L9	Q9b919 carabus hum
131	237	13	Q7ZML3	Q7zml3 xenopus lae	204	7	1.0	355	8	Q9GBK8	Q9gbk8 carabus sma
132	238	3	Q7Z721	Q7z721 inocybe ste	205	7	1.0	355	8	Q9M1Z5	Q9m1z5 carabus lop
133	238	16	Q8CW43	Q8cw43 escherichia	206	7	1.0	355	8	Q9TEA3	Q9tea3 carabus bla
134	239	13	Q91218	Q91218 oncorhynch	207	7	1.0	355	8	Q9TE05	Q9te05 carabus can
135	239	16	Q9KOD6	Q9k0d6 vibrio chol	208	7	1.0	355	8	Q9M1Z7	Q9m1z7 carabus sma
136	240	16	Q891B3	Q891b3 bradyrhizob	209	7	1.0	355	8	Q9TE93	Q9te93 carabus bla
137	241	16	Q8FRK8	Q8frk8 corynebacte	210	7	1.0	355	8	Q9MR80	Q9mr80 carabus por
138	244	10	Q7X990	Q7x990 oryza sativ	211	7	1.0	355	8	Q9TB99	Q9tb99 carabus bla
139	247	16	Q8XG07	Q8xg07 escherichia	212	7	1.0	355	8	Q9GBN2	Q9gbn2 carabus nan
140	247	16	Q8FCQ3	Q8fcq3 escherichia	213	7	1.0	355	8	Q9TE04	Q9te04 carabus can
141	248	16	Q83PU8	Q83pu8 shigella fl	214	7	1.0	355	8	Q9TEA9	Q9tea9 carabus bla
142	248	10	Q49138	Q49138 arabidopsis	215	7	1.0	355	8	Q9MR79	Q9mr79 carabus por
143	249	11	Q8C1Q8	Q8c1q8 mus musculu	216	7	1.0	355	8	Q9TDY5	Q9tdy5 carabus cya
144	250	10	Q8ZFK6	Q8zfk6 yersinia pe	217	7	1.0	355	8	Q9B9R9	Q9b9r9 carabus lac
145	253	16	Q89UG6	Q89ug6 bradyrhizob	218	7	1.0	355	8	Q37444	Q37444 carabus bla
146	255	3	Q9Y7A9	Q9y7a9 metarhizium	219	7	1.0	355	8	Q9TE86	Q9te86 carabus bla
147	255	12	Q84700	Q84700 pea early b	220	7	1.0	355	8	Q9TE85	Q9te85 carabus bla
148	259	16	Q8HDL2	Q8hdl2 agrobacteri	221	7	1.0	355	8	Q47486	Q47486 carabus sic
149	265	2	Q07812	Q07812 mycobacteri	222	7	1.0	355	8	Q9B9S4	Q9b9s4 carabus kad
150	265	16	Q07181	Q07181 mycobacteri	223	7	1.0	355	8	Q9TEA5	Q9tea5 carabus bla
151	265	16	Q7U190	Q7u190 mycobacteri	224	7	1.0	355	8	Q9M1Z4	Q9m1z4 carabus gen
152	266	12	Q81916	Q81916 biomia trop	225	7	1.0	355	8	Q47484	Q47484 carabus vir
153	266	12	Q9QU80	Q9qu80 ct virus. o	226	7	1.0	355	8	Q9TDY2	Q9tdy2 carabus arr
154	268	5	Q9XY56	Q9xy56 ctenocephal	227	7	1.0	355	8	Q9GBL6	Q9gb16 carabus arl
155	271	4	Q9NPM7	Q9npm7 homo sapien	228	7	1.0	355	8	Q9TEA2	Q9tea2 carabus bla
156	272	2	Q51013	Q51013 neisseria g	229	7	1.0	355	8	Q9TEA0	Q9tea0 carabus bla
157	273	16	Q83DW2	Q83dw2 coxiella bu	230	7	1.0	355	8	Q9TE08	Q9te08 carabus bel
158	278	2	Q84C08	Q84c08 pseudomonas	231	7	1.0	355	8	Q9TDY8	Q9tdy8 carabus con
159	280	16	Q87X78	Q87x78 pseudomonas	232	7	1.0	355	8	Q37443	Q37443 carabus bla
160	281	17	Q8U4H8	Q8u4h8 pyrococcus	233	7	1.0	355	8	Q37447	Q37447 carabus bla
161	282	12	Q8UXE9	Q8uxe9 rosellinia	234	7	1.0	355	8	Q78724	Q78724 carabus bla
162	284	5	Q96089	Q96089 haemaphysal	235	7	1.0	355	8	Q9TEA7	Q9tea7 carabus bla



236	1.0	355	8	09GBL0	09gb10 carabus ale	309	7	1.0	355	8	09TE10	09te10 carabus gcl
237	1.0	355	8	09B9S1	09b9s1 carabus aen	310	7	1.0	355	8	09GBK5	09gbk5 carabus con
238	1.0	355	8	09TDY0	09tdy0 carabus cle	311	7	1.0	355	8	09BDY9	09bdy9 carabus con
239	1.0	355	8	09B9S3	09b9s3 carabus lin	312	7	1.0	355	8	09TDY5	09tdy5 carabus bla
240	1.0	355	8	09GBK6	09gbk6 carabus gly	313	7	1.0	355	8	09B9R7	09b9r7 carabus bal
241	1.0	355	8	09GBL8	09gb18 carabus cra	314	7	1.0	355	8	09TE89	09te89 carabus bla
242	1.0	355	8	09TEA6	09tea6 carabus tra	315	7	1.0	355	8	09TE13	09te13 carabus sem
243	1.0	355	8	09TDY1	09tdy1 carabus lrl	316	7	1.0	355	8	09TE45	09te45 carabus por
244	1.0	355	8	09TDY7	09tdy7 carabus tuk	317	7	1.0	355	8	09G0S4	09g0s4 carabus por
245	1.0	355	8	09TEB4	09teb4 carabus bla	318	7	1.0	355	8	09MTZ3	09mtz3 carabus geh
246	1.0	355	8	09TEB4	09teb4 carabus bor	319	7	1.0	355	8	09GBN1	09gbn1 carabus ema
247	1.0	355	8	09TEB1	09teb1 carabus bor	320	7	1.0	355	8	09GBL4	09gb14 carabus pot
248	1.0	355	8	09TEB1	09teb1 carabus bor	321	7	1.0	355	8	09TEB0	09teb0 carabus bla
249	1.0	355	8	09TEB1	09teb1 carabus bor	322	7	1.0	355	8	09MR78	09mr78 carabus por
250	1.0	355	8	09GBL2	09gb12 carabus hae	323	7	1.0	355	8	09GBM3	09gbm3 carabus ign
251	1.0	355	8	09TEB9	09teb9 carabus bel	324	7	1.0	355	8	09GBM8	09gbm8 carabus hum
252	1.0	355	8	09GBL5	09gb15 carabus ari	325	7	1.0	355	8	09GBK7	09gbk7 carabus gly
253	1.0	355	8	09MR77	09mr77 carabus por	326	7	1.0	355	8	09GBL9	09gb19 carabus gra
254	1.0	355	8	09MR76	09mr76 carabus por	327	7	1.0	355	8	09TEB1	09teb1 carabus sel
255	1.0	355	8	09TDY6	09tdy6 carabus tou	328	7	1.0	355	8	09TEB7	09teb7 carabus bla
256	1.0	355	8	09TEB6	09teb6 carabus bla	329	7	1.0	355	8	09TE95	09te95 carabus bla
257	1.0	355	8	09B9M0	09b9m0 carabus hum	330	7	1.0	355	8	09MT07	09mt07 carabus van
258	1.0	355	8	09TEB2	09teb2 carabus bla	331	7	1.0	355	8	09MR81	09mr81 carabus por
259	1.0	355	8	09TEB2	09teb2 carabus bla	332	7	1.0	355	8	09B9R8	09b9r8 carabus str
260	1.0	355	8	09GBM0	09gbm0 carabus uen	333	7	1.0	355	8	09B9R8	09b9r8 carabus bla
261	1.0	355	8	09TEA8	09tea8 carabus bla	334	7	1.0	355	8	09GBK9	09gbk9 carabus ale
262	1.0	355	8	09TEA8	09tea8 carabus bla	335	7	1.0	355	8	09B9S6	09b9s6 carabus str
263	1.0	355	8	09GBM5	09gbm5 carabus oia	336	7	1.0	355	8	09TEB3	09teb3 carabus bla
264	1.0	355	8	09GBL7	09gb17 carabus exl	337	7	1.0	355	8	09GBM4	09gbm4 carabus mir
265	1.0	355	8	09B101	09b101 carabus lep	338	7	1.0	355	8	09TE12	09te12 carabus sem
266	1.0	355	8	09GBM2	09gbm2 carabus bra	339	7	1.0	355	8	09TE91	09te91 carabus bla
267	1.0	355	8	09TEA9	09tea9 carabus bla	340	7	1.0	355	8	09TE95	09te95 carabus tit
268	1.0	355	8	09TDY4	09tdy4 carabus lao	341	7	1.0	355	8	09TE97	09te97 carabus bla
269	1.0	355	8	09TEA8	09tea8 carabus gen	342	7	1.0	355	8	09GBM6	09gbm6 carabus oia
270	1.0	355	8	09TEA8	09tea8 carabus gen	343	7	1.0	355	8	09TEB3	09teb3 carabus bla
271	1.0	355	8	09TEA8	09tea8 carabus gen	344	7	1.0	355	8	09TEA4	09tea4 carabus bla
272	1.0	355	8	09TEA8	09tea8 carabus gen	345	7	1.0	355	8	09TEA4	09tea4 carabus bla
273	1.0	355	8	09TEA8	09tea8 carabus gen	346	7	1.0	355	8	09TEA4	09tea4 carabus bla
274	1.0	355	8	09TEA8	09tea8 carabus gen	347	7	1.0	355	8	09TEA4	09tea4 carabus bla
275	1.0	355	8	09TEA8	09tea8 carabus gen	348	7	1.0	355	8	09TEA4	09tea4 carabus bla
276	1.0	355	8	09TEA8	09tea8 carabus gen	349	7	1.0	355	8	09TEA4	09tea4 carabus bla
277	1.0	355	8	09TEA8	09tea8 carabus gen	350	7	1.0	355	8	09TEA4	09tea4 carabus bla
278	1.0	355	8	09TEA8	09tea8 carabus gen	351	7	1.0	355	8	09TEA4	09tea4 carabus bla
279	1.0	355	8	09TEA8	09tea8 carabus gen	352	7	1.0	355	8	09TEA4	09tea4 carabus bla
280	1.0	355	8	09TEA8	09tea8 carabus gen	353	7	1.0	355	8	09TEA4	09tea4 carabus bla
281	1.0	355	8	09TEA8	09tea8 carabus gen	354	7	1.0	355	8	09TEA4	09tea4 carabus bla
282	1.0	355	8	09TEA8	09tea8 carabus gen	355	7	1.0	355	8	09TEA4	09tea4 carabus bla
283	1.0	355	8	09TEA8	09tea8 carabus gen	356	7	1.0	355	8	09TEA4	09tea4 carabus bla
284	1.0	355	8	09TEA8	09tea8 carabus gen	357	7	1.0	355	8	09TEA4	09tea4 carabus bla
285	1.0	355	8	09TEA8	09tea8 carabus gen	358	7	1.0	355	8	09TEA4	09tea4 carabus bla
286	1.0	355	8	09TEA8	09tea8 carabus gen	359	7	1.0	355	8	09TEA4	09tea4 carabus bla
287	1.0	355	8	09TEA8	09tea8 carabus gen	360	7	1.0	355	8	09TEA4	09tea4 carabus bla
288	1.0	355	8	09TEA8	09tea8 carabus gen	361	7	1.0	355	8	09TEA4	09tea4 carabus bla
289	1.0	355	8	09TEA8	09tea8 carabus gen	362	7	1.0	355	8	09TEA4	09tea4 carabus bla
290	1.0	355	8	09TEA8	09tea8 carabus gen	363	7	1.0	355	8	09TEA4	09tea4 carabus bla
291	1.0	355	8	09TEA8	09tea8 carabus gen	364	7	1.0	355	8	09TEA4	09tea4 carabus bla
292	1.0	355	8	09TEA8	09tea8 carabus gen	365	7	1.0	355	8	09TEA4	09tea4 carabus bla
293	1.0	355	8	09TEA8	09tea8 carabus gen	366	7	1.0	355	8	09TEA4	09tea4 carabus bla
294	1.0	355	8	09TEA8	09tea8 carabus gen	367	7	1.0	355	8	09TEA4	09tea4 carabus bla
295	1.0	355	8	09TEA8	09tea8 carabus gen	368	7	1.0	355	8	09TEA4	09tea4 carabus bla
296	1.0	355	8	09TEA8	09tea8 carabus gen	369	7	1.0	355	8	09TEA4	09tea4 carabus bla
297	1.0	355	8	09TEA8	09tea8 carabus gen	370	7	1.0	355	8	09TEA4	09tea4 carabus bla
298	1.0	355	8	09TEA8	09tea8 carabus gen	371	7	1.0	355	8	09TEA4	09tea4 carabus bla
299	1.0	355	8	09TEA8	09tea8 carabus gen	372	7	1.0	355	8	09TEA4	09tea4 carabus bla
300	1.0	355	8	09TEA8	09tea8 carabus gen	373	7	1.0	355	8	09TEA4	09tea4 carabus bla
301	1.0	355	8	09TEA8	09tea8 carabus gen	374	7	1.0	355	8	09TEA4	09tea4 carabus bla
302	1.0	355	8	09TEA8	09tea8 carabus gen	375	7	1.0	355	8	09TEA4	09tea4 carabus bla
303	1.0	355	8	09TEA8	09tea8 carabus gen	376	7	1.0	355	8	09TEA4	09tea4 carabus bla
304	1.0	355	8	09TEA8	09tea8 carabus gen	377	7	1.0	355	8	09TEA4	09tea4 carabus bla
305	1.0	355	8	09TEA8	09tea8 carabus gen	378	7	1.0	355	8	09TEA4	09tea4 carabus bla
306	1.0	355	8	09TEA8	09tea8 carabus gen	379	7	1.0	355	8	09TEA4	09tea4 carabus bla
307	1.0	355	8	09TEA8	09tea8 carabus gen	380	7	1.0	355	8	09TEA4	09tea4 carabus bla
308	1.0	355	8	09TEA8	09tea8 carabus gen	381	7	1.0	355	8	09TEA4	09tea4 carabus bla

382	7	1.0	355	8	085G10	085G10 carabus tor	455	7	1.0	413	17	029192	029192 archaeoglob
383	7	1.0	355	8	085G19	085G19 carabus tor	456	7	1.0	416	16	088RT5	088RT5 pseudomonas
384	7	1.0	355	8	085G17	085G17 carabus tor	457	7	1.0	416	13	078T79	078T79 actinomyces
385	7	1.0	355	8	085G18	085G18 carabus tor	458	7	1.0	437	2	051640	051640 burkholderia
386	7	1.0	355	8	085G16	085G16 carabus tor	459	7	1.0	437	16	07UDY7	07UDY7 rhodospirillum
387	7	1.0	355	8	085G15	085G15 carabus tor	460	7	1.0	437	16	091Y67	091Y67 arabidopsis
388	7	1.0	355	8	085G12	085G12 carabus tor	461	7	1.0	442	13	0804X1	0804X1 fugu rubrip
389	7	1.0	355	8	085G10	085G10 carabus tor	462	7	1.0	447	11	08TA85	08TA85 homo sapien
390	7	1.0	355	8	085G10	085G10 carabus tor	463	7	1.0	449	11	08BIT8	08BIT8 mus musculu
391	7	1.0	355	8	085G19	085G19 carabus tor	464	7	1.0	453	16	08P1B8	08P1B8 xanthomonas
392	7	1.0	355	8	085G18	085G18 carabus tor	465	7	1.0	453	16	08P704	08P704 xanthomonas
393	7	1.0	355	8	085G17	085G17 carabus tor	466	7	1.0	459	10	063349	063349 brassica na
394	7	1.0	355	8	085G16	085G16 carabus tor	467	7	1.0	461	16	006380	006380 mycobacteri
395	7	1.0	355	8	085G15	085G15 carabus tor	468	7	1.0	461	16	07TM31	07TM31 mycobacteri
396	7	1.0	355	8	085G14	085G14 carabus tor	469	7	1.0	463	10	08M671	08M671 homo sapien
397	7	1.0	355	8	085G13	085G13 carabus tor	470	7	1.0	465	10	08GM44	08GM44 arabidopsis
398	7	1.0	355	8	085G12	085G12 carabus tor	471	7	1.0	465	10	084XL8	084XL8 xerophyta h
399	7	1.0	355	8	085G11	085G11 carabus tor	472	7	1.0	469	10	08LEG9	08LEG9 arabidopsis
400	7	1.0	355	8	085G10	085G10 carabus tor	473	7	1.0	469	16	081NL2	081NL2 bacillus an
401	7	1.0	355	8	085G09	085G09 carabus tor	474	7	1.0	472	5	096657	096657 caenorhabdi
402	7	1.0	355	8	085G08	085G08 carabus tor	475	7	1.0	476	16	081B16	081B16 bacillus ce
403	7	1.0	355	8	085G07	085G07 carabus tor	476	7	1.0	479	16	099RL5	099RL5 utaphylloc
404	7	1.0	355	8	085G06	085G06 carabus tor	477	7	1.0	483	16	089BC3	089BC3 bradyrhizob
405	7	1.0	355	8	085G05	085G05 carabus tor	478	7	1.0	487	16	08ET76	08ET76 oceanobacil
406	7	1.0	355	8	085G04	085G04 carabus tor	479	7	1.0	489	12	091Q01	091Q01 soybean dwa
407	7	1.0	355	8	085G03	085G03 carabus tor	480	7	1.0	490	16	07VH13	07VH13 helicobacte
408	7	1.0	355	8	085G02	085G02 carabus tor	481	7	1.0	492	5	046659	046659 caenorhabdi
409	7	1.0	355	8	085G01	085G01 carabus tor	482	7	1.0	492	16	088Z15	088Z15 lactobacilli
410	7	1.0	355	8	085G00	085G00 carabus tor	483	7	1.0	493	13	090XP7	090XP7 brachydanio
411	7	1.0	355	8	085G00	085G00 carabus tor	484	7	1.0	493	17	0972W0	0972W0 eulfolobus
412	7	1.0	355	8	085G00	085G00 carabus tor	485	7	1.0	494	11	09ER20	09ER20 mus musculu
413	7	1.0	355	8	085G00	085G00 carabus tor	486	7	1.0	494	11	091X69	091X69 mus musculu
414	7	1.0	355	8	085G00	085G00 carabus tor	487	7	1.0	494	11	08VDV0	08VDV0 mus musculu
415	7	1.0	355	8	085G00	085G00 carabus tor	488	7	1.0	494	11	08BMS0	08BMS0 mus musculu
416	7	1.0	355	8	085G00	085G00 carabus tor	489	7	1.0	497	2	054706	054706 streptococ
417	7	1.0	355	8	085G00	085G00 carabus tor	490	7	1.0	497	16	054749	054749 streptococ
418	7	1.0	355	8	085G00	085G00 carabus tor	491	7	1.0	497	16	051503	051503 botryella bu
419	7	1.0	355	8	085G00	085G00 carabus tor	492	7	1.0	497	16	09A1S4	09A1S4 streptococ
420	7	1.0	355	8	085G00	085G00 carabus tor	493	7	1.0	501	5	09NDP6	09NDP6 riftia pach
421	7	1.0	355	8	085G00	085G00 carabus tor	494	7	1.0	505	8	09SEA3	09SEA3 gymnocalyet
422	7	1.0	355	8	085G00	085G00 carabus tor	495	7	1.0	507	8	094P31	094P31 haagocetereu
423	7	1.0	355	8	085G00	085G00 carabus tor	496	7	1.0	507	8	095E88	095E88 eriohyce eu
424	7	1.0	355	8	085G00	085G00 carabus tor	497	7	1.0	507	8	095E84	095E84 brownlingia
425	7	1.0	355	8	085G00	085G00 carabus tor	498	7	1.0	507	8	095E88	095E88 poreklopora
426	7	1.0	355	8	085G00	085G00 carabus tor	499	7	1.0	507	8	095E96	095E96 matucana in
427	7	1.0	355	8	085G00	085G00 carabus tor	500	7	1.0	507	8	095E89	095E89 eriohyce is
428	7	1.0	355	8	085G00	085G00 carabus tor	501	7	1.0	507	8	095E90	095E90 eriohyce is
429	7	1.0	355	8	085G00	085G00 carabus tor	502	7	1.0	507	8	095E91	095E91 eriohyce is
430	7	1.0	355	8	085G00	085G00 carabus tor	503	7	1.0	507	8	095E92	095E92 eriohyce is
431	7	1.0	355	8	085G00	085G00 carabus tor	504	7	1.0	507	8	095E93	095E93 eriohyce is
432	7	1.0	355	8	085G00	085G00 carabus tor	505	7	1.0	507	8	095E94	095E94 eriohyce is
433	7	1.0	355	8	085G00	085G00 carabus tor	506	7	1.0	507	8	095E95	095E95 eriohyce is
434	7	1.0	355	8	085G00	085G00 carabus tor	507	7	1.0	507	8	095E96	095E96 eriohyce is
435	7	1.0	355	8	085G00	085G00 carabus tor	508	7	1.0	507	8	095E97	095E97 eriohyce is
436	7	1.0	355	8	085G00	085G00 carabus tor	509	7	1.0	507	8	095E98	095E98 eriohyce is
437	7	1.0	355	8	085G00	085G00 carabus tor	510	7	1.0	507	8	095E99	095E99 eriohyce is
438	7	1.0	355	8	085G00	085G00 carabus tor	511	7	1.0	507	8	095E90	095E90 eriohyce is
439	7	1.0	355	8	085G00	085G00 carabus tor	512	7	1.0	507	8	095E91	095E91 eriohyce is
440	7	1.0	355	8	085G00	085G00 carabus tor	513	7	1.0	507	8	095E92	095E92 eriohyce is
441	7	1.0	355	8	085G00	085G00 carabus tor	514	7	1.0	508	2	093SM9	093SM9 eriohyce is
442	7	1.0	355	8	085G00	085G00 carabus tor	515	7	1.0	508	8	095E93	095E93 eriohyce is
443	7	1.0	355	8	085G00	085G00 carabus tor	516	7	1.0	509	8	095E94	095E94 eriohyce is
444	7	1.0	355	8	085G00	085G00 carabus tor	517	7	1.0	509	8	095E95	095E95 eriohyce is
445	7	1.0	355	8	085G00	085G00 carabus tor	518	7	1.0	509	8	095E96	095E96 eriohyce is
446	7	1.0	355	8	085G00	085G00 carabus tor	519	7	1.0	509	8	095E97	095E97 eriohyce is
447	7	1.0	355	8	085G00	085G00 carabus tor	520	7	1.0	509	8	095E98	095E98 eriohyce is
448	7	1.0	355	8	085G00	085G00 carabus tor	521	7	1.0	509	8	095E99	095E99 eriohyce is
449	7	1.0	355	8	085G00	085G00 carabus tor	522	7	1.0	509	8	095E90	095E90 eriohyce is
450	7	1.0	355	8	085G00	085G00 carabus tor	523	7	1.0	509	8	095E91	095E91 eriohyce is
451	7	1.0	355	8	085G00	085G00 carabus tor	524	7	1.0	509	8	095E92	095E92 eriohyce is
452	7	1.0	355	8	085G00	085G00 carabus tor	525	7	1.0	509	8	095E93	095E93 eriohyce is
453	7	1.0	355	8	085G00	085G00 carabus tor	526	7	1.0	509	8	095E94	095E94 eriohyce is
454	7	1.0	355	8	085G00	085G00 carabus tor	527	7	1.0	509	8	095E95	095E95 eriohyce is

528	7	1.0	509	8	095B91	095e91 parodia oct	601	7	1.0	708	2	087239	087239 laccococcus
529	7	1.0	509	8	095B83	095e83 leptemium c	602	7	1.0	735	13	057381	057381 xenopus lae
530	7	1.0	509	8	095ED4	095e04 biosfeldia	603	7	1.0	746	16	097R74	097R74 streptococ
531	7	1.0	509	8	095EE0	095e00 austrocylia	604	7	1.0	749	13	097G88	097G88 oncothymu
532	7	1.0	509	8	095EC1	095e01 leptococcus	605	7	1.0	754	10	049144	049144 arabiopsis
533	7	1.0	509	8	095E85	095e85 rhippallia f	606	7	1.0	765	16	08XY74	08XY74 talstonia s
534	7	1.0	509	8	095EB1	095e01 echinocoreu	607	7	1.0	783	13	086LL3	086LL3 giardia lam
535	7	1.0	509	8	095ED3	095e03 frailea gra	608	7	1.0	783	12	09EJ26	09EJ26 cercoplithec
536	7	1.0	509	8	095EB8	095e08 austrocactu	609	7	1.0	787	5	09NFK1	09NFK1 drosophila
537	7	1.0	509	8	095EC2	095e02 amatocoreu	610	7	1.0	790	4	08N5Z2	08N5Z2 homo sapien
538	7	1.0	509	8	095EB9	095e09 neoraimondi	611	7	1.0	791	10	049139	049139 arabiopsis
539	7	1.0	509	8	095EA7	095e07 seelencereu	612	7	1.0	791	10	050073	050073 arabiopsis
540	7	1.0	509	8	095EB3	095e03 pfeiffera m	613	7	1.0	791	10	049137	049137 arabiopsis
541	7	1.0	509	8	095EB2	095e02 pereskia st	614	7	1.0	799	16	08NSU9	08NSU9 corynebacte
542	7	1.0	509	8	095EB6	095e06 corryocactu	615	7	1.0	805	5	09SRK7	09SRK7 drosophila
543	7	1.0	509	8	095EB3	095e03 pereskia gu	616	7	1.0	805	16	081WV6	081WV6 bacillus an
544	7	1.0	509	8	095EB4	095e04 talinum pan	617	7	1.0	806	16	081A60	081A60 bacillus co
545	7	1.0	509	8	095E92	095e92 parodia mic	618	7	1.0	808	10	0987D1	0987D1 arabiopsis
546	7	1.0	509	8	095ED1	095e01 echinocactu	619	7	1.0	826	10	09T041	09T041 arabiopsis
547	7	1.0	509	8	095EA6	095e06 discococcus	620	7	1.0	826	17	08TQX6	08TQX6 methanobarc
548	7	1.0	509	8	095ED2	095e02 frailea pha	621	7	1.0	826	17	08PUP4	08PUP4 methanobarc
549	7	1.0	509	8	095EA8	095e08 hylocereus	622	7	1.0	842	10	09LS88	09LS88 arabiopsis
550	7	1.0	524	13	07SKX8	07skx8 brachydantio	623	7	1.0	867	5	021186	021186 caenorhabdi
551	7	1.0	526	4	094900	094900 homo sapien	624	7	1.0	869	5	081G55	081G55 caenorhabdi
552	7	1.0	526	4	096AV5	096av5 homo sapien	625	7	1.0	873	2	09S024	09S024 escherichia
553	7	1.0	527	16	09P606	09p606 xanthomonas	626	7	1.0	917	5	09VAB8	09VAB8 drosophila
554	7	1.0	529	5	097403	097403 caenorhabdi	627	7	1.0	921	5	09VJ29	09VJ29 drosophila
555	7	1.0	532	17	09YDB4	09yde4 aeropyrum p	628	7	1.0	921	6	09BDU0	09BDU0 dendrocyrax
556	7	1.0	533	2	09B147	09b147 caenorhabdi	629	7	1.0	950	10	08RZX0	08RZX0 oryza sativ
557	7	1.0	535	2	09JP77	09jp77 thermomonos	630	7	1.0	961	5	08SVH3	08SVH3 oncocephalito
558	7	1.0	540	2	09X2V0	09x2v0 agrobacteri	631	7	1.0	970	10	09AYF2	09AYF2 oryza sativ
559	7	1.0	541	16	08RFL3	08rf13 fusobacteri	632	7	1.0	970	10	07XEP23	07XEP23 oryza sativ
560	7	1.0	541	16	07WPA4	07wpa4 bordetella	633	7	1.0	977	13	091925	091925 xenopus lae
561	7	1.0	544	12	08TFN9	08tfn9 emerticella	634	7	1.0	980	5	022088	022088 caenorhabdi
562	7	1.0	549	12	09DW53	09dw53 rat cytoleg	635	7	1.0	991	4	08TDH1	08TDH1 homo sapien
563	7	1.0	553	16	097810	097810 streptococ	636	7	1.0	1007	13	08U128	08U128 xenopus lae
564	7	1.0	553	16	08DOR3	08dgr3 streptococ	637	7	1.0	1031	16	08G5X2	08G5X2 bifidobacte
565	7	1.0	556	11	09CVK0	09cvk0 mus musculu	638	7	1.0	1047	10	09FKM9	09FKM9 arabiopsis
566	7	1.0	560	10	049141	049141 arabiopsis	639	7	1.0	1048	5	09NAV1	09NAV1 caenorhabdi
567	7	1.0	560	10	050057	050057 arabiopsis	640	7	1.0	1074	16	083125	083125 antrococtu
568	7	1.0	561	16	09RXX1	09rx1 delinococcus	641	7	1.0	1081	11	08BZ19	08BZ19 mus musculu
569	7	1.0	561	16	09KYS9	09kys9 streptomyce	642	7	1.0	1100	4	08BDH1	08BDH1 homo sapien
570	7	1.0	568	16	088W64	088w64 lactobacilli	643	7	1.0	1111	9	08S5Z2	08S5Z2 mycobacteri
571	7	1.0	580	10	09ZOP6	09zop6 arabiopsis	644	7	1.0	1120	16	08FP97	08FP97 corynebacte
572	7	1.0	581	10	09LKH1	09lkh1 mesembryant	645	7	1.0	1136	5	08IDJ8	08IDJ8 plasmodium
573	7	1.0	581	16	08D7C1	08d7c1 vibrio vuln	646	7	1.0	1240	5	08T6Z7	08T6Z7 drosophila
574	7	1.0	582	10	023492	023492 arabiopsis	647	7	1.0	1240	5	08T6Z6	08T6Z6 drosophila
575	7	1.0	584	10	09SQZ0	09sqz0 arabiopsis	648	7	1.0	1240	5	09W084	09W084 arabiopsis
576	7	1.0	585	5	017491	017491 caenorhabdi	649	7	1.0	1243	11	065468	065468 arabiopsis
577	7	1.0	585	5	08SZY4	08szv4 drosophila	650	7	1.0	1243	11	035954	035954 mus musculu
578	7	1.0	600	16	093GX8	093gx8 streptomyce	651	7	1.0	1300	3	08XOV5	08XOV5 neurospora
579	7	1.0	606	10	07XSS0	07xss0 oryza sativ	652	7	1.0	1340	5	09GWA4	09GWA4 anophelo g
580	7	1.0	608	6	09GMB0	09gmb0 bus scrota	653	7	1.0	1346	2	09ZG12	09ZG12 streptomyco
581	7	1.0	612	13	0804W7	0804w7 fugu rubrip	654	7	1.0	1544	3	086ZB3	086ZB3 botrytis ci
582	7	1.0	613	11	080VE0	080ve0 mus musculu	655	7	1.0	1568	5	09FHD0	09FHD0 arabiopsis
583	7	1.0	617	17	097UG5	097ug5 sulfolobus	656	7	1.0	1609	5	095VA5	095VA5 drosophila
584	7	1.0	618	11	P704Z3	P704z3 mus musculu	657	7	1.0	1631	16	08DZ37	08DZ37 streptococ
585	7	1.0	620	10	038940	038940 arabiopsis	658	7	1.0	1640	3	086Z91	086Z91 gibberolla
586	7	1.0	622	4	07Z7P3	07z7p3 homo sapien	659	7	1.0	1660	10	0947Z9	0947Z9 oryza sativ
587	7	1.0	624	10	094CF4	094cf4 arabiopsis	660	7	1.0	1660	10	07XFK3	07XFK3 oryza sativ
588	7	1.0	629	16	087VG1	087vg1 pseudomonas	661	7	1.0	1666	10	08LP68	08LP68 chlamydomon
589	7	1.0	633	13	090Z56	090z56 scopthalamu	662	7	1.0	1768	5	09N8K7	09N8K7 trypanosoma
590	7	1.0	633	13	09NKKD7	09nkd7 drosophila	663	7	1.0	1831	4	086T77	086T77 homo sapien
591	7	1.0	658	10	065466	065466 arabiopsis	664	7	1.0	1863	4	081VX2	081VX2 homo sapien
592	7	1.0	663	17	08U2H8	08u2h8 pyrococcus	665	7	1.0	1865	4	07Z401	07Z401 homo sapien
593	7	1.0	674	10	09C3S9	09c3s9 arabiopsis	666	7	1.0	1877	5	09XW1	09XW1 plasmodium
594	7	1.0	678	16	09A4E2	09a4e2 caulobacter	667	7	1.0	1903	5	09UON7	09UON7 plasmodium
595	7	1.0	680	10	08GXL8	08gx18 arabiopsis	668	7	1.0	1952	5	095SN5	095SN5 drosophila
596	7	1.0	682	16	08EMF4	08emf4 mycoplasma	669	7	1.0	1966	5	09NHX6	09NHX6 drosophila
597	7	1.0	683	5	09VIE8	09vie8 drosophila	670	7	1.0	1966	5	081QA6	081QA6 drosophila
598	7	1.0	684	10	080709	080709 arabiopsis	671	7	1.0	1968	3	08XOC5	08XOC5 neurospora
599	7	1.0	700	16	08ECU0	08ecu0 thewanelia	672	7	1.0	1985	3	09VSK5	09VSK5 drosophila
600	7	1.0	703	16	08R917	08r917 thermomater	673	7	1.0	1985	5	08T9N4	08T9N4 drosophila

674	7	1.0	1988	5	Q86BH2	Q86bh2 drosophila
675	7	1.0	2393	5	Q81461	Q81461 plasmodium
676	7	1.0	2605	2	Q50858	Q50858 myxococcus
677	7	1.0	2906	11	Q9WUH9	Q9Wuh9 rictus notv
678	7	1.0	3306	10	Q9FT44	Q9ft44 arabidopsis
679	7	1.0	3446	5	Q86AC8	Q86ac8 dicycostell
680	7	1.0	3564	11	Q923L3	Q923l3 mus musculu
681	7	1.0	3972	16	Q9S0R8	Q9s0r8 streptomyce
682	7	1.0	4567	5	Q9W433	Q9w433 drosophila
683	7	1.0	4899	5	Q9VR91	Q9vr91 drosophila
684	6	0.8	33	12	Q8B9R9	Q8b9r9 emilliania h
685	6	0.8	33	12	Q8B9R8	Q8b9r8 emilliania h
686	6	0.8	33	12	Q8B9R7	Q8b9r7 emilliania h
687	6	0.8	33	12	Q8B9R6	Q8b9r6 emilliania h
688	6	0.8	33	12	Q8B9R5	Q8b9r5 emilliania h
689	6	0.8	33	12	Q8B9R4	Q8b9r4 emilliania h
690	6	0.8	33	12	Q8B9R3	Q8b9r3 emilliania h
691	6	0.8	33	12	Q8B9R2	Q8b9r2 emilliania h
692	6	0.8	33	16	Q8FZEO	Q8fzeo bruceella su
693	6	0.8	35	16	Q9KSL5	Q9ksl5 vibrio chol
694	6	0.8	36	3	Q96W36	Q96w36 ophiostoma
695	6	0.8	37	15	Q9DRP2	Q9drp2 human immun
696	6	0.8	38	16	Q7W966	Q7w966 haemophilus
697	6	0.8	39	6	Q29360	Q29360 sus scrofa
698	6	0.8	40	2	Q9R4D0	Q9r4d0 thermus aqu
699	6	0.8	40	15	Q8UM87	Q8um87 human immun
700	6	0.8	40	15	Q8USM4	Q8usm4 human immun

## ALIGNMENTS

RESULT 1  
Q96JW2 PRELIMINARY; PRT; 737 AA.

AC Q96JW2; 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein FLJ1935.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placental;  
 RA Isegal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Shiraori A., Sudo H.,  
 RA Magatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takahashi M., Chiba Y., Ichida S., Murakawa K., Ono Y., Takiguchi S.,  
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Maehiro Y.,  
 RA Niimura Y., Iwayanagi T.,  
 RT "MEDO human cDNA sequencing project."  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
 DR EMBL; AK027841; BAB55404.1; -  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000859; CUB.  
 DR InterPro; IPR009003; Cys\_ser\_trypsin.  
 DR InterPro; IPR007424; EGF\_2.  
 DR InterPro; IPR006209; EGF\_1like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR001254; Peptidase S1.  
 DR InterPro; IPR001314; Peptidase S1A.  
 DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
 DR Pfam; PF00431; CUB; 1.  
 DR Pfam; PF00008; EGF; 1.

DR Pfam; PF00084; sushi; 2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYOTRYP SIN.  
 DR SMART; SM00032; CCP; 2.  
 DR SMART; SM00042; CUB; 1.  
 DR SMART; SM00181; EGF; 2.  
 DR SMART; SM00020; TRYP\_SPC; 1.  
 DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS00022; EGF\_2; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS0240; TRYPSIN\_DOM; 1.  
 DR Hypothetical protein; EGF-like domain; Hydrolase; Protease;  
 KW Serine protease.  
 SQ SEQUENCE 737 AA; 81952 MW; 4F51689C5EB32B44 CRC64;

Query Match 61.9%; Score 446; DB 4; Length 737;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

275 LERRNCSDPGPVNGYOKITGPGGLINGRAKIGTVVAFPCNNSYVLSGNERKTCQNGE 334  
 292 LERRNCSDPGPVNGYOKITGPGGLINGRAKIGTVVAFPCNNSYVLSGNERKTCQNGE 351  
 335 WSGKOPICIKACREPKISDLYRRVLPVQVQSETPHLQLYSAFSGKQLGAPTKKPL 394  
 352 WSGKOPICIKACREPKISDLYRRVLPVQVQSETPHLQLYSAFSGKQLGAPTKKPL 411  
 395 PRGDLPMGVQHTLQLOVYECISPFYRLGSSRRCTLRGKSGRAPSCPIGKLENTA 454  
 412 PRGDLPMGVQHTLQLOVYECISPFYRLGSSRRCTLRGKSGRAPSCPIGKLENTA 471  
 455 PRTGGLRMPQOAIYRRTSGVADGSLHKGAFLVCSGALNERTVVAACHVTDLGKVTM 514  
 472 PRTGGLRMPQOAIYRRTSGVADGSLHKGAFLVCSGALNERTVVAACHVTDLGKVTM 531  
 515 IKTADLKVLGKFRYRDDDEKTIQSLQISAILHPNVDPILLDDIALIKLIDKARIST 574  
 532 IKTADLKVLGKFRYRDDDEKTIQSLQISAILHPNVDPILLDDIALIKLIDKARIST 591  
 575 RYQPTCLASRLSTSFQSHITVAGWNLADVRSQFNDLRSGVSVVDLCEEQH 634  
 592 RYQPTCLASRLSTSFQSHITVAGWNLADVRSQFNDLRSGVSVVDLCEEQH 651  
 635 EDHGIPVSTVDNMFCSWEPPTAPSDICTAETGIAVSEFGRAPEPRHMLGLVMSYD 694  
 652 EDHGIPVSTVDNMFCSWEPPTAPSDICTAETGIAVSEFGRAPEPRHMLGLVMSYD 711  
 695 KTCSHRLSTAFKVLPEKWMIRNMK 720  
 712 KTCSHRLSTAFKVLPEKWMIRNMK 737

## RESULT 2

Q9Y432 PRELIMINARY; PRT; 181 AA.  
 AC Q9Y432; 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN DKFZP586H2123.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RA Ansoorge W., Winkner U., Mewes H.W., Gassenhuber J., Wiemann S.,  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL050214; CAB4317.1; -  
 DR FIR; T08805; T08805.  
 DR HSP; P00742; IHCG.

DR MEROPS; S01.998; -  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR009003; Cys\_ser\_trypsin.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 KM Hypothetical protein; Hydrolase; Protease; Serine protease.  
 FT NON\_TER  
 SQ SEQUENCE 181 AA; 19962 MW; ABC793BBE682D439 CRC64;  
 Query Match 24.7%; Score 178; DB 4; Length 181;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-179; Indels 0; Gaps 0;  
 Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 543 ISAILHNYDPIILDADIAIKLIDKARISTRVOPICLAASRDISTSFQESHITVAGWN 602  
 DB 4 ISAILHNYDPIILDADIAIKLIDKARISTRVOPICLAASRDISTSFQESHITVAGWN 63  
 QY 603 VLADVRSGFKNQDTLRSGVSVVDSLCEQEHEDHGIPVSVDNMFCSMEPTASDICT 662  
 DB 64 VLADVRSGFKNQDTLRSGVSVVDSLCEQEHEDHGIPVSVDNMFCSMEPTASDICT 123  
 QY 663 AETGGAIVSPGRASPEPRHLMGLVSWSYDTCGSHRLSTAFKVLPEKDIERNMK 720  
 DB 124 AETGGAIVSPGRASPEPRHLMGLVSWSYDTCGSHRLSTAFKVLPEKDIERNMK 181  
 RESULT 3  
 Q8BU25 PRELIMINARY; PRT; 720 AA.  
 ID Q8BU25  
 AC Q8BU25  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DE Hypothetical EGF-like domain.  
 GN E43002GOSRIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NOJ; TISSUE=Thymus;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573 (2002).  
 DR EMBL; AK088017; BAC40098.1; -  
 DR MGI; MGI:2445082; E430002GOSRIK.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000859; CUB\_Ser\_trypsin.  
 DR InterPro; IPR009003; Cys\_ser\_trypsin.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR000436; Sush1\_SCR\_CCP.  
 DR Pfam; PF00431; CUB; 1.  
 DR Pfam; PF00008; EGF; 1.  
 DR Pfam; PF00084; Sush1; 2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00033; CCP; 2.  
 DR SMART; SM00042; CUB; 1.  
 DR SMART; SM00181; EGF; 2.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 KM Hypothetical protein.  
 SQ SEQUENCE 720 AA; 80300 MW; C098E076D903A5A0 CRC64;  
 Query Match 8.5%; Score 61; DB 11; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-55; Indels 0; Gaps 0;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 74 NECDSCLIHPGCTIFENCKSCRNCSWGGLDDFYVKGFCACRAGMYGSDCMRCGVLR 133  
 DB 74 NECDSCLIHPGCTIFENCKSCRNCSWGGLDDFYVKGFCACRAGMYGSDCMRCGVLR 133  
 QY 134 A 134  
 DB 134 A 134  
 RESULT 4  
 Q8K2B8 PRELIMINARY; PRT; 720 AA.  
 ID Q8K2B8  
 AC Q8K2B8  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Similar to DKFZP566H2123 protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strubeberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
 DR EMBL; BC031841; AAH1841.1; -  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000859; CUB\_Ser\_trypsin.  
 DR InterPro; IPR009003; Cys\_ser\_trypsin.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR000436; Sush1\_SCR\_CCP.  
 DR Pfam; PF00431; CUB; 1.  
 DR Pfam; PF00008; EGF; 1.  
 DR Pfam; PF00084; Sush1; 2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00033; CCP; 2.  
 DR SMART; SM00042; CUB; 2.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 KM EGF-like domain; Hydrolase; Protease; Serine protease.  
 SQ SEQUENCE 720 AA; 80377 MW; 7172B7F1E690FD08 CRC64;  
 Query Match 5.7%; Score 41; DB 11; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-34; Indels 0; Gaps 0;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR SMART; SM00181; EGF; 2.  
 DR SMART; SM00179; EGF\_Ca; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 KM Hypothetical protein.  
 SQ SEQUENCE 720 AA; 80300 MW; C098E076D903A5A0 CRC64;  
 Query Match 8.5%; Score 61; DB 11; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-55; Indels 0; Gaps 0;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 74 NECDSCLIHPGCTIFENCKSCRNCSWGGLDDFYVKGFCACRAGMYGSDCMRCGVLR 133  
 DB 74 NECDSCLIHPGCTIFENCKSCRNCSWGGLDDFYVKGFCACRAGMYGSDCMRCGVLR 133  
 QY 134 A 134  
 DB 134 A 134  
 RESULT 4  
 Q8K2B8 PRELIMINARY; PRT; 720 AA.  
 ID Q8K2B8  
 AC Q8K2B8  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Similar to DKFZP566H2123 protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strubeberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.  
 DR EMBL; BC031841; AAH1841.1; -  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000859; CUB\_Ser\_trypsin.  
 DR InterPro; IPR009003; Cys\_ser\_trypsin.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR000436; Sush1\_SCR\_CCP.  
 DR Pfam; PF00431; CUB; 1.  
 DR Pfam; PF00008; EGF; 1.  
 DR Pfam; PF00084; Sush1; 2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00033; CCP; 2.  
 DR SMART; SM00042; CUB; 2.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 KM EGF-like domain; Hydrolase; Protease; Serine protease.  
 SQ SEQUENCE 720 AA; 80377 MW; 7172B7F1E690FD08 CRC64;  
 Query Match 5.7%; Score 41; DB 11; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-34; Indels 0; Gaps 0;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 FL0LLISLSPREXTVINEACPGAEANINMCRCECEPDIEC 53  
 |||||  
 DB 13 FL0LLISLSPREXTVINEACPGAEANINMCRCECEPDIEC 53

## RESULT 5

O91WZ0 PRELIMINARY; PRT; 222 AA.  
 AC O91WZ0.  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Bone morphogenetic protein 1 (Fragment).  
 GN BMP-1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NC NCB1\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Metar; TISSUE=Embryo;  
 RA Kataoka H., Enomoto K.,  
 RT "Partial CDNA sequence isolated by RT-PCR."  
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.  
 DR EMBL; AB073100; BAB6961.1; -  
 DR GO; GO:0008533; F:astacin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000859; COB.  
 DR InterPro; IPR001506; Peptidase\_M2A.  
 DR Pfam; PF01400; Astacin; 1.  
 DR Pfam; PF00431; CUB; 2.  
 DR SMART; SM00042; CUB; 2.  
 DR PROSITE; PS01180; CUB; 2.  
 FT NON\_TER 1  
 FT NON\_TER 222  
 SQ SEQUENCE 222 AA; 25426 MW; 66A9052DA98BB57A CRC64;

Query Match 1.2%; Score 9; DB 11; Length 222;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 179 YDYVEVRDG 187  
 |||||  
 DB 80 YDYVEVRDG 88

## RESULT 6

ID O86553 PRELIMINARY; PRT; 276 AA.  
 AC O86553;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Putative dehydrogenase.  
 GN SC0619 OR SCIF2.16C.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 NC NCB1\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Seeger K.J., Harris D.,  
 RT Submitted (AUG-1998) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Parthill J., Barrell B.G., Rajandream M.A.,  
 RL Submitted (AUG-1998) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);

RX MEDLINE=97000351; PubMed=8843436;  
 RA Redenbach M., Kleiser H.M., Denaplatte D., Eichner A., Cullum J.,  
 RA Kinashi H., Hopwood D.A.;  
 RT "A set of ordered cosmids and a detailed genetic and physical map for  
 the 8 Mb Streptomyces coelicolor A3(2) chromosome."  
 RL Mol. Microbiol. 21:77-96(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2) / M145;  
 RX MEDLINE=21996410; PubMed=12000953;  
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
 RA Thompson N.R., James K.D., Harris D.E., Quail M.A., Kleiser H.,  
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 RA Huang C.-H., Kleiser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabbittowitch E., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete Streptomyces  
 coelicolor A3(2)."  
 RL Nature 417:141-147(2002).  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 (SDR) FAMILY.  
 DR EMBL; AL939128; CAA20507.1; -  
 DR PIR; T29125; T29125.  
 DR HSP; O64105; IOAA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 DR PRINTS; PR00080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; 1.  
 DR Oxidoreductase; Complete proteome.  
 SQ SEQUENCE 276 AA; 29010 MW; 30F038B70D63C7C CRC64;

Query Match 1.2%; Score 9; DB 16; Length 276;  
 Best Local Similarity 100.0%; Pred. No. 2.4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 670 AVSFPGRAS 678  
 |||||  
 DB 225 AVSFPGRAS 233

## RESULT 7

ID O57658 PRELIMINARY; PRT; 691 AA.  
 AC O57658;  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Bone morphogenetic protein 1 (Fragment).  
 GN BMP1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NC NCB1\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20267865; PubMed=10806368;  
 RA Reynolds S.D., Zhang D., Puzas J.E., O'Keefe R.J., Rosier R.N.,  
 RA Reynolds P.R.;  
 RT "Cloning of the chick BMP1/Tolloid CDNA and expression in skeletal  
 tissues."  
 RL Gene 248:233-243(2000).  
 CC -1- SIMILARITY: CONTAINS 3 CUB DOMAINS.  
 DR EMBL; U75331; AAC02259.1; -  
 DR HSP; P00736; IAPQ.  
 DR MEROPS; M12.005; -  
 DR GO; GO:0008533; F:astacin activity; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO:0008237; F:metallopeptidase activity; IEA.  
 DR GO:0008270; F:zinc ion binding; IEA.  
 DR GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro: IPR00152; Asx\_hydroxyl\_3.  
 DR InterPro: IPR00859; CUB.  
 DR InterPro: IPR01881; EGF\_Ca.  
 DR InterPro: IPR06209; EGF-like.  
 DR InterPro: IPR06026; Peptidase M.  
 DR InterPro: IPR01506; Peptidase M12A.  
 DR InterPro: IPR06025; Pept\_M\_zn\_BS.  
 DR Pfam: PF01400; Ascatin; 1.  
 DR Pfam: PF00431; CUB; 3.  
 DR Pfam: PF00008; EGF; 1.  
 DR PRINTS: PRO0480; ASFCIN.  
 DR SMART: SM00042; CUB; 3.  
 DR SMART: SM00235; ZMec; 1.  
 DR SMART: SM00179; EGF\_CA; 1.  
 DR PROSITE: PS0010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS01180; CUB; 3.  
 DR PROSITE: PS01186; EGF\_2; 1.  
 DR PROSITE: PS01187; EGF\_CA; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 DR EGF-like domain.  
 KW EGF-like domain.  
 FT NON TER 1  
 SQ SEQUENCE 691 AA; 77843 MW; 01245982B8DC8F28 CRC64;

Query Match 1.2%; Score 9; DB 13; Length 691;  
 Best Local Similarity 100.0%; Pred. No. 5.7;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 179 YDYVEVRDQ 187  
 |||||  
 DB 338 YDYVEVRDQ 346

RESULT 8  
 O8QFX6 PRELIMINARY; PRT; 923 AA.  
 AC O8QFX6;  
 DT 01-JUN-2002 (TRENBLrel. 21, Created)  
 DT 01-OCT-2003 (TRENBLrel. 21, Last annotation update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Neurophilin-1.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NC NCB1\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lee P., Goshl K., Davidson A., Mannix R., Zon L., Klagsbrun M.;  
 RT "Neurophilin-1 is required for normal vascular development and is a  
 mediator of VEGF-dependent angiogenesis in zebrafish."  
 RL Submitted (Nov-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE NEUROPHILIN FAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 CUB DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 F5/F8 TYPE C DOMAIN.  
 DR EMBL: AY064213; AAL40862.1; -.  
 DR GO: GO:0016021; C:integral to membrane; IEA.  
 DR GO: GO:0004872; F:receptor activity; IEA.  
 DR GO: GO:0007155; P:cell adhesion; IEA.  
 DR InterPro: IPR000859; CUB.  
 DR InterPro: IPR000421; FAS8\_C.  
 DR InterPro: IPR008979; Gal\_bind\_like.  
 DR InterPro: IPR000998; MAM\_domain.  
 DR Pfam: PF00431; CUB; 2.  
 DR Pfam: PF00754; F5\_F8\_type\_C; 2.  
 DR Pfam: PF00629; MAM; 1.  
 DR SMART: SM00042; CUB; 2.  
 DR SMART: SM00331; MAM; 1.  
 DR SMART: SM00137; MAM; 1.

DR PROSITE: PS01180; CUB; 2.  
 DR PROSITE: PS01285; FAS8C\_1; 1.  
 DR PROSITE: PS01286; FAS8C\_2; 2.  
 DR PROSITE: PS50022; FAS8C\_3; 2.  
 DR PROSITE: PS00740; MAM\_1; 1.  
 DR PROSITE: PS50060; MAM\_2; 1.  
 DR Glycoprotein; Receptor; Transmembrane.  
 KW Glycoprotein; Receptor; Transmembrane.  
 SQ SEQUENCE 923 AA; 102492 MW; 2ED84B129AA92B2D CRC64;

Query Match 1.2%; Score 9; DB 13; Length 923;  
 Best Local Similarity 100.0%; Pred. No. 7.5;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 179 YDYVEVRDQ 187  
 |||||  
 DB 82 YDYVEVRDQ 90

RESULT 9  
 O8AXP1 PRELIMINARY; PRT; 923 AA.  
 ID O8AXP1;  
 AC O8AXP1;  
 DT 01-MAR-2003 (TRENBLrel. 23, Created)  
 DT 01-MAR-2003 (TRENBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Neurophilin-1.  
 GN NP-1.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NC NCB1\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shoji W., Tawarayama H.;  
 RT "The cloning and expression of neurophilin-1."  
 RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AB088776; BAC53657.1; -.  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0007155; P:cell adhesion; IEA.  
 DR InterPro: IPR000859; CUB.  
 DR InterPro: IPR000421; FAS8\_C.  
 DR InterPro: IPR008979; Gal\_bind\_like.  
 DR InterPro: IPR000998; MAM\_domain.  
 DR Pfam: PF00431; CUB; 2.  
 DR Pfam: PF00754; F5\_F8\_type\_C; 2.  
 DR Pfam: PF00629; MAM; 1.  
 DR SMART: SM00042; CUB; 2.  
 DR SMART: SM00231; FAS8C\_2.  
 DR SMART: SM00137; MAM; 1.  
 DR PROSITE: PS01180; CUB; 1.  
 DR PROSITE: PS01285; FAS8C\_1; 1.  
 DR PROSITE: PS01286; FAS8C\_2; 2.  
 DR PROSITE: PS50022; FAS8C\_3; 2.  
 DR PROSITE: PS00740; MAM\_1; 1.  
 DR PROSITE: PS50060; MAM\_2; 1.  
 SQ SEQUENCE 923 AA; 102541 MW; 0E6CE33ED28A21F7 CRC64;

Query Match 1.2%; Score 9; DB 13; Length 923;  
 Best Local Similarity 100.0%; Pred. No. 7.5;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 179 YDYVEVRDQ 187  
 |||||  
 DB 82 YDYVEVRDQ 90

RESULT 10  
 O9UQ00 PRELIMINARY; PRT; 926 AA.  
 ID O9UQ00;  
 AC O9UQ00;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)



DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE Hypothetical protein KIAA0932 (Fragment).  
 GN KIAA0932.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NX NCBI\_TaxID=9606;  
 RL [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=9246063; PubMed=1021032; Kikuno R., Hirose M.,  
 RA Miyagawa T., Ishikawa K., Suyama M., Kishimoto N., Ohara O.,  
 RA Nagajima N., Tanaka A., Koltan H., Nomura N., Ohara O.,  
 RT "Prediction of the coding sequences of unidentified human genes. XIII.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro."  
 RL DNA Ref. 6:63-70(1999).  
 CC -1- SIMILARITY: CONTAINS 5 CUB DOMAINS.  
 DR EMBL; AB023149; BAA76776.1; -.  
 DR HSSP; P00736; IAPQ.  
 DR MEROPS; M12.018; -.  
 DR GO; GO:0008533; F:actin activity; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0008237; F:metalloproteinase activity; IEA.  
 DR GO; GO:0008270; F:zinc ion binding; IEA.  
 DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.  
 DR InterPro: IPR000152; Asx\_hydroxyl\_S.  
 DR InterPro: IPR000859; CUB.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR006209; EGF-like.  
 DR InterPro: IPR006026; Peptidase\_M.  
 DR InterPro: IPR001506; Peptidase\_M12A.  
 DR InterPro: IPR006025; Pept\_M\_Zn\_BS.  
 DR Pfam; PF01400; Astacin; 1.  
 DR Pfam; PF00431; CUB; 5.  
 DR Pfam; PF00008; EGF; 2.  
 DR PRINTS; PR00480; ASTACIN.  
 DR SMART; SM00042; CUB; 5.  
 DR SMART; SM00179; EGF\_CA; 2.  
 DR SMART; SM00235; Zmnc; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 2.  
 DR PROSITE; PS01180; CUB; 5.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 2.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 KM Hypothetical protein; EGF-like domain.  
 FT NON\_TER  
 SQ SEQUENCE 926 AA; 103873 MW; 58FA35CDD10970B CRC64;  
 Query Match 1.2%; Score 9; DB 4; Length 926;  
 Best Local Similarity 100.0%; Pred. No. 7.5;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187  
 DB 317 YDYVEVRDG 325

RESULT 11  
 QY6L7 PRELIMINARY; PRT; 1015 AA.  
 AC QY6L7;  
 DT 01-NOV-1999 (TREMblrel. 12, Created)  
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE Tolloid-like 2 protein.  
 GN TLL2.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NX NCBI\_TaxID=9606;  
 RL [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;  
 RX MEDLINE=99447609; PubMed=10516436;  
 RA Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Eddy R.L.,  
 RA Shows T.B., Greenspan D.S.,  
 RT "Assignment of TLL1 and TLL2, which encode human BMP-1/Tolloid-  
 RT related metalloproteinases, to chromosomes 4q32-q33 and 10q23-q24 and  
 RT assignment of murine Tll2 to chromosome 19."  
 RL Cytogenet. Cell Genet. 86:64-65(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=99410337; PubMed=10479448;  
 RA Scott I.C., Biltz I.L., Pappano W.N., Clark T.G., Steigltz B.M.,  
 RA Thomas C.L., Maas S.A., Takahara K., Cho K.W.Y., Greenspan D.S.,  
 RT "Mammalian BMP-1/Tolloid-related metalloproteinases, including novel  
 RT family member mammalian tollid-like 2, have differential enzymatic  
 RT activities and distributions of expression relevant to patterning and  
 RT skeletogenesis."  
 RL Dev. Biol. 213:283-300(1999).  
 CC -1- SIMILARITY: CONTAINS 5 CUB DOMAINS.  
 DR EMBL; AF059516; AAD4297.1; -.  
 DR HSSP; P00736; IAPQ.  
 DR MEROPS; M12.018; -.  
 DR GO; GO:0008533; F:actin activity; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0008237; F:metalloproteinase activity; IEA.  
 DR GO; GO:0008270; F:zinc ion binding; IEA.  
 DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.  
 DR InterPro: IPR000152; Asx\_hydroxyl\_S.  
 DR InterPro: IPR000859; CUB.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR006209; EGF-like.  
 DR InterPro: IPR006026; Peptidase\_M.  
 DR InterPro: IPR001506; Peptidase\_M12A.  
 DR InterPro: IPR006025; Pept\_M\_Zn\_BS.  
 DR Pfam; PF01400; Astacin; 1.  
 DR Pfam; PF00431; CUB; 5.  
 DR Pfam; PF00008; EGF; 2.  
 DR PRINTS; PR00480; ASTACIN.  
 DR SMART; SM00042; CUB; 5.  
 DR SMART; SM00179; EGF\_CA; 2.  
 DR SMART; SM00235; Zmnc; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 2.  
 DR PROSITE; PS01180; CUB; 5.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 2.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
 KM EGF-like domain.  
 FT NON\_TER  
 SQ SEQUENCE 1015 AA; 113556 MW; 25F5B23065861593 CRC64;  
 Query Match 1.2%; Score 9; DB 4; Length 1015;  
 Best Local Similarity 100.0%; Pred. No. 8.2;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187  
 DB 406 YDYVEVRDG 414

RESULT 12  
 Q23995 PRELIMINARY; PRT; 1464 AA.  
 AC Q23995;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE TOLLID related 1.  
 GN TOK OR TLLR-1 OR CG8683.  
 OS Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.



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OX NCBI_TaxID=7227;
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON S;
RA MEDLINE=95113176; PubMed=7813777;
RA Nguyen T., Jamal J., Shmell M.J., Arora K., O'Connor M.B.;
RT "Characterization of tolloid-related-1: a BMP-1-like product that is
RL required during larval and pupal stages of Drosophila development.";
RL Dev. Biol. 166:569-586(1994).
CC -1 SIMILARITY: CONTAINS 5 CUB DOMAINS.
DR EMBL; U12634; AAA70057.1; -.
DR HSSP; P00736; IAPQ.
DR MEROPS; M12.011; -.
DR FlyBase; FBgn0004885; tok.
DR GO; GO:0008533; F:actinin activity; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0008237; F:metalloproteinase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001506; Peptidase_M12A.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01400; Actacin; 1.
DR Pfam; PF00431; CUB; 5.
DR Pfam; PF00008; EGF; 2.
DR PRINTS; PR00480; ASTACTIN.
DR SMART; SM00042; CUB; 5.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00235; ZmC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01180; CUB; 5.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW EGF-like domain.
SQ SEQUENCE 1464 AA; 165053 MW; 94373260D3862E6 CRC64;

Query Match 1.2%; Score 9; DB 5; Length 1464;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
DB 897 YDYVEVRDG 905

RESULT 13
Q9VC47 PRELIMINARY; PRT; 1464 AA.
AC Q9VC47;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE TOK protein (GH23184P).
GN TOK OR CG6863.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

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RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Aspayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintoy S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Broctler P.,
RA Burkova D., Butcher D., Butler H., Cadieu E., Cantor A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo S., Delcher A., Deng Z., Dey A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Houston K.A., Howland T.J., Wei M.-H., Iodgwan C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Mishina N.V., Mobarry C., Moritz J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhu Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).

[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Aspayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: CONTAINS 5 CUB DOMAINS.
DR EMBL; AE003749; AAF56328.1; -.
DR EMBL; AY051585; AAK93009.1; -.
DR HSSP; P00736; IAPQ.
DR MEROPS; M12.011; -.
DR FlyBase; FBgn0004885; tok.
DR GO; GO:0008533; F:actinin activity; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0008237; F:metalloproteinase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001506; Peptidase_M12A.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01400; Actacin; 1.
DR Pfam; PF00431; CUB; 5.
DR Pfam; PF00008; EGF; 2.
DR PRINTS; PR00480; ASTACTIN.
DR SMART; SM00042; CUB; 5.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00235; ZmC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01180; CUB; 5.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW EGF-like domain; Hydrolyase; Metal-binding; Metalloprotease; Protease;

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KW Zinc.  
SQ SEQUENCE 1464 AA; 165218 MW; 029BE1560DBE9056 CRC64;  
Query Match 1.2%; Score 9; DB 5; Length 1464;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 179 YDYVEVRDG 187  
DB 897 YDYVEVRDG 905  
RESULT 14  
Q24132 PRELIMINARY; PRT; 1464 AA.  
AC Q24132;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE TOLKIN.  
GN TOK OR TOLKIN OR CG6863.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96042912; PubMed=8536976;  
RA Finelli A.L., Xie T., Bossie C.A., Blackman R.K., Padgett R.W.;  
RT "The tolkin gene is a tollid/BMP-1 homologue that is essential for  
RT Drosophila development.";  
RC Genotice 141:271-281(1995).  
CC -I- SIMILARITY: CONTAINS 5 CUB DOMAINS.  
DR EMBL; U34777; AAC47015.1; --  
DR PIR; S58984; S58984.  
DR HSP; P00736; IAPQ.  
DR MEROPS; M12.011; --  
DR FlyBase; Fgn0004885; tok.  
DR GO; GO:000533; F:astacin activity; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0008237; F:metallopeptidase activity; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR GO; GO:0005508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000182; ASX\_hydroxyl\_S.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR006026; Peptidase\_M.  
DR InterPro; IPR001506; Peptidase\_M12A.  
DR InterPro; IPR006025; Pept\_M\_2n\_BS.  
DR Pfam; PF01400; Astacin; 1.  
DR Pfam; PF00431; CUB; 5.  
DR Pfam; PF00008; EGF; 2.  
DR PRINTS; PR00480; ASTACIN.  
DR SMART; SM00042; CUB; 5.  
DR SMART; SM00179; EGF\_CA; 2.  
DR SMART; SM00235; ZnMG; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 2.  
DR PROSITE; PS01180; CUB; 5.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_CA; 2.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW EGF-like domain.  
SQ SEQUENCE 1464 AA; 165106 MW; 5955B6DEA9E37170 CRC64;

Query Match 1.2%; Score 9; DB 5; Length 1464;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 179 YDYVEVRDG 187  
DB 897 YDYVEVRDG 905

RESULT 15  
O16004 PRELIMINARY; PRT; 2531 AA.  
AC O16004;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Notch homolog.  
OS Lytechinus variegatus (Sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;  
OC Lytechinus.  
OX NCBI\_TaxID=7654;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97454256; PubMed=9310331;  
RA Sherwood D.R., McClay D.R.;  
RT "Identification and localization of a sea urchin Notch homologue:  
RT insights into vegetal plate regionalization and Notch receptor  
RT regulation.";  
RL Development 124:3363-3374(1997).  
DR EMBL; AF000634; AAB82088.1; --  
DR HSP; P01132; IEGF.  
DR GO; GO:0006020; C:membrane; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:00030154; P:cell differentiation; IEA.  
DR InterPro; IPR002110; ANK.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001438; EGF\_II.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR008297; Notch.  
DR InterPro; IPR000800; Notch\_dom.  
DR Pfam; PF00023; ank; 6.  
DR Pfam; PF00008; EGF; 34.  
DR Pfam; PF00066; notch; 3.  
DR PRINTS; PR00010; EGFLOOD.  
DR PRINTS; PR01452; NOTCH.  
DR SMART; SM00248; ANK; 5.  
DR SMART; SM00179; EGF\_CA; 23.  
DR SMART; SM00004; NL; 3.  
DR PROSITE; PS50088; ANK\_REPEAT; 5.  
DR PROSITE; PS50297; ANK\_REPEAT; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 21.  
DR PROSITE; PS00022; EGF\_1; 33.  
DR PROSITE; PS01186; EGF\_2; 25.  
DR PROSITE; PS01187; EGF\_CA; 20.  
DR PIRSF; PIRSF002279; Notch; 1.  
KW ANK repeat; EGF-like domain; Repeat.  
SQ SEQUENCE 2531 AA; 273982 MW; 5BF42BEC627CA303 CRC64;

Query Match 1.2%; Score 9; DB 5; Length 2531;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 260 CACLAGYTG 268  
DB 537 CACLAGYTG 545

Search completed: August 18, 2004, 16:33:39  
Job time : 59 secs

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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:25:04 ; Search time 50 Seconds  
(without alignments)

4520.551 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 720

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1292805 seqs, 313927144 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 700 summaries

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Published Applications AA:\*

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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pdb.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pdb.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pdb.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pdb.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pdb.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pdb.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pdb.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pdb.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pdb.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pdb.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pdb.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pdb.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pdb.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pdb.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pdb.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pdb.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	720	100.0	720	9	US-09-989-722-231
2	720	100.0	720	9	US-09-989-723-231
3	720	100.0	720	9	US-09-989-729-231
4	720	100.0	720	9	US-09-989-727-231
5	720	100.0	720	9	US-09-989-731-231
6	720	100.0	720	9	US-09-989-732-231
7	720	100.0	720	9	US-09-991-073-231
8	720	100.0	720	9	US-09-990-442-231
9	720	100.0	720	9	US-09-991-163-231
10	720	100.0	720	9	US-09-993-604-231
11	720	100.0	720	9	US-09-990-456-231
12	720	100.0	720	9	US-09-989-721-231
13	720	100.0	720	9	US-09-992-598-231
14	720	100.0	720	9	US-09-989-293A-231
15	720	100.0	720	9	US-09-989-735-231

16	720	100.0	720	9	US-09-990-444-231	Sequence 231, App
17	720	100.0	720	9	US-09-991-181-231	Sequence 231, App
18	720	100.0	720	9	US-09-989-730-231	Sequence 231, App
19	720	100.0	720	9	US-09-990-436-231	Sequence 231, App
20	720	100.0	720	9	US-09-993-687-231	Sequence 231, App
21	720	100.0	720	10	US-09-989-734-231	Sequence 231, App
22	720	100.0	720	10	US-09-997-653-231	Sequence 231, App
23	720	100.0	720	10	US-09-993-667-231	Sequence 231, App
24	720	100.0	720	10	US-09-997-428-231	Sequence 231, App
25	720	100.0	720	10	US-09-997-666-231	Sequence 231, App
26	720	100.0	720	10	US-09-990-438-231	Sequence 231, App
27	720	100.0	720	10	US-09-990-562-231	Sequence 231, App
28	720	100.0	720	10	US-09-990-711-231	Sequence 231, App
29	720	100.0	720	10	US-09-989-726-231	Sequence 231, App
30	720	100.0	720	10	US-09-998-156-231	Sequence 231, App
31	720	100.0	720	10	US-09-990-437-231	Sequence 231, App
32	720	100.0	720	10	US-09-991-157-231	Sequence 231, App
33	720	100.0	720	10	US-09-997-514-231	Sequence 231, App
34	720	100.0	720	10	US-09-997-573-231	Sequence 231, App
35	720	100.0	720	10	US-09-991-172-231	Sequence 231, App
36	720	100.0	720	10	US-09-990-726-231	Sequence 231, App
37	720	100.0	720	10	US-09-997-559-231	Sequence 231, App
38	720	100.0	720	10	US-09-997-601-231	Sequence 231, App
39	720	100.0	720	10	US-09-990-443-231	Sequence 231, App
40	720	100.0	720	10	US-09-991-854-231	Sequence 231, App
41	720	100.0	720	10	US-09-997-628-231	Sequence 231, App
42	720	100.0	720	10	US-09-997-683-231	Sequence 231, App
43	720	100.0	720	10	US-09-989-729A-231	Sequence 231, App
44	720	100.0	720	10	US-09-997-349-231	Sequence 231, App
45	720	100.0	720	10	US-09-997-440-231	Sequence 231, App
46	720	100.0	720	10	US-09-990-440-231	Sequence 231, App
47	720	100.0	720	10	US-09-993-463-231	Sequence 231, App
48	720	100.0	720	10	US-09-997-542-231	Sequence 231, App
49	720	100.0	720	10	US-09-993-748-231	Sequence 231, App
50	720	100.0	720	10	US-09-990-429-231	Sequence 231, App
51	720	100.0	720	10	US-09-990-437-231	Sequence 231, App
52	720	100.0	720	10	US-09-989-328-231	Sequence 231, App
53	720	100.0	720	10	US-09-993-583-231	Sequence 231, App
54	720	100.0	720	10	US-09-941-992-231	Sequence 231, App
55	720	100.0	720	10	US-09-992-521-231	Sequence 231, App
56	720	100.0	720	10	US-09-997-333-231	Sequence 231, App
57	720	100.0	720	10	US-09-997-384-231	Sequence 231, App
58	720	100.0	720	10	US-09-998-041-231	Sequence 231, App
59	720	100.0	720	10	US-09-997-585-231	Sequence 231, App
60	720	100.0	720	10	US-09-997-614-231	Sequence 231, App
61	720	100.0	720	10	US-09-989-862-231	Sequence 231, App
62	720	100.0	720	10	US-09-997-529-231	Sequence 231, App
63	720	100.0	720	10	US-09-989-725-231	Sequence 231, App
64	720	100.0	720	11	US-09-989-733-231	Sequence 231, App
65	720	100.0	720	11	US-09-992-643-231	Sequence 231, App
66	720	100.0	720	12	US-10-206-915-170	Sequence 170, App
67	720	100.0	720	12	US-10-199-670-170	Sequence 170, App
68	720	100.0	720	12	US-10-201-858-170	Sequence 170, App
69	720	100.0	720	12	US-10-205-890-170	Sequence 170, App
70	720	100.0	720	12	US-10-208-024-170	Sequence 170, App
71	720	100.0	720	12	US-10-201-853-170	Sequence 170, App
72	720	100.0	720	12	US-10-063-745-38	Sequence 38, App1
73	720	100.0	720	12	US-09-989-724-231	Sequence 231, App
74	720	100.0	720	12	US-09-989-728-231	Sequence 231, App
75	720	100.0	720	12	US-09-990-441-231	Sequence 231, App
76	720	100.0	720	12	US-10-063-513-38	Sequence 38, App1
77	720	100.0	720	12	US-10-063-513-38	Sequence 38, App1
78	720	100.0	720	12	US-10-063-515-38	Sequence 38, App1
79	720	100.0	720	12	US-10-063-549-38	Sequence 38, App1
80	720	100.0	720	12	US-10-063-569-38	Sequence 38, App1
81	720	100.0	720	12	US-10-063-551-38	Sequence 38, App1
82	720	100.0	720	12	US-10-174-581-170	Sequence 170, App
83	720	100.0	720	12	US-10-176-483-170	Sequence 170, App
84	720	100.0	720	12	US-10-176-749-170	Sequence 170, App
85	720	100.0	720	12	US-10-176-914-170	Sequence 170, App
86	720	100.0	720	12	US-10-176-915-170	Sequence 170, App
87	720	100.0	720	12	US-09-997-857-231	Sequence 231, App
88	720	100.0	720	12	US-10-063-555-38	Sequence 38, App1

89	720	100.0	720	12	US-10-063-563-38	Sequence 38, App1	162	720	100.0	720	14	US-10-184-658-170	Sequence 170, App
90	720	100.0	720	12	US-10-063-594-38	Sequence 38, App1	163	720	100.0	720	14	US-10-176-991-170	Sequence 170, App
91	720	100.0	720	12	US-10-063-553-38	Sequence 38, App1	164	720	100.0	720	14	US-10-173-695-170	Sequence 170, App
92	720	100.0	720	12	US-10-063-554-38	Sequence 38, App1	165	720	100.0	720	14	US-10-173-697-170	Sequence 170, App
93	720	100.0	720	12	US-10-176-484-170	Sequence 170, App	166	720	100.0	720	14	US-10-173-705-170	Sequence 170, App
94	720	100.0	720	12	US-10-180-550-170	Sequence 170, App	167	720	100.0	720	14	US-10-174-576-170	Sequence 170, App
95	720	100.0	720	12	US-10-183-014-170	Sequence 170, App	168	720	100.0	720	14	US-10-174-585-170	Sequence 170, App
96	720	100.0	720	12	US-10-187-738-170	Sequence 170, App	169	720	100.0	720	14	US-10-174-585-170	Sequence 170, App
97	720	100.0	720	12	US-10-187-740-170	Sequence 170, App	170	720	100.0	720	14	US-10-175-741-170	Sequence 170, App
98	720	100.0	720	12	US-10-187-883-170	Sequence 170, App	171	720	100.0	720	14	US-10-176-481-170	Sequence 170, App
99	720	100.0	720	12	US-10-194-363-170	Sequence 170, App	172	720	100.0	720	14	US-10-176-485-170	Sequence 170, App
100	720	100.0	720	12	US-10-194-460-170	Sequence 170, App	173	720	100.0	720	14	US-10-176-487-170	Sequence 170, App
101	720	100.0	720	12	US-10-194-463-170	Sequence 170, App	174	720	100.0	720	14	US-10-176-493-170	Sequence 170, App
102	720	100.0	720	12	US-10-194-484-170	Sequence 170, App	175	720	100.0	720	14	US-10-176-756-170	Sequence 170, App
103	720	100.0	720	12	US-10-195-884-170	Sequence 170, App	176	720	100.0	720	14	US-10-176-911-170	Sequence 170, App
104	720	100.0	720	12	US-10-195-896-170	Sequence 170, App	177	720	100.0	720	14	US-10-176-913-170	Sequence 170, App
105	720	100.0	720	12	US-10-196-744-170	Sequence 170, App	178	720	100.0	720	14	US-10-176-925-170	Sequence 170, App
106	720	100.0	720	12	US-10-196-755-170	Sequence 170, App	179	720	100.0	720	14	US-10-176-978-170	Sequence 170, App
107	720	100.0	720	12	US-10-196-757-170	Sequence 170, App	180	720	100.0	720	14	US-10-179-510-170	Sequence 170, App
108	720	100.0	720	12	US-10-197-704-170	Sequence 170, App	181	720	100.0	720	14	US-10-180-543-170	Sequence 170, App
109	720	100.0	720	12	US-10-197-710-170	Sequence 170, App	182	720	100.0	720	14	US-10-180-543-170	Sequence 170, App
110	720	100.0	720	12	US-10-198-758-170	Sequence 170, App	183	720	100.0	720	14	US-10-180-546-170	Sequence 170, App
111	720	100.0	720	12	US-10-198-766-170	Sequence 170, App	184	720	100.0	720	14	US-10-180-547-170	Sequence 170, App
112	720	100.0	720	12	US-10-199-304-170	Sequence 170, App	185	720	100.0	720	14	US-10-180-549-170	Sequence 170, App
113	720	100.0	720	12	US-10-199-309-170	Sequence 170, App	186	720	100.0	720	14	US-10-180-555-170	Sequence 170, App
114	720	100.0	720	12	US-10-199-313-170	Sequence 170, App	187	720	100.0	720	14	US-10-180-559-170	Sequence 170, App
115	720	100.0	720	12	US-10-199-456-170	Sequence 170, App	188	720	100.0	720	14	US-10-181-000-170	Sequence 170, App
116	720	100.0	720	12	US-10-201-329-170	Sequence 170, App	189	720	100.0	720	14	US-10-183-010-170	Sequence 170, App
117	720	100.0	720	12	US-10-202-412-170	Sequence 170, App	190	720	100.0	720	14	US-10-183-012-170	Sequence 170, App
118	720	100.0	720	12	US-10-206-919-170	Sequence 170, App	191	720	100.0	720	14	US-10-184-614-170	Sequence 170, App
119	720	100.0	720	12	US-10-206-922-170	Sequence 170, App	192	720	100.0	720	14	US-10-184-623-170	Sequence 170, App
120	720	100.0	720	12	US-10-206-924-170	Sequence 170, App	193	720	100.0	720	14	US-10-184-635-170	Sequence 170, App
121	720	100.0	720	12	US-10-206-928-170	Sequence 170, App	194	720	100.0	720	14	US-10-184-637-170	Sequence 170, App
122	720	100.0	720	12	US-10-207-914-170	Sequence 170, App	195	720	100.0	720	14	US-10-184-646-170	Sequence 170, App
123	720	100.0	720	12	US-10-207-921-170	Sequence 170, App	196	720	100.0	720	14	US-10-184-647-170	Sequence 170, App
124	720	100.0	720	12	US-10-207-922-170	Sequence 170, App	197	720	100.0	720	14	US-10-184-652-170	Sequence 170, App
125	720	100.0	720	12	US-10-208-027-170	Sequence 170, App	198	720	100.0	720	14	US-10-187-594-170	Sequence 170, App
126	720	100.0	720	12	US-09-997-641-231	Sequence 231, App	199	720	100.0	720	14	US-10-187-596-170	Sequence 170, App
127	720	100.0	720	12	US-09-991-150-231	Sequence 231, App	200	720	100.0	720	14	US-10-187-745-170	Sequence 170, App
128	720	100.0	720	12	US-10-174-570-170	Sequence 170, App	201	720	100.0	720	14	US-10-187-885-170	Sequence 170, App
129	720	100.0	720	12	US-10-163-005-170	Sequence 170, App	202	720	100.0	720	14	US-10-187-886-170	Sequence 170, App
130	720	100.0	720	12	US-10-006-867-38	Sequence 38, App1	203	720	100.0	720	14	US-10-199-464-170	Sequence 170, App
131	720	100.0	720	13	US-10-032-886-170	Sequence 170, App	204	720	100.0	720	14	US-10-196-756-170	Sequence 170, App
132	720	100.0	720	13	US-10-063-547-38	Sequence 38, App1	205	720	100.0	720	14	US-10-176-751-170	Sequence 170, App
133	720	100.0	720	14	US-10-174-590-170	Sequence 170, App	206	720	100.0	720	14	US-10-176-760-170	Sequence 170, App
134	720	100.0	720	14	US-10-176-758-170	Sequence 170, App	207	720	100.0	720	14	US-10-176-990-170	Sequence 170, App
135	720	100.0	720	14	US-10-175-737-170	Sequence 170, App	208	720	100.0	720	14	US-10-180-541-170	Sequence 170, App
136	720	100.0	720	14	US-10-063-616-38	Sequence 38, App1	209	720	100.0	720	14	US-10-180-542-170	Sequence 170, App
137	720	100.0	720	14	US-10-173-706-170	Sequence 170, App	210	720	100.0	720	14	US-10-180-548-170	Sequence 170, App
138	720	100.0	720	14	US-10-175-738-170	Sequence 170, App	211	720	100.0	720	14	US-10-180-551-170	Sequence 170, App
139	720	100.0	720	14	US-10-175-752-170	Sequence 170, App	212	720	100.0	720	14	US-10-180-998-170	Sequence 170, App
140	720	100.0	720	14	US-10-176-482-170	Sequence 170, App	213	720	100.0	720	14	US-10-180-999-170	Sequence 170, App
141	720	100.0	720	14	US-10-176-757-170	Sequence 170, App	214	720	100.0	720	14	US-10-183-013-170	Sequence 170, App
142	720	100.0	720	14	US-10-176-913-170	Sequence 170, App	215	720	100.0	720	14	US-10-184-612-170	Sequence 170, App
143	720	100.0	720	14	US-10-180-552-170	Sequence 170, App	216	720	100.0	720	14	US-10-184-616-170	Sequence 170, App
144	720	100.0	720	14	US-10-180-557-170	Sequence 170, App	217	720	100.0	720	14	US-10-184-622-170	Sequence 170, App
145	720	100.0	720	14	US-10-063-502-38	Sequence 38, App1	218	720	100.0	720	14	US-10-184-628-170	Sequence 170, App
146	720	100.0	720	14	US-10-173-700-170	Sequence 170, App	219	720	100.0	720	14	US-10-184-629-170	Sequence 170, App
147	720	100.0	720	14	US-10-174-572-170	Sequence 170, App	220	720	100.0	720	14	US-10-184-629-170	Sequence 170, App
148	720	100.0	720	14	US-10-174-579-170	Sequence 170, App	221	720	100.0	720	14	US-10-184-630-170	Sequence 170, App
149	720	100.0	720	14	US-10-174-582-170	Sequence 170, App	222	720	100.0	720	14	US-10-184-631-170	Sequence 170, App
150	720	100.0	720	14	US-10-174-588-170	Sequence 170, App	223	720	100.0	720	14	US-10-184-632-170	Sequence 170, App
151	720	100.0	720	14	US-10-175-739-170	Sequence 170, App	224	720	100.0	720	14	US-10-184-636-170	Sequence 170, App
152	720	100.0	720	14	US-10-175-740-170	Sequence 170, App	225	720	100.0	720	14	US-10-184-640-170	Sequence 170, App
153	720	100.0	720	14	US-10-175-743-170	Sequence 170, App	226	720	100.0	720	14	US-10-184-650-170	Sequence 170, App
154	720	100.0	720	14	US-10-176-488-170	Sequence 170, App	227	720	100.0	720	14	US-10-184-651-170	Sequence 170, App
155	720	100.0	720	14	US-10-176-492-170	Sequence 170, App	228	720	100.0	720	14	US-10-187-588-170	Sequence 170, App
156	720	100.0	720	14	US-10-176-747-170	Sequence 170, App	229	720	100.0	720	14	US-10-187-597-170	Sequence 170, App
157	720	100.0	720	14	US-10-176-750-170	Sequence 170, App	230	720	100.0	720	14	US-10-187-598-170	Sequence 170, App
158	720	100.0	720	14	US-10-176-985-170	Sequence 170, App	231	720	100.0	720	14	US-10-187-600-170	Sequence 170, App
159	720	100.0	720	14	US-10-176-987-170	Sequence 170, App	232	720	100.0	720	14	US-10-187-601-170	Sequence 170, App
160	720	100.0	720	14	US-10-176-992-170	Sequence 170, App	233	720	100.0	720	14	US-10-187-602-170	Sequence 170, App
161	720	100.0	720	14	US-10-176-993-170	Sequence 170, App	234	720	100.0	720	14	US-10-187-603-170	Sequence 170, App

235	720	100.0	720	14	US-10-187-741-170	Sequence 170, App	308	720	100.0	720	14	US-10-194-425-170	Sequence 170, App
236	720	100.0	720	14	US-10-187-743-170	Sequence 170, App	309	720	100.0	720	14	US-10-194-485-170	Sequence 170, App
237	720	100.0	720	14	US-10-187-746-170	Sequence 170, App	310	720	100.0	720	14	US-10-195-885-170	Sequence 170, App
238	720	100.0	720	14	US-10-187-747-170	Sequence 170, App	311	720	100.0	720	14	US-10-195-899-170	Sequence 170, App
239	720	100.0	720	14	US-10-187-751-170	Sequence 170, App	312	720	100.0	720	14	US-10-196-748-170	Sequence 170, App
240	720	100.0	720	14	US-10-187-753-170	Sequence 170, App	313	720	100.0	720	14	US-10-196-750-170	Sequence 170, App
241	720	100.0	720	14	US-10-187-754-170	Sequence 170, App	314	720	100.0	720	14	US-10-197-699-170	Sequence 170, App
242	720	100.0	720	14	US-10-187-757-170	Sequence 170, App	315	720	100.0	720	14	US-10-197-700-170	Sequence 170, App
243	720	100.0	720	14	US-10-187-764-170	Sequence 170, App	316	720	100.0	720	14	US-10-197-705-170	Sequence 170, App
244	720	100.0	720	14	US-10-188-687-170	Sequence 170, App	317	720	100.0	720	14	US-10-197-708-170	Sequence 170, App
245	720	100.0	720	14	US-10-188-769-170	Sequence 170, App	318	720	100.0	720	14	US-10-198-764-170	Sequence 170, App
246	720	100.0	720	14	US-10-188-770-170	Sequence 170, App	319	720	100.0	720	14	US-10-198-765-170	Sequence 170, App
247	720	100.0	720	14	US-10-188-773-170	Sequence 170, App	320	720	100.0	720	14	US-10-198-768-170	Sequence 170, App
248	720	100.0	720	14	US-10-188-781-170	Sequence 170, App	321	720	100.0	720	14	US-10-198-769-170	Sequence 170, App
249	720	100.0	720	14	US-10-194-361-170	Sequence 170, App	322	720	100.0	720	14	US-10-199-305-170	Sequence 170, App
250	720	100.0	720	14	US-10-194-423-170	Sequence 170, App	323	720	100.0	720	14	US-10-199-306-170	Sequence 170, App
251	720	100.0	720	14	US-10-195-897-170	Sequence 170, App	324	720	100.0	720	14	US-10-199-310-170	Sequence 170, App
252	720	100.0	720	14	US-10-195-901-170	Sequence 170, App	325	720	100.0	720	14	US-10-199-311-170	Sequence 170, App
253	720	100.0	720	14	US-10-195-902-170	Sequence 170, App	326	720	100.0	720	14	US-10-199-314-170	Sequence 170, App
254	720	100.0	720	14	US-10-196-743-170	Sequence 170, App	327	720	100.0	720	14	US-10-199-317-170	Sequence 170, App
255	720	100.0	720	14	US-10-196-760-170	Sequence 170, App	328	720	100.0	720	14	US-10-199-665-170	Sequence 170, App
256	720	100.0	720	14	US-10-173-708-170	Sequence 170, App	329	720	100.0	720	14	US-10-199-666-170	Sequence 170, App
257	720	100.0	720	14	US-10-176-479-170	Sequence 170, App	330	720	100.0	720	14	US-10-199-669-170	Sequence 170, App
258	720	100.0	720	14	US-10-176-748-170	Sequence 170, App	331	720	100.0	720	14	US-10-201-534-170	Sequence 170, App
259	720	100.0	720	14	US-10-176-916-170	Sequence 170, App	332	720	100.0	720	14	US-10-201-770-170	Sequence 170, App
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677	720	100.0	720	14	US-10-063-655-38	Sequence 38, Appl	/	PRIOR APPLICATION NUMBER: 60/075945
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679	720	100.0	720	14	US-10-063-658-38	Sequence 38, Appl	/	PRIOR APPLICATION NUMBER: 60/078910
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681	720	100.0	720	14	US-10-063-568-38	Sequence 38, Appl	/	PRIOR APPLICATION NUMBER: 60/083322
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## ALIGNMENTS

RESULT 1  
US-09-989-722-231  
Sequence 231, Application US/09989722  
Patent No. US20020072067A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deeneyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12



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; PRIOR FILING DATE: 1998-07-09  
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Patent No. US20020072092A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
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APPLICANT: Eaton, Dan L.  
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APPLICANT: Godowski, Paul J.  
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APPLICANT: Gurney, Austin L.  
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APPLICANT: Pan, James  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C62  
CURRENT APPLICATION NUMBER: US/09/989,723  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
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Query Match 100.0%; Score 720; DB 9; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGCTGTLGTLFQLLLISSIPREYTVINEACPAEWNIMRECCEYDQIECVCPGKRE 60  
 DB 1 MELGCTGTLGTLFQLLLISSIPREYTVINEACPAEWNIMRECCEYDQIECVCPGKRE 60  
 QY 61 VGVYTI PCRNENECDSCLHHPGCTIFENCKSCRNCSWGGLDDFYVKGFYCAECRAGW 120  
 DB 61 VGVYTI PCRNENECDSCLHHPGCTIFENCKSCRNCSWGGLDDFYVKGFYCAECRAGW 120  
 QY 121 YGGDCMRGQVLRAPKQGLLESYPLNAHCEWTHAKPGFVQLRPFVMSLEFDYMCQYD 180  
 DB 121 YGGDCMRGQVLRAPKQGLLESYPLNAHCEWTHAKPGFVQLRPFVMSLEFDYMCQYD 180  
 QY 181 YVEVDGNRQGIITKRVCGNERPAPIOSIGSSLHVLPHSDGSKNFDGFHAIYEITACS 240  
 DB 181 YVEVDGNRQGIITKRVCGNERPAPIOSIGSSLHVLPHSDGSKNFDGFHAIYEITACS 240

QY 241 SSPCFHDGTCVLDKAGSYKACACLAGVTGQRCENLLERNCSDFGGPVNGYQKITGGPGLI 300  
 DB 241 SSPCFHDGTCVLDKAGSYKACACLAGVTGQRCENLLERNCSDFGGPVNGYQKITGGPGLI 300  
 QY 301 NGRHAKIGTVVSFFCNNSVYLSGNEKRTCOQNGWSGKQPICIKACREPKISDLVRRVRL 360  
 DB 301 NGRHAKIGTVVSFFCNNSVYLSGNEKRTCOQNGWSGKQPICIKACREPKISDLVRRVRL 360  
 QY 361 PMQVQSRETPHLQLYSAAFSKQKLSQAPTKKQALPGDLPNGYQHLLHTQLQYECISPFYR 420  
 DB 361 PMQVQSRETPHLQLYSAAFSKQKLSQAPTKKQALPGDLPNGYQHLLHTQLQYECISPFYR 420  
 QY 421 RLGSRRRTCLRTCKWSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSL 480  
 DB 421 RLGSRRRTCLRTCKWSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSL 480  
 QY 481 HKGAWFLVCSGALVNERVTVAHAHCVTDLGKVTMIKTADLVKLVGFYRDDDDREKTIQS 540  
 DB 481 HKGAWFLVCSGALVNERVTVAHAHCVTDLGKVTMIKTADLVKLVGFYRDDDDREKTIQS 540  
 QY 541 LQISAILHPNYPDILLADADIALKLLDKARISTRVQPICLAASRDLSSTFQESHITVAG 600  
 DB 541 LQISAILHPNYPDILLADADIALKLLDKARISTRVQPICLAASRDLSSTFQESHITVAG 600  
 QY 601 WNVLDVRSFGKNDTLRSQVSVVSDLSLCEOEHDHGIPVSVTDNMFCASWEPTAPSDI 660  
 DB 601 WNVLDVRSFGKNDTLRSQVSVVSDLSLCEOEHDHGIPVSVTDNMFCASWEPTAPSDI 660  
 QY 661 CTAETGGIAAVSPGRASPEPRWHLMLGLVSWSDYDKTCSHRLSTAFKVLFPKDWIERNMK 720  
 DB 661 CTAETGGIAAVSPGRASPEPRWHLMLGLVSWSDYDKTCSHRLSTAFKVLFPKDWIERNMK 720

RESULT 3

US-09-989-279-231  
 ; Sequence 231, Application US/09989279  
 ; Patent No. US20020072496A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas P.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P27301C56  
 ; CURRENT APPLICATION NUMBER: US/09/989,279  
 ; CURRENT FILING DATE: 2001-11-19  
 ; PRIOR APPLICATION NUMBER: 60/049787  
 ; PRIOR FILING DATE: 1997-06-16  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/065186



;; PRIOR FILING DATE: 1998-07-01.  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match		100.0%;	Score 720;	DB 9;	Length 720;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 720;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MELGCTQLGTLFTQLLLISLPREYTVINEACPGAENIMCRECCEDQIECVCPKRE	60		
Db	1	MELGCTQLGTLFTQLLLISLPREYTVINEACPGAENIMCRECCEDQIECVCPKRE	60		
Qy	61	VVGTYIPCCRNENECDSCLHPGCTIFENCKSCRNCSWGGLDDFVVGKGYCAECRAGW	120		
Db	61	VVGTYIPCCRNENECDSCLHPGCTIFENCKSCRNCSWGGLDDFVVGKGYCAECRAGW	120		
Qy	121	YGGDCMRGQVLRAPKGGILLESYPLNAHCWTTHAKPGFVIQRFVWLSLEFFYMCQYD	180		
Db	121	YGGDCMRGQVLRAPKGGILLESYPLNAHCWTTHAKPGFVIQRFVWLSLEFFYMCQYD	180		
Qy	181	YVEVRDGNRQGIILKRVCGNERPAPICQSSLSHLVLFHSDGSKNPGFHAIVEIITACS	240		
Db	181	YVEVRDGNRQGIILKRVCGNERPAPICQSSLSHLVLFHSDGSKNPGFHAIVEIITACS	240		
Qy	241	SSPCFHDGTCVLDKAGSYKCAACLAGYTGQRCENLLEERNCSDDPGPVNGYQKITGGPGLI	300		
Db	241	SSPCFHDGTCVLDKAGSYKCAACLAGYTGQRCENLLEERNCSDDPGPVNGYQKITGGPGLI	300		
Qy	301	NGRIAKIGTVVSPFCNNSYVLSGNEKRTCCQNGWSGKQPTICIKACREPKISDLVRRVL	360		
Db	301	NGRIAKIGTVVSPFCNNSYVLSGNEKRTCCQNGWSGKQPTICIKACREPKISDLVRRVL	360		
Qy	361	PMQVQSRRTPLHQLYSAAFSKQKLSAPTKKPPALPFGDLPMGYQHLHTQLQYECISPFYR	420		
Db	361	PMQVQSRRTPLHQLYSAAFSKQKLSAPTKKPPALPFGDLPMGYQHLHTQLQYECISPFYR	420		
Qy	421	RLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRTSGVHDGSL	480		
Db	421	RLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRTSGVHDGSL	480		
Qy	481	HKGAWFLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVLGKGFYRDDDRDEKTIQS	540		
Db	481	HKGAWFLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVLGKGFYRDDDRDEKTIQS	540		
Qy	541	LQISAILHPNYDPTLLDADAILKLDKARISRVQPICAASRDLSSTFQESHITVAG	600		
Db	541	LQISAILHPNYDPTLLDADAILKLDKARISRVQPICAASRDLSSTFQESHITVAG	600		
Qy	601	WNVLADVRSPGKNDTLRSRGVSVVDSLLCEQHEHDGIPVSVTDNNMFCASWEPTAPSDI	660		
Db	601	WNVLADVRSPGKNDTLRSRGVSVVDSLLCEQHEHDGIPVSVTDNNMFCASWEPTAPSDI	660		
Qy	661	CTAETGGTAAVSPGRASPEPRHMLGLVSVSYDKTCSHRLSTFTKVLPPKDWIERNMK	720		
Db	661	CTAETGGTAAVSPGRASPEPRHMLGLVSVSYDKTCSHRLSTFTKVLPPKDWIERNMK	720		

;; Sequence 231, Application US/09989727  
;; Patent No. US20020072497A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kljavin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P27301C65  
;; CURRENT APPLICATION NUMBER: US/09/989,727  
;; CURRENT FILING DATE: 2001-11-19  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/065186  
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;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088033

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2 PRIOR FILING DATE: 1998-06-24  
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8 PRIOR FILING DATE: 1998-06-24  
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18 PRIOR FILING DATE: 1998-06-24  
19 PRIOR APPLICATION NUMBER: 60/090557  
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21 PRIOR APPLICATION NUMBER: 60/090676  
22 PRIOR FILING DATE: 1998-06-25  
23 PRIOR APPLICATION NUMBER: 60/090678  
24 PRIOR FILING DATE: 1998-06-25  
25 PRIOR APPLICATION NUMBER: 60/090690  
26 PRIOR FILING DATE: 1998-06-25  
27 PRIOR APPLICATION NUMBER: 60/090694  
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34 PRIOR FILING DATE: 1998-06-26  
35 PRIOR APPLICATION NUMBER: 60/090863  
36 PRIOR FILING DATE: 1998-06-26  
37 PRIOR APPLICATION NUMBER: 60/091360  
38 PRIOR FILING DATE: 1998-07-01  
39 PRIOR APPLICATION NUMBER: 60/091478  
40 PRIOR FILING DATE: 1998-07-02  
41 PRIOR APPLICATION NUMBER: 60/091544  
42 PRIOR FILING DATE: 1998-07-01  
43 PRIOR APPLICATION NUMBER: 60/091519  
44 PRIOR FILING DATE: 1998-07-02  
45 PRIOR APPLICATION NUMBER: 60/091626  
46 PRIOR FILING DATE: 1998-07-02  
47 PRIOR APPLICATION NUMBER: 60/091633  
48 PRIOR FILING DATE: 1998-07-02  
49 PRIOR APPLICATION NUMBER: 60/091978  
50 PRIOR FILING DATE: 1998-07-07  
51 PRIOR APPLICATION NUMBER: 60/091982  
52 PRIOR FILING DATE: 1998-07-07  
53 PRIOR APPLICATION NUMBER: 60/092182  
54 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 720; DB 9; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MELGCTWTLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60  
Db 1 MELGCTWTLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60  
Qy 61 VVGTYTPCCRNEENECDSLHPGCTTIFENCKSCRNSGWTGTLDDFYVKGFFYCAECRAGW 120  
Db 61 VVGTYTPCCRNEENECDSLHPGCTTIFENCKSCRNSGWTGTLDDFYVKGFFYCAECRAGW 120  
Qy 121 YGDCMRCQVLRAPKQIILLESYFLNAHCEWTTHAKPGFVQLRFVMLSLEFDYMCQYD 180  
Db 121 YGDCMRCQVLRAPKQIILLESYFLNAHCEWTTHAKPGFVQLRFVMLSLEFDYMCQYD 180  
Qy 181 YVEVDGNRDGQIIKRVCGNERPAPIOSIGSSHLVPHSDGSKNFDGPHATYEETACS 240

DB 181 YVEVRDGDNRDQGIKRVCGNERPAPIQSIGSLHLVLFHSDGSKDPGPHAIYEBITACS 240  
QY 241 SSPCFHDGTCVLDDKAGSYKACIAGYTGORCENLLERNCSDPGGPPVNGYQKITGPGIJI 300  
DB 241 SSPCFHDGTCVLDDKAGSYKACIAGYTGORCENLLERNCSDPGGPPVNGYQKITGPGIJI 300  
QY 301 NGRHAKIGTVVSPFCNNSTVLSGNEKRTCCQNGWSGKQPCICACREPKISDLVRRVYL 360  
DB 301 NGRHAKIGTVVSPFCNNSTVLSGNEKRTCCQNGWSGKQPCICACREPKISDLVRRVYL 360  
QY 361 PMOVQSRFPLHQLYSAASKOKQAPTKKAPLPGDLPNGVQHLLHTLOQYECISPFYR 420  
DB 361 PMOVQSRFPLHQLYSAASKOKQAPTKKAPLPGDLPNGVQHLLHTLOQYECISPFYR 420  
QY 421 RLGSRRTRCRLTKGWSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYVRTSGVHDGSL 480  
DB 421 RLGSRRTRCRLTKGWSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYVRTSGVHDGSL 480  
QY 481 HKGAWFLVCSGALVNRVTWVAACHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQS 540  
DB 481 HKGAWFLVCSGALVNRVTWVAACHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQS 540  
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DB 541 LQISAILHPNDPIILDDADIALTKLLDKARISTRVQPCILASRDLSFSQESHITVAG 600  
QY 601 WNYLADVRSPGKNDTLRSQVSVSDLLCEEQHDHGIPVSVTDNMFCASWEPTAPSDI 660  
DB 601 WNYLADVRSPGKNDTLRSQVSVSDLLCEEQHDHGIPVSVTDNMFCASWEPTAPSDI 660  
QY 661 CTAETGGIAVSPGRASPEPRHMLGLVSWSDYKTCSHRLSTAFPTKVLFFKDWIERNMK 720  
DB 661 CTAETGGIAVSPGRASPEPRHMLGLVSWSDYKTCSHRLSTAFPTKVLFFKDWIERNMK 720

RESULT 5  
US-09-989-731-231  
Sequence 231, Application US/09989731  
Patent No. US20020103125A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Garber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C70  
CURRENT APPLICATION NUMBER: US/09/989,731  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
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PRIOR FILING DATE: 1998-06-02  
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 / PRIOR APPLICATION NUMBER: 60/091982
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 / PRIOR APPLICATION NUMBER: 60/092182
 / PRIOR FILING DATE: 1998-07-09

 Query Match 100.0%; Score 720; DB 9; Length 720;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRCECYDQIECVCPGKRE 60
 Db 1 MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRCECYDQIECVCPGKRE 60

 QY 61 VVGTYIPCCNEENECDSLIHPGCTTFENCKSCRNGSWGSTLDDFYVKGYPYCAECRAGW 120
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 QY 121 YGGDMRCGQVLRAPKQIILLESYPLNAHCEWTTHAKPGFVIQLRFVWLSLEFDMCOYD 180
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 QY 181 YVEVRDGDNRDQIIKRVCGNERPAPIQSGSSLHVLFHSDGSKNFGFHAIVEITACS 240
 Db 181 YVEVRDGDNRDQIIKRVCGNERPAPIQSGSSLHVLFHSDGSKNFGFHAIVEITACS 240

 QY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGRCENLLEERNCSDDPGPVNGYKQITGGPGLI 300
 Db 241 SSPCFHDGTCVLDKAGSYKACLAGYTGRCENLLEERNCSDDPGPVNGYKQITGGPGLI 300

 QY 301 NGRHAKIGTVVSPFCNNNSYVLSGNEKRTCOQGEWSGKOPICIKACREPKISDLVRRVL 360
 Db 301 NGRHAKIGTVVSPFCNNNSYVLSGNEKRTCOQGEWSGKOPICIKACREPKISDLVRRVL 360

 QY 361 PMQVQSRETPHLQYSAAFSKQLQSAPTKKPAALPFGDLPMGYOHLHTQLQYECISPPYR 420
 Db 361 PMQVQSRETPHLQYSAAFSKQLQSAPTKKPAALPFGDLPMGYOHLHTQLQYECISPPYR 420

 QY 421 RLGSRRRTCLRTGWSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRTSGVHDGSL 480
 Db 421 RLGSRRRTCLRTGWSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRTSGVHDGSL 480

 QY 481 HKGAFLVCSGALVNERTVVVAACHVTDLGKVTMIKTADLKVLGKFRVDRDDREKTIQS 540
 Db 481 HKGAFLVCSGALVNERTVVVAACHVTDLGKVTMIKTADLKVLGKFRVDRDDREKTIQS 540

 QY 541 LQISAILHPNYPDILLADIAILKLDKARISTRVQPICLAASRDISTSQESHITVAG 600
 Db 541 LQISAILHPNYPDILLADIAILKLDKARISTRVQPICLAASRDISTSQESHITVAG 600

 QY 601 WNLADVRSFGKNDTLRSQVSVVDSILLCEQHEHGIPIVSVTDNMFCAWETAAPSDI 660
 Db 601 WNLADVRSFGKNDTLRSQVSVVDSILLCEQHEHGIPIVSVTDNMFCAWETAAPSDI 660

 QY 661 CTATETGGIAAVSFFGRASPEPRWHLMLGVNSYDKTCSHRLSTAFKVLFPKDWIERNMK 720
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 RESULT 6



US-09-989-732-231  
 / Sequence 231, Application US/09989732  
 / Patent No. US20020123463A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Aghkenazi, Avi J.  
 / APPLICANT: Baker, Kevin P.  
 / APPLICANT: Botstein, David  
 / APPLICANT: Desnoyers, Luc  
 / APPLICANT: Eaton, Dan L.  
 / APPLICANT: Ferrara, Napoleone  
 / APPLICANT: Fong, Sherman  
 / APPLICANT: Gerber, Hanspeter  
 / APPLICANT: Gertitsen, Mary E.  
 / APPLICANT: Goddard, Audrey  
 / APPLICANT: Godowski, Paul J.  
 / APPLICANT: Grimaldi, J. Christopher  
 / APPLICANT: Gurney, Austin L.  
 / APPLICANT: Kijavlin, Ivar J.  
 / APPLICANT: Napier, Mary A.  
 / APPLICANT: Pan, James  
 / APPLICANT: Paoni, Nicholas F.  
 / APPLICANT: Roy, Margaret Ann  
 / APPLICANT: Stewart, Timothy A.  
 / APPLICANT: Tumas, Daniel  
 / APPLICANT: Watanabe, Colin K.  
 / APPLICANT: Williams, P. Mickey  
 / APPLICANT: Wood, William I.  
 / APPLICANT: Zhang, Zemin  
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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 / FILE REFERENCE: P2730PIC57  
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 / CURRENT FILING DATE: 2001-11-19  
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1 PRIOR APPLICATION NUMBER: 60/092182  
1 PRIOR FILING DATE: 1998-07-09

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DB 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSIGSLHVLPHSDGSKNDFGHAIYEEITACS 240  
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QY 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL 480  
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QY 481 HKGAWFLVCSGALVNERTVVAACHCVTDLGKVTWIKTADLKVLGKFYRDDDRDEKTIQS 540  
DB 481 HKGAWFLVCSGALVNERTVVAACHCVTDLGKVTWIKTADLKVLGKFYRDDDRDEKTIQS 540  
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QY 601 MNVLADVRSPGKNDTLRSVGVVSDLSLCEQEHEDHGIPVSVTDNMFCASWEPTAPSDI 660  
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RESULT 7

US-09-991-073-231  
Sequence 231, Application US/09991073  
Patent No. US2002012756A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C15  
CURRENT APPLICATION NUMBER: US/09/991,073  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250



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/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09

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Db 181 YVEVRGDNRDGOILKRVCCNERPAPQISGSLHVLFSHDSKNGDFGHAIYEEITACS 240

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Db 241 SSFCFHDGTCLVDKAGSYKACLAGYTGQRCENLLEERNCSDFGPGVNGYKQITGGPGLI 300

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Db 361 PMOVQSRTEPLHOLYSAAFSKQKLOSAPTKPKALPGCDLPMGYOHLHTLOVECSIPFVR 420

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Db 421 RLGSRRRTCLRTGKWSGRAPSCIPICCKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSL 480

Qy 481 HKGAWFLVCSGALVWERTVVAACHVTDLGKVTWKITADLKVLGKPYRDDDRDEKTIQS 540
Db 481 HKGAWFLVCSGALVWERTVVAACHVTDLGKVTWKITADLKVLGKPYRDDDRDEKTIQS 540

Qy 541 LQISAILHPNYDPIILLDADIALIKLLDKARISTRVQPICLAASRDLSFQESHITVAG 600
Db 541 LQISAILHPNYDPIILLDADIALIKLLDKARISTRVQPICLAASRDLSFQESHITVAG 600

Qy 601 WNVLADVRSPGKNDTLRSQVWSVDSLLCEEQHEHDHGI PVSVTDNMFCAWSEFTAPS DI 660
Db 601 WNVLADVRSPGKNDTLRSQVWSVDSLLCEEQHEHDHGI PVSVTDNMFCAWSEFTAPS DI 660

Qy 661 CTAETGGAIVSPFGRASPPRHLMLGWSVSDYKTCSHRLSTAFKVLPPKDWIERNMK 720
Db 661 CTAETGGAIVSPFGRASPPRHLMLGWSVSDYKTCSHRLSTAFKVLPPKDWIERNMK 720

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RESULT 8
US-09-990-442-231
; Sequence 231, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030

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; PRIOR FILING DATE: 1998-06-04  
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; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 720; DB 9; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	VVGVTIPCCNEENECDSCLIHFGCTIFENCKSCRNCSWGTTLDDFVVKGFYCAECRAGW	120
Qy	121	YGGDCMRCGQVLRAPKQGIILLESYPLNAHCEWTHAKPGFVIQLRFVWLSLEPFYMCQYD	180
Db	121	YGGDCMRCGQVLRAPKQGIILLESYPLNAHCEWTHAKPGFVIQLRFVWLSLEPFYMCQYD	180

QY 181 YVEVRDGNDRDQIIKRVCGNERPAPIQSIQSSHLVLFHSDGSKNFDGPHAIYEEITACS 240  
Db 181 YVEVRDGNDRDQIIKRVCGNERPAPIQSIQSSHLVLFHSDGSKNFDGPHAIYEEITACS 240  
QY 241 SSPCFHDGTCTVLDKAGSYKACLAGYTGQRCENLLBERNCSDPGPVNGYQKITGPGPLI 300  
Db 241 SSPCFHDGTCTVLDKAGSYKACLAGYTGQRCENLLBERNCSDPGPVNGYQKITGPGPLI 300  
QY 301 NGRHAKITGVVSPFCNNSYVLSGNEKRTCOQNGEWSGKQPCICAKCREPKISDLVRRVRL 360  
Db 301 NGRHAKITGVVSPFCNNSYVLSGNEKRTCOQNGEWSGKQPCICAKCREPKISDLVRRVRL 360  
QY 361 PMQVQSBETPLHQLYSAPSKQLOSAPTKPPALPGDLPNGYOHLLTQLOVEICISPEYR 420  
Db 361 PMQVQSBETPLHQLYSAPSKQLOSAPTKPPALPGDLPNGYOHLLTQLOVEICISPEYR 420  
QY 421 RLSSRRTCLRTGKWSRAPSCIPICGKIENITAPKTQGLRWPMQAAIYVRTSGVHDGSL 480  
Db 421 RLSSRRTCLRTGKWSRAPSCIPICGKIENITAPKTQGLRWPMQAAIYVRTSGVHDGSL 480  
QY 481 HKGAWFLVCSGALVWERTVVAACHVTDLGKVTMIKTADLKVVLGKPYRDDREKTIQS 540  
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QY 541 LQISAITLHPNYPIILLDADIAIKLLDKARISTRVQPICLAASRDLSFQESHITVAG 600  
Db 541 LQISAITLHPNYPIILLDADIAIKLLDKARISTRVQPICLAASRDLSFQESHITVAG 600  
QY 601 WNVLDVRSFGKNDTLRSVSVSDLLCEEQHEHDGIPVSVTDNMFCASWEPTAPSDI 660  
Db 601 WNVLDVRSFGKNDTLRSVSVSDLLCEEQHEHDGIPVSVTDNMFCASWEPTAPSDI 660  
QY 661 CTABTGIAAVSPGRASPSPRHLMLGLVNSWYDKTCSHRLSTAFKVLFPKDWIERNMK 720  
Db 661 CTABTGIAAVSPGRASPSPRHLMLGLVNSWYDKTCSHRLSTAFKVLFPKDWIERNMK 720

RESULT 9  
US-09-991-163-231  
; Sequence 231, Application US/09991163  
; Patent No. US20020132253A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: KJavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C17  
; CURRENT APPLICATION NUMBER: US/09/991,163  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16

; PRIOR FILING DATE: 1998-06-16  
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 ; PRIOR FILING DATE: 1998-06-16  
 ; PRIOR APPLICATION NUMBER: 60/089514  
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 ; PRIOR APPLICATION NUMBER: 60/091978  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/091982  
 ; PRIOR FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 60/092182  
 ; PRIOR FILING DATE: 1998-07-09  
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 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 MELGCTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKRE 60  
 QY 61 VVGYYTIPCCRNEENECDSCLIHPGCTTIFENCKSCRMGGTLLDDFYVVGFCYCAECRAG 120  
 Db 61 VVGYYTIPCCRNEENECDSCLIHPGCTTIFENCKSCRMGGTLLDDFYVVGFCYCAECRAG 120  
 QY 121 YGGDCMRCQGVLRAPKQIILLESYPLNAHCEWTIHAKEGFIQLRFVWLSLEFDYMCQYD 180  
 Db 121 YGGDCMRCQGVLRAPKQIILLESYPLNAHCEWTIHAKEGFIQLRFVWLSLEFDYMCQYD 180  
 QY 181 YVEVRDGNRDQIIRKVCNERPAPIQSIGSLHVLPHSDGSKNPDGPHAIYEETACS 240  
 Db 181 YVEVRDGNRDQIIRKVCNERPAPIQSIGSLHVLPHSDGSKNPDGPHAIYEETACS 240  
 QY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGORCENLLEERNCSPPGGVNGYQKITGPGGLI 300  
 Db 241 SSPCFHDGTCVLDKAGSYKACLAGYTGORCENLLEERNCSPPGGVNGYQKITGPGGLI 300  
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 Db 361 PMQVQSRETPHLQLYSAAFSKQKLSAFTKPKALPGDLPNGYQHLLHTQLQYECISPFYR 420  
 QY 421 RLGSRRRTCLRTGKSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRYSVGHGSL 480  
 Db 421 RLGSRRRTCLRTGKSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRYSVGHGSL 480  
 QY 481 HKGAWFLVCSGALVNBRTVVAAHCVTDLGKVTMIKTADLVKLVGKPYRDDDEKTIQS 540  
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RESULT 10  
US-09-993-604-231  
Sequence 231, Application US/09993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
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APPLICANT: Godowski, Paul J.  
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APPLICANT: Gurney, Austin L.  
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APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C25  
CURRENT APPLICATION NUMBER: US/09/993,604  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
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Qy	61	VGVYTI PCRNENECSDLIHPGCTTIPENCKSRNGSWGTLDDFYVKGPFYCAECRAGW	120		
Db	61	VGVYTI PCRNENECSDLIHPGCTTIPENCKSRNGSWGTLDDFYVKGPFYCAECRAGW	120		
Qy	121	YGGDCMRGCVLRAPKGGQILLESPLNNAHCWTTHAKPGFVIQLRFVWLSLEFDYMCQYD	180		
Db	121	YGGDCMRGCVLRAPKGGQILLESPLNNAHCWTTHAKPGFVIQLRFVWLSLEFDYMCQYD	180		

Qy	181	YVEVRDGDNRDQIIKRVCGNERPAPIQSIGSSHLVLFHSDGSKNPDGPHAIYEETACS	240		
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Qy	241	SSPCFHDGTCLVDKAGSYKACACLAGYTGORCENLLEERNCSDPGGPVNGYOKITGGPGLI	300		
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Qy	301	NGRHAKIGTVVSPFFCNNSYVLSGNEKRTCOQNGESGKQPICIKACREPKISDLVERRVL	360		
Db	301	NGRHAKIGTVVSPFFCNNSYVLSGNEKRTCOQNGESGKQPICIKACREPKISDLVERRVL	360		
Qy	361	PMQVQSRETPHLQLYSAAFSKOKLASAPTKKPPALPPGDLPMGYQHHLTOLQYECISPPFYR	420		
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Qy	421	RLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL	480		
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Qy	541	LQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASRDLSFSFESHITVAG	600		
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Qy	601	WNVLADVRSPGKNDTLRSGVSVVDSILCEQHEHDHGI PVSVTDNMFCASWEPTAPSDI	660		
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; Sequence 231, Application US/09990456					
; Patent No. US20020137890A1					
; GENERAL INFORMATION:					
; APPLICANT: Ashkenazi, Avi J.					
; APPLICANT: Baker, Kevin P.					
; APPLICANT: Botstein, David					
; APPLICANT: Desnoyers, Luc					
; APPLICANT: Eaton, Dan L.					
; APPLICANT: Ferrara, Napoleone					
; APPLICANT: Fong, Sherman					
; APPLICANT: Gerber, Hanspeter					
; APPLICANT: Gerritsen, Mary E.					
; APPLICANT: Goddard, Audrey					
; APPLICANT: Godowski, Paul J.					
; APPLICANT: Grimaldi, J. Christopher					
; APPLICANT: Gurney, Austin L.					
; APPLICANT: Kljavin, Ivar J.					
; APPLICANT: Napier, Mary A.					
; APPLICANT: Pan, James					
; APPLICANT: Paoni, Nicholas P.					
; APPLICANT: Roy, Margaret Ann					
; APPLICANT: Stewart, Timothy A.					
; APPLICANT: Tumas, Daniel					
; APPLICANT: Watanabe, Colin K.					
; APPLICANT: Williams, P. Mickey					
; APPLICANT: Wood, William I.					
; APPLICANT: Zhang, Zemin					
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic					
; TITLE OF INVENTION: Acids Encoding the Same					
; FILE REFERENCE: P2730P1C22					
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; CURRENT FILING DATE: 2001-11-14					
; PRIOR APPLICATION NUMBER: 60/049787					

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56	56	PRIOR FILING DATE: 1998-06-10	56	56	PRIOR FILING DATE:

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Qy	Db	121 YGGDCMRGQVLRAPKGQILLESPLNACHCWTTHAKPGFVIOIRFVNLSEFFDMCOYD 180					
Qy	Db	181 YVEVRDGNRQDQIIKRVCGNERPAPIQSIGSSHLVLFHSDGSKNFDGFHAIYEITACS 240					
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Patent No. US20020142961A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Grittisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
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TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C55  
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17	PRIOR FILING DATE: 1998-06-09
18	PRIOR APPLICATION NUMBER: 60/088734
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69	PRIOR FILING DATE: 1998-06-22

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54	PRIOR FILING DATE: 1998-07-07
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56	PRIOR FILING DATE: 1998-07-07
57	PRIOR APPLICATION NUMBER: 60/092182
58	PRIOR FILING DATE: 1998-07-09

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Qy	61	VWGYYTPCCRNENECDSCLIHPGCCTIFENCCKSRNGSGGTLLDDFPVKGIFYCAECRAGW	120			
Dd	61	VWGYYTPCCRNENECDSCLIHPGCCTIFENCCKSRNGSGGTLLDDFPVKGIFYCAECRAGW	120			
Qy	121	YGSDCMRCGGVLRAPKGOILLSESYPLNANCWTIHAKPGFVIOLRFVMLSLFFDYMCQYD	180			

121	YGGDCMRCQGVUBAPKGOILLSEYPLNHCWVTHAKPGVFIQLRFVMLUSLEDPYMCQVD	180
181	YVEVRDGNRDQOIIKRYVCGNERPAPIQSIQSSLHVLFHSDGSKNFDGFHAIYEETIACS	240
181	YVEVRDGNRDQOIIKRYVCGNERPAPIQSIQSSLHVLFHSDGSKNFDGFHAIYEETIACS	240
241	SSPCFHDGTCVULDKAGSYKCACLAGYTGQRCENLLEBRNCSDPGPGVNGYKQITGGPGILI	300
241	SSPCFHDGTCVULDKAGSYKCACLAGYTGQRCENLLEBRNCSDPGPGVNGYKQITGGPGILI	300
301	NGRHAKITGVISFFCNSYVLSGNEKRTCOQNGSWSGKQPICIKACREPKISDLVRRVYL	360
301	NGRHAKITGVISFFCNSYVLSGNEKRTCOQNGSWSGKQPICIKACREPKISDLVRRVYL	360
361	PMQVOSRETPLHOLYSAAFSKQKLSQSAFTKPKPALPFGDLPMGVOHLHTLOLQYECISPPFYR	420
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421	RLGSSRRTCRLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQWAAIYVRTSGVHDSGL	480
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541	LQISAILIHPNYDPIILLDADTALLKLUDKARISTRVQPICLAASRDLSFTSQESHITVAG	600
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661	CTAETGCGIAAVSFFPGRASPERRWHLMGLVSVSYDKTCSHRLSTAFTKVLPFKDWIERNNK	720
661	CTAETGCGIAAVSFFPGRASPERRWHLMGLVSVSYDKTCSHRLSTAFTKVLPFKDWIERNNK	720

## RESULT 13

US-09-992-598-231  
 ; Sequence 231, Application US/09992598  
 ; Patent No. US20020160384A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Achkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kijavini, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2730PIC20  
 ; CURRENT APPLICATION NUMBER: US/09/992,598  
 ; CURRENT FILING DATE: 2001-11-14

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 / PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 720; DB 9; Length 720;  
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 DB 61 VVGVTIPCCRNENECDSCLIHGCTIIFENCKSCNCGSGTLDPPYKGFYCAECRAGW 120  
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 DB 121 YGDCMRCQGVLRAPKQIILLESYPLNAHCEWTIHAKEGFIQLRFLVMSLEFDYMCQYD 180  
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 DB 181 YVEVRDGNRDQIIKRVCGNERPAPIOSIGSSHLVLFHSDGSKNFDGFHAIYEITACS 240  
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 DB 241 SSPCFHDGTCLVDKAGSYKACLAGYTGRCENLLEERNCSDPGGVNGYQKITGGPGLI 300  
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 DB 301 NGRHAKIGTVVSFFCNSYVLSGNEKRTCOQNGESGKQPICIKACREPKISDLVRRVYL 360  
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 DB 361 PMQVQSRETPHLQYSAAPSKOKLQSAPTKKPALPFGDLPMGYQHLHTLOLQYECISPFYR 420  
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 DB 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTGLRWPQAAIYRRISGVHDGSL 480  
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 DB 481 HKGANFLVCSGALVNERTVVAAHCVTDLGKVTMTKTADLKVLGKGYRDDRDEKTIQS 540  
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 DB 541 LOISAILHPNYDPIILLDADIAILKLLDKARISTRVQPICLAASRDLSFQESHITVAG 600  
 QY 601 WNVLDVRSFGPKNDTLRSVVSVVDSLLCEQHEDHGIPVSVTDMNMFCASEPTAPSDI 660  
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Db 661 CTAETGCIASVFPGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFKVLFPFKDWIERNMK 720

## RESULT 14

US-09-989-293A-231

/ Sequence 231, Application US/09989293A

/ Patent No. US20020177164A1

/ GENERAL INFORMATION:

/ APPLICANT: Ashkenazi, Avi J.

/ APPLICANT: Baker, Kevin P.

/ APPLICANT: Botstein, David

/ APPLICANT: Deenoyers, Luc

/ APPLICANT: Eaton, Dan L.

/ APPLICANT: Ferrara, Napoleone

/ APPLICANT: Fong, Sherman

/ APPLICANT: Gerber, Hanspeter

/ APPLICANT: Gertschen, Mary E.

/ APPLICANT: Goddard, Audrey

/ APPLICANT: Godowski, Paul J.

/ APPLICANT: Grimaldi, J. Christopher

/ APPLICANT: Gurney, Austin L.

/ APPLICANT: Kljavin, Ivar J.

/ APPLICANT: Napier, Mary A.

/ APPLICANT: Pan, James

/ APPLICANT: Paoni, Nicholas F.

/ APPLICANT: Roy, Margaret Ann

/ APPLICANT: Stewart, Timothy A.

/ APPLICANT: Tumas, Daniel

/ APPLICANT: Watanabe, Colin K.

/ APPLICANT: Williams, P. Mickey

/ APPLICANT: Wood, William I.

/ APPLICANT: Zhang, Zemin

/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

/ ACIDS

/ FILE REFERENCE: P2730P1C66

/ CURRENT APPLICATION NUMBER: US/09/989,293A

/ PRIOR APPLICATION NUMBER: 60/049787

/ PRIOR FILING DATE: 1997-06-16

/ PRIOR APPLICATION NUMBER: 60/062250

/ PRIOR FILING DATE: 1997-10-17

/ PRIOR APPLICATION NUMBER: 60/065186

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PRIOR APPLICATION NUMBER: 60/092182									
PRIOR FILING DATE: 1998-07-09									
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Db	1	MELGCTQLGLTFLQLLLISLPREYTVINEACPGAENIMWCECEYDQIECVCPKRE	60						
Qy	61	VWGYTTPCCNEECDSCLHFGCTIFENCKSCRNWSGGTLDLDPVYKGFYCAECBAGW	120						
Db	61	VWGYTTPCCNEECDSCLHFGCTIFENCKSCRNWSGGTLDLDPVYKGFYCAECBAGW	120						
Qy	121	YGGDCMRGQVLRAPKQILLESYPLNAHCETWTHAKPGFVIQLRFVMLSLEFDYMCQYD	180						

Db	121	YGGDCMRGQVLRAPKQILLESYPLNAHCETWTHAKPGFVIQLRFVMLSLEFDYMCQYD	180
Qy	181	YVEVRDGNRDQIIRKVCGRNPAPIOSIGSSLHVLFSDGSKNFDGFHAIYEITACS	240
Db	181	YVEVRDGNRDQIIRKVCGRNPAPIOSIGSSLHVLFSDGSKNFDGFHAIYEITACS	240
Qy	241	SSPCFHDGTCLVDKAGSYKCAACLAGYTGORCENLLBERNCSDPGGPNVGYQKITGGPGLI	300
Db	241	SSPCFHDGTCLVDKAGSYKCAACLAGYTGORCENLLBERNCSDPGGPNVGYQKITGGPGLI	300
Qy	301	NGRHAKIGTVVSFFCNSYVLSGNEKRTCQQNGESGKQPICIKACREPKISDLVRRRVL	360
Db	301	NGRHAKIGTVVSFFCNSYVLSGNEKRTCQQNGESGKQPICIKACREPKISDLVRRRVL	360
Qy	361	PMQVQSRETFPLHQLYSAAFSKOKLQSAPTKKPALPFGDLPNGYQHLHTQLQYECISPPFYR	420
Db	361	PMQVQSRETFPLHQLYSAAFSKOKLQSAPTKKPALPFGDLPNGYQHLHTQLQYECISPPFYR	420
Qy	421	RLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSL	480
Db	421	RLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSL	480
Qy	481	HKGAWFLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIOS	540
Db	481	HKGAWFLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIOS	540
Qy	541	LQISAIILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASRDLSFQESHITVAG	600
Db	541	LQISAIILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASRDLSFQESHITVAG	600
Qy	601	MNVLDVRSFGPKNDTLRSVVVSDSLCEBQHEHDGIPVSVTDMNMFCAWEPAPSII	660
Db	601	MNVLDVRSFGPKNDTLRSVVVSDSLCEBQHEHDGIPVSVTDMNMFCAWEPAPSII	660
Qy	661	CTAETGGIAAVSFPGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNNK	720
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US-09-989-735-231			
; Sequence 231, Application US/09989735			
; Publication No. US20020193299A1			
; GENERAL INFORMATION:			
; APPLICANT: Ashkenazi, Avi J.			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan L.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, J. Christopher			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Kljavin, Ivar J.			
; APPLICANT: Napier, Mary A.			
; APPLICANT: Pan, James			
; APPLICANT: Paoni, Nicholas F.			
; APPLICANT: Roy, Margaret Ann			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Watanabe, Colin K.			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William I.			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
; TITLE OF INVENTION: Acids Encoding the Same			
; FILE REFERENCE: P2730PIC61			
; CURRENT APPLICATION NUMBER: US/09/989,735			

1	PRIOR APPLICATION NUMBER: 60/089105	
2	PRIOR FILING DATE: 1998-06-12	
3	PRIOR APPLICATION NUMBER: 60/089440	
4	PRIOR FILING DATE: 1998-06-16	
5	PRIOR APPLICATION NUMBER: 60/089512	
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46	PRIOR FILING DATE: 1998-06-24	
47	PRIOR APPLICATION NUMBER: 60/090435	
48	PRIOR FILING DATE: 1998-06-24	
49	PRIOR APPLICATION NUMBER: 60/090444	
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63	PRIOR APPLICATION NUMBER: 60/090676	
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Query Match 100.0%; Score 720; DB 9; Length 720;  
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QY 61 VVGTYTIPCCRNENECDSCLIHGCTIPENCKSCRNCSWGGTLDFFYVKGFCYACBACRAGW 120  
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QY 121 YGDCMRCQVLRAPKQILLESYPLNAHCEWTIAKPGFVIQLRFVMLSLEFDYMCQYD 180  
DB 121 YGDCMRCQVLRAPKQILLESYPLNAHCEWTIAKPGFVIQLRFVMLSLEFDYMCQYD 180

QY 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSLHVLPHSDGSKNFDGPHAIYEBITACS 240  
DB 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSLHVLPHSDGSKNFDGPHAIYEBITACS 240

QY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGORCENLLEERNCSDFGPGVNGYQKITGGPGLI 300  
DB 241 SSPCFHDGTCVLDKAGSYKACLAGYTGORCENLLEERNCSDFGPGVNGYQKITGGPGLI 300

QY 301 NGRHAKIGTVWSFFCNNSVVLGNEKRTCCQNGEWSGKQPICIKACREPKISDLVRRRL 360  
DB 301 NGRHAKIGTVWSFFCNNSVVLGNEKRTCCQNGEWSGKQPICIKACREPKISDLVRRRL 360

QY 361 PMQVQSRETPHLQYSAAFSKQLQSAPTKPALPFGDLPNGYQHLTLQYECISPPFYR 420  
DB 361 PMQVQSRETPHLQYSAAFSKQLQSAPTKPALPFGDLPNGYQHLTLQYECISPPFYR 420

QY 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL 480  
DB 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL 480

QY 481 HKGANFLVCSGALVNERTVVAACHCVTDLGKVTMIKTADLVKGFYRDDDRDEKTIOS 540  
DB 481 HKGANFLVCSGALVNERTVVAACHCVTDLGKVTMIKTADLVKGFYRDDDRDEKTIOS 540

QY 541 LQISAILHPNYDPIILLDADIAILKLLDKARISTRVQPICLAASRDLSFQESHITVAG 600  
DB 541 LQISAILHPNYDPIILLDADIAILKLLDKARISTRVQPICLAASRDLSFQESHITVAG 600

QY 601 WNVLADVRSFGKNDTLRSQVSVVDSLACEBOHEDHGI PVSVTNNMFCASWEPAPS DI 660  
DB 601 WNVLADVRSFGKNDTLRSQVSVVDSLACEBOHEDHGI PVSVTNNMFCASWEPAPS DI 660

QY 661 CTAETGGIAAVSPGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK 720

DB 661 CTAETGGIAAVSPGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK 720

Search completed: August 18, 2004, 16:30:55  
Job time : 55 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:22:34 ; Search time 19 Seconds  
(without alignments)  
1956.353 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 720

Sequence: 1 MELGWTQLGLTFLQLLLIS.....LSTAFKVLFPKDWIERNMK 720

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 700 summaries

Databao : Issued Patents AA.\*  
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5: /cgn2\_6/ptodata/2/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	1.2	101	3	US-09-374-135-4
2	9	1.2	110	4	US-09-341-461-28
3	9	1.2	730	3	US-08-872-757-2
4	9	1.2	730	4	US-09-850-048A-2
5	9	1.2	788	1	US-08-572-225-1
6	9	1.2	986	4	US-09-285-385C-19
7	9	1.2	1015	4	US-09-285-385C-2
8	8	1.1	51	3	US-09-188-930-342
9	8	1.1	51	4	US-09-312-283C-342
10	8	1.1	96	4	US-09-472-087-99
11	8	1.1	152	3	US-09-188-930-187
12	8	1.1	152	4	US-09-312-283C-187
13	8	1.1	155	4	US-09-472-087-20
14	8	1.1	155	4	US-09-472-087-112
15	8	1.1	1019	1	US-08-296-014A-4
16	8	1.1	1019	2	US-08-596-405-4
17	8	1.1	1019	2	US-08-877-620-4
18	8	1.1	1019	4	US-09-287-368A-2
19	8	1.1	1083	1	US-08-296-014A-2
20	8	1.1	1083	2	US-08-596-405-2
21	8	1.1	1083	2	US-08-877-620-2
22	8	1.1	1083	4	US-09-287-368-2
23	8	1.1	3571	4	US-09-911-842A-2
24	7	1.0	42	1	US-08-293-778-11
25	7	1.0	80	4	US-09-621-976-4542
26	7	1.0	83	4	US-09-543-681A-5389
27	7	1.0	105	4	US-09-187-859-18

28	7	1.0	105	4	US-09-839-542B-18	Sequence 18, Appl
29	7	1.0	105	4	US-09-535-852-18	Sequence 18, Appl
30	7	1.0	111	4	US-09-252-991A-23343	Sequence 23343, A
31	7	1.0	121	4	US-09-252-991A-22436	Sequence 22436, A
32	7	1.0	121	4	US-09-621-976-5058	Sequence 5058, Ap
33	7	1.0	142	4	US-09-489-039A-10461	Sequence 10461, A
34	7	1.0	144	3	US-08-906-763-153	Sequence 153, App
35	7	1.0	144	3	US-08-906-616-153	Sequence 153, App
36	7	1.0	144	3	US-08-639-075A-153	Sequence 153, App
37	7	1.0	144	3	US-09-004-731-81	Sequence 81, Appl
38	7	1.0	144	3	US-09-012-431-153	Sequence 153, App
39	7	1.0	144	3	US-08-749-699-81	Sequence 81, Appl
40	7	1.0	144	3	US-09-012-692-153	Sequence 153, App
41	7	1.0	144	3	US-08-906-613-153	Sequence 153, App
42	7	1.0	144	3	US-09-004-729-81	Sequence 81, Appl
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44	7	1.0	187	4	US-09-107-532A-6736	Sequence 6736, Ap
45	7	1.0	210	4	US-09-198-452A-869	Sequence 869, App
46	7	1.0	214	4	US-09-543-681A-4600	Sequence 4600, Ap
47	7	1.0	226	4	US-09-489-039A-7662	Sequence 7662, Ap
48	7	1.0	233	3	US-09-004-731-27	Sequence 27, Appl
49	7	1.0	233	3	US-08-749-699-27	Sequence 27, Appl
50	7	1.0	233	4	US-09-004-729-27	Sequence 27, Appl
51	7	1.0	245	4	US-09-252-991A-26491	Sequence 26491, A
52	7	1.0	255	4	US-09-540-236-2829	Sequence 2829, Ap
53	7	1.0	257	4	US-09-328-352-7049	Sequence 7049, Ap
54	7	1.0	259	3	US-08-944-483-52	Sequence 52, Appl
55	7	1.0	265	4	US-09-050-739-16	Sequence 16, Appl
56	7	1.0	266	3	US-09-004-731-24	Sequence 24, Appl
57	7	1.0	266	3	US-08-749-699-24	Sequence 24, Appl
58	7	1.0	266	4	US-09-004-729-24	Sequence 24, Appl
59	7	1.0	288	3	US-09-032-215-42	Sequence 42, Appl
60	7	1.0	295	3	US-08-338-368-2	Sequence 2, Appl1
61	7	1.0	310	4	US-09-107-532A-4185	Sequence 4185, Ap
62	7	1.0	314	4	US-09-636-382A-2	Sequence 2, Appl1
63	7	1.0	376	2	US-08-558-269-10	Sequence 10, Appl
64	7	1.0	376	3	US-09-410-882-10	Sequence 10, Appl
65	7	1.0	399	4	US-09-252-991A-28974	Sequence 28974, A
66	7	1.0	422	4	US-09-489-039A-12443	Sequence 12443, A
67	7	1.0	437	4	US-09-489-039A-7612	Sequence 7612, Ap
68	7	1.0	448	4	US-09-328-352-5694	Sequence 5694, Ap
69	7	1.0	503	4	US-09-071-035-360	Sequence 360, App
70	7	1.0	525	4	US-09-252-991A-23870	Sequence 23870, A
71	7	1.0	556	4	US-08-795-691-2	Sequence 2, Appli
72	7	1.0	579	1	US-08-295-411-4	Sequence 4, Appli
73	7	1.0	579	2	US-08-955-471-4	Sequence 4, Appli
74	7	1.0	579	3	PCT-US92-10242-4	Sequence 14, Appl
75	7	1.0	579	5	US-09-117-708-14	Sequence 14, Appl
76	7	1.0	615	1	US-07-998-972A-3	Sequence 3, Appli
77	7	1.0	615	1	US-08-463-953-3	Sequence 3, Appli
78	7	1.0	615	1	US-08-462-261-3	Sequence 3, Appli
79	7	1.0	615	5	PCT-US92-11357-3	Sequence 3, Appli
80	7	1.0	622	3	US-08-952-967-8	Sequence 8, Appli
81	7	1.0	805	4	US-09-252-991A-17822	Sequence 2, Appli
82	7	1.0	808	4	US-09-565-909-2	Sequence 2, Appli
83	7	1.0	986	3	US-08-872-757-4	Sequence 4, Appli
84	7	1.0	986	4	US-09-850-048A-4	Sequence 4, Appli
85	7	1.0	1074	4	US-09-071-035-358	Sequence 358, App
86	7	1.0	1074	4	US-09-071-035-394	Sequence 394, App
87	7	1.0	1096	4	US-09-134-000C-5764	Sequence 5764, Ap
88	7	1.0	1346	3	US-09-320-878-4	Sequence 4, Appli
89	7	1.0	1346	3	US-09-105-537-37	Sequence 37, Appl
90	7	1.0	1346	4	US-09-141-908-5	Sequence 5, Appli
91	7	1.0	1346	4	US-09-657-440-4	Sequence 4, Appli
92	7	1.0	11877	3	US-09-105-537-6	Sequence 6, Appli
93	6	0.8	11	3	US-08-464-961-2	Sequence 2, Appli
94	6	0.8	11	3	US-08-957-130-17	Sequence 17, Appl
95	6	0.8	11	3	US-08-969-315-2	Sequence 2, Appli
96	6	0.8	11	5	PCT-US96-08233-2	Sequence 2, Appli
97	6	0.8	12	4	US-09-205-258-304	Sequence 304, App
98	6	0.8	13	1	US-08-179-481-87	Sequence 87, Appl
99	6	0.8	17	1	US-08-205-938A-14	Sequence 14, Appl
100	6	0.8	17	5	PCT-US95-02626-14	Sequence 14, Appl

101	6	0.8	20	1	US-08-305-938A-13	Sequence 13, Appl	174	6	0.8	94	4	US-08-328-500-10	Sequence 10, Appl
102	6	0.8	20	5	PCT-US95-02626-13	Sequence 13, Appl	175	6	0.8	96	3	US-09-230-637-44	Sequence 44, Appl
103	6	0.8	25	4	US-09-660-587-28	Sequence 28, Appl	176	6	0.8	101	4	US-09-390-134B-42	Sequence 42, Appl
104	6	0.8	25	4	US-09-361-358A-28	Sequence 28, Appl	177	6	0.8	103	4	US-09-199-637A-271	Sequence 271, Appl
105	6	0.8	25	4	US-09-301-458-20	Sequence 20, Appl	178	6	0.8	103	4	US-09-252-991A-32642	Sequence 32642, A
106	6	0.8	25	4	US-09-811-007A-28	Sequence 28, Appl	179	6	0.8	103	4	US-09-543-681A-8232	Sequence 8232, Ap
107	6	0.8	35	1	US-08-145-708A-15	Sequence 15, Appl	180	6	0.8	103	4	US-09-621-976-4109	Sequence 4109, Ap
108	6	0.8	35	2	US-08-331-454-15	Sequence 15, Appl	181	6	0.8	106	4	US-09-087-031E-13	Sequence 13, Appl
109	6	0.8	37	2	US-09-066-074-14	Sequence 14, Appl	182	6	0.8	107	4	US-09-732-210-230	Sequence 230, Appl
110	6	0.8	37	2	US-08-555-912A-14	Sequence 14, Appl	183	6	0.8	107	4	US-09-489-039A-9954	Sequence 9954, Ap
111	6	0.8	37	3	US-08-348-518C-24	Sequence 24, Appl	184	6	0.8	108	4	US-09-489-039A-9392	Sequence 9392, Ap
112	6	0.8	37	3	US-08-476-509B-24	Sequence 24, Appl	185	6	0.8	108	4	US-09-489-039A-11679	Sequence 11679, A
113	6	0.8	37	4	US-09-252-404A-39	Sequence 39, Appl	186	6	0.8	109	4	US-09-134-000C-6718	Sequence 6718, Ap
114	6	0.8	37	4	US-09-275-900-14	Sequence 14, Appl	187	6	0.8	110	4	US-09-376-330-24	Sequence 24, Appl
115	6	0.8	37	4	US-09-821-861-16	Sequence 16, Appl	188	6	0.8	111	4	US-09-252-991A-17096	Sequence 17096, A
116	6	0.8	38	1	US-08-145-708A-14	Sequence 14, Appl	189	6	0.8	112	4	US-09-107-532A-7068	Sequence 7068, Ap
117	6	0.8	38	2	US-08-331-454-14	Sequence 14, Appl	190	6	0.8	121	1	US-08-307-498-7	Sequence 7, Appl
118	6	0.8	40	3	US-08-706-344C-19	Sequence 19, Appl	191	6	0.8	121	3	US-09-298-268-7	Sequence 7, Appl
119	6	0.8	40	4	US-08-469-260A-467	Sequence 467, App	192	6	0.8	122	4	US-09-732-210-598	Sequence 598, App
120	6	0.8	40	4	US-08-488-446-467	Sequence 467, App	193	6	0.8	122	4	US-09-732-210-600	Sequence 600, App
121	6	0.8	40	4	US-08-467-344A-467	Sequence 467, App	194	6	0.8	123	3	US-09-124-900-10	Sequence 10, Appl
122	6	0.8	41	1	US-08-168-091A-41	Sequence 41, Appl	195	6	0.8	123	3	US-09-134-001C-3283	Sequence 3283, Ap
123	6	0.8	42	1	US-09-066-330-3	Sequence 3, Appl	196	6	0.8	124	4	US-08-311-731A-202	Sequence 202, App
124	6	0.8	42	1	US-07-398-003A-73	Sequence 73, Appl	197	6	0.8	125	4	US-09-543-681A-1777	Sequence 1777, Ap
125	6	0.8	43	1	US-08-453-274B-73	Sequence 73, Appl	198	6	0.8	127	4	US-09-134-001C-2936	Sequence 2936, Ap
126	6	0.8	43	1	US-08-453-695A-73	Sequence 73, Appl	199	6	0.8	127	4	US-09-134-001C-2937	Sequence 2937, Ap
127	6	0.8	43	1	US-08-268-161A-73	Sequence 73, Appl	200	6	0.8	127	4	US-09-809-739-10	Sequence 10, Appl
128	6	0.8	43	2	US-08-453-702A-73	Sequence 73, Appl	201	6	0.8	128	4	US-09-134-001C-2881	Sequence 2881, Ap
129	6	0.8	43	2	US-08-751-305-4	Sequence 4, Appl	202	6	0.8	128	4	US-09-134-000C-3953	Sequence 3953, Ap
130	6	0.8	43	3	US-09-099-639-73	Sequence 73, Appl	203	6	0.8	132	4	US-09-252-991A-29618	Sequence 29618, A
131	6	0.8	43	5	PCT-US93-12588-73	Sequence 73, Appl	204	6	0.8	133	4	US-09-252-991A-32343	Sequence 32343, A
132	6	0.8	43	5	PCT-US95-08071-73	Sequence 73, Appl	205	6	0.8	134	4	US-09-134-001C-3817	Sequence 3817, Ap
133	6	0.8	44	3	US-09-220-528-85	Sequence 85, Appl	206	6	0.8	134	4	US-09-252-991A-24835	Sequence 24835, A
134	6	0.8	45	3	US-08-899-437-13	Sequence 13, Appl	207	6	0.8	136	4	US-09-252-991A-24892	Sequence 24892, A
135	6	0.8	45	3	US-09-126-121-13	Sequence 13, Appl	208	6	0.8	138	3	US-08-630-172-1	Sequence 1, Appl
136	6	0.8	46	3	US-08-753-007A-16	Sequence 16, Appl	209	6	0.8	138	3	US-09-375-419-1	Sequence 1, Appl
137	6	0.8	46	3	US-09-398-496-16	Sequence 16, Appl	210	6	0.8	139	3	US-08-444-818-174	Sequence 174, App
138	6	0.8	46	4	US-09-083-541-4	Sequence 4, Appl	211	6	0.8	140	4	US-09-252-991A-31623	Sequence 31623, A
139	6	0.8	50	3	US-09-004-406C-10	Sequence 10, Appl	212	6	0.8	140	4	US-08-906-769-135	Sequence 135, App
140	6	0.8	50	3	US-09-004-406C-11	Sequence 11, Appl	213	6	0.8	141	3	US-08-906-616-135	Sequence 135, App
141	6	0.8	52	1	US-08-294-189-17	Sequence 17, Appl	214	6	0.8	141	3	US-08-639-075A-135	Sequence 135, App
142	6	0.8	56	4	US-09-055-075C-48	Sequence 48, Appl	215	6	0.8	141	3	US-09-012-431-135	Sequence 135, App
143	6	0.8	56	4	US-09-319-124-48	Sequence 48, Appl	216	6	0.8	141	3	US-09-012-692-135	Sequence 135, App
144	6	0.8	56	4	US-09-765-815-9	Sequence 9, Appl	217	6	0.8	141	3	US-08-906-613-135	Sequence 135, App
145	6	0.8	59	4	US-09-800-729-163	Sequence 163, App	218	6	0.8	144	4	US-09-199-637A-17	Sequence 17, Appl
146	6	0.8	62	4	US-09-107-532A-5665	Sequence 5665, Ap	219	6	0.8	144	4	US-09-134-001C-4218	Sequence 4218, Ap
147	6	0.8	62	4	US-09-497-491-27	Sequence 27, Appl	220	6	0.8	146	4	US-09-252-991A-18563	Sequence 18563, A
148	6	0.8	64	4	US-09-482-273-117	Sequence 117, App	221	6	0.8	146	4	US-09-252-991A-18563	Sequence 18563, A
149	6	0.8	64	4	US-09-352-991A-17573	Sequence 17573, A	222	6	0.8	149	2	US-08-038-364-18	Sequence 18, Appl
150	6	0.8	70	4	US-09-732-210-883	Sequence 883, App	223	6	0.8	149	3	US-09-158-710-18	Sequence 18, Appl
151	6	0.8	72	4	US-09-540-236-2199	Sequence 2199, App	224	6	0.8	150	4	US-09-252-991A-17720	Sequence 17720, A
152	6	0.8	74	4	US-09-543-681A-8341	Sequence 8341, Ap	225	6	0.8	151	4	US-08-679-493A-74	Sequence 74, Appl
153	6	0.8	74	4	US-09-134-000C-6316	Sequence 6316, Ap	226	6	0.8	153	4	US-09-288-143-123	Sequence 123, App
154	6	0.8	76	4	US-09-328-352-4331	Sequence 4331, Ap	227	6	0.8	153	4	US-09-252-991A-23634	Sequence 23634, A
155	6	0.8	77	3	US-08-718-904-6	Sequence 6, Appl	228	6	0.8	153	4	US-09-134-000C-5186	Sequence 5186, Ap
156	6	0.8	77	4	US-09-449-249-6	Sequence 6, Appl	229	6	0.8	154	4	US-09-387-418A-8	Sequence 8, Appl
157	6	0.8	85	4	US-09-732-210-1467	Sequence 1467, Ap	230	6	0.8	156	1	US-08-469-667-20	Sequence 20, Appl
158	6	0.8	86	1	US-07-847-743B-19	Sequence 19, Appl	231	6	0.8	156	4	US-09-224-110-20	Sequence 20, Appl
159	6	0.8	86	1	US-08-456-201-19	Sequence 19, Appl	232	6	0.8	156	4	US-09-252-991A-24413	Sequence 24413, A
160	6	0.8	86	2	US-08-330-161-17	Sequence 17, Appl	233	6	0.8	156	5	PCT-US95-07289-20	Sequence 20, Appl
161	6	0.8	86	2	US-08-456-241-19	Sequence 19, Appl	234	6	0.8	157	2	US-08-811-949-41	Sequence 41, Appl
162	6	0.8	86	2	US-08-440-401-17	Sequence 17, Appl	235	6	0.8	157	3	US-08-872-855-6	Sequence 6, Appl
163	6	0.8	86	2	US-08-419-878B-17	Sequence 17, Appl	236	6	0.8	157	3	US-08-981-392-68	Sequence 68, Appl
164	6	0.8	86	4	US-09-134-001C-3359	Sequence 3359, Ap	237	6	0.8	159	3	US-09-071-035-446	Sequence 446, Appl
165	6	0.8	86	4	US-09-173-480-17	Sequence 17, Appl	238	6	0.8	159	3	US-08-796-792-2	Sequence 2, Appl
166	6	0.8	86	4	US-09-252-991A-29383	Sequence 29383, A	239	6	0.8	159	4	US-09-491-795-2	Sequence 29, Appl
167	6	0.8	86	5	PCT-US92-04295A-19	Sequence 19, Appl	240	6	0.8	162	1	US-08-266-451B-29	Sequence 29, Appl
168	6	0.8	87	4	US-09-352-991A-28740	Sequence 28740, A	241	6	0.8	162	2	US-08-748-725-29	Sequence 29, Appl
169	6	0.8	90	4	US-09-352-991A-24074	Sequence 24074, A	242	6	0.8	164	4	US-09-540-236-2636	Sequence 2636, Ap
170	6	0.8	93	4	US-09-252-991A-17535	Sequence 17535, A	243	6	0.8	164	4	US-09-489-039A-11750	Sequence 11750, A
171	6	0.8	94	3	US-08-946-329A-79	Sequence 79, Appl	244	6	0.8	170	4	US-09-252-991A-22362	Sequence 22362, A
172	6	0.8	94	3	US-08-466-368-5	Sequence 5, Appl	245	6	0.8	172	4	US-09-252-991A-29480	Sequence 29480, A
173	6	0.8	94	4	US-08-470-598-2	Sequence 2, Appl	246	6	0.8	172	4	US-09-328-352-5591	Sequence 5591, Ap

247	6	0.8	176	4	US-09-252-991A-24281	Sequence 24281, A	320	6	0.8	208	4	US-09-518-950-2	Sequence 2, Appli
248	6	0.8	176	4	US-09-252-991A-24805	Sequence 24805, A	321	6	0.8	208	4	US-09-449-249-5	Sequence 5, Appli
249	6	0.8	176	4	US-09-489-039A-12706	Sequence 12706, A	322	6	0.8	208	4	US-09-449-249-7	Sequence 7, Appli
250	6	0.8	177	2	US-08-770-544-20	Sequence 20, Appl	323	6	0.8	208	4	US-09-252-991A-23641	Sequence 23641, A
251	6	0.8	177	4	US-09-579-259-20	Sequence 20, Appl	324	6	0.8	208	4	US-10-138-158-18	Sequence 18, Appl
252	6	0.8	177	4	US-09-543-681A-5159	Sequence 5159, Ap	325	6	0.8	209	3	US-08-375-762-71	Sequence 71, Appl
253	6	0.8	177	4	US-09-650-324A-20	Sequence 20, Appl	326	6	0.8	209	3	US-09-295-028-71	Sequence 71, Appl
254	6	0.8	179	3	US-09-612-126-11	Sequence 11, Appl	327	6	0.8	209	4	US-09-106-582-71	Sequence 71, Appl
255	6	0.8	180	4	US-09-543-681A-7669	Sequence 7669, Ap	328	6	0.8	209	4	US-09-311-311C-20	Sequence 20, Appl
256	6	0.8	181	4	US-09-252-991A-17818	Sequence 17818, A	329	6	0.8	209	4	US-09-252-991A-23571	Sequence 23571, A
257	6	0.8	181	4	US-09-134-000C-4633	Sequence 4633, Ap	330	6	0.8	209	4	US-09-159-469-71	Sequence 71, Appl
258	6	0.8	183	3	US-09-621-976-4025	Sequence 4025, Ap	331	6	0.8	209	4	US-09-693-542-71	Sequence 71, Appl
259	6	0.8	184	3	US-08-907-800A-2	Sequence 2, Appli	332	6	0.8	210	3	US-09-162-184-33	Sequence 33, Appl
260	6	0.8	184	3	US-08-969-317-2	Sequence 2, Appli	333	6	0.8	210	3	US-09-489-777A-33	Sequence 33, Appl
261	6	0.8	185	3	US-08-975-762-11	Sequence 11, Appl	334	6	0.8	210	4	US-09-252-991A-27171	Sequence 27171, A
262	6	0.8	185	3	US-08-821-324-11	Sequence 11, Appl	335	6	0.8	211	3	US-09-252-991A-28553	Sequence 28553, A
263	6	0.8	185	3	US-09-295-028-11	Sequence 11, Appl	336	6	0.8	212	3	US-08-861-774E-22	Sequence 22, Appl
264	6	0.8	185	4	US-09-106-582-11	Sequence 11, Appl	337	6	0.8	212	3	US-08-861-774E-34	Sequence 34, Appl
265	6	0.8	185	4	US-09-159-469-11	Sequence 11, Appl	338	6	0.8	213	3	US-08-861-774E-60	Sequence 60, Appl
266	6	0.8	185	4	US-09-693-542-11	Sequence 11, Appl	339	6	0.8	213	3	US-08-861-774E-64	Sequence 64, Appl
267	6	0.8	186	3	US-09-612-126-8	Sequence 8, Appli	340	6	0.8	213	3	US-08-861-774E-72	Sequence 72, Appl
268	6	0.8	187	4	US-08-635-886C-207	Sequence 207, App	341	6	0.8	214	3	US-08-861-774E-30	Sequence 30, Appl
269	6	0.8	187	4	US-08-635-886C-208	Sequence 208, App	342	6	0.8	214	3	US-08-861-774E-32	Sequence 32, Appl
270	6	0.8	187	4	US-08-635-886C-209	Sequence 209, App	343	6	0.8	214	3	US-08-861-774E-44	Sequence 44, Appl
271	6	0.8	187	4	US-08-974-690C-207	Sequence 207, App	344	6	0.8	214	3	US-08-861-774E-48	Sequence 48, Appl
272	6	0.8	187	4	US-08-974-690C-208	Sequence 208, App	345	6	0.8	214	3	US-08-861-774E-54	Sequence 54, Appl
273	6	0.8	187	4	US-08-974-690C-209	Sequence 209, App	346	6	0.8	214	3	US-08-861-774E-66	Sequence 66, Appl
274	6	0.8	191	2	US-08-230-665A-187	Sequence 187, App	347	6	0.8	214	3	US-08-861-774E-76	Sequence 76, Appl
275	6	0.8	191	2	US-08-230-665A-189	Sequence 189, App	348	6	0.8	214	3	US-08-861-774E-78	Sequence 78, Appl
276	6	0.8	191	2	US-08-230-665A-190	Sequence 190, App	349	6	0.8	214	5	PCT-US96-08950-2	Sequence 2, Appli
277	6	0.8	191	5	PCT-US95-10398-187	Sequence 187, App	350	6	0.8	214	5	PCT-US96-09127-2	Sequence 2, Appli
278	6	0.8	191	5	PCT-US95-10398-189	Sequence 189, App	351	6	0.8	215	1	US-08-266-451B-27	Sequence 27, Appl
279	6	0.8	191	5	PCT-US95-10398-190	Sequence 190, App	352	6	0.8	215	1	US-08-748-725-27	Sequence 27, Appl
280	6	0.8	192	4	US-09-138-452A-276	Sequence 276, App	353	6	0.8	215	3	US-08-861-774E-40	Sequence 40, Appl
281	6	0.8	193	1	US-08-248-466B-14	Sequence 14, Appl	354	6	0.8	216	3	US-08-861-774E-58	Sequence 58, Appl
282	6	0.8	193	3	US-09-041-889-5	Sequence 5, Appli	355	6	0.8	216	3	US-08-861-774E-62	Sequence 62, Appl
283	6	0.8	193	3	US-08-837-058-5	Sequence 5, Appli	356	6	0.8	218	3	US-08-861-774E-46	Sequence 46, Appl
284	6	0.8	193	4	US-09-417-264-5	Sequence 5, Appli	357	6	0.8	218	3	US-08-861-774E-50	Sequence 50, Appl
285	6	0.8	193	4	US-08-635-886C-210	Sequence 210, App	358	6	0.8	218	4	US-09-134-000C-3898	Sequence 3898, Ap
286	6	0.8	193	4	US-08-974-690C-210	Sequence 210, App	359	6	0.8	218	4	US-09-828-303-23	Sequence 23, Appl
287	6	0.8	194	4	US-09-516-914-9	Sequence 9, Appli	360	6	0.8	219	3	US-08-861-774E-70	Sequence 70, Appl
288	6	0.8	194	4	US-09-489-039A-8286	Sequence 8286, Ap	361	6	0.8	219	4	US-09-252-991A-28228	Sequence 28228, A
289	6	0.8	196	3	US-08-931-392-35	Sequence 35, Appl	362	6	0.8	219	4	US-09-198-452A-634	Sequence 634, App
290	6	0.8	198	4	US-09-252-991A-22691	Sequence 22691, A	363	6	0.8	221	4	US-09-874-926-2	Sequence 2, Appli
291	6	0.8	199	4	US-09-252-991A-31135	Sequence 31135, A	364	6	0.8	222	4	US-09-252-991A-24147	Sequence 24147, A
292	6	0.8	200	4	US-09-101-272G-73	Sequence 73, Appl	365	6	0.8	223	4	US-09-252-991A-19065	Sequence 19065, A
293	6	0.8	200	4	US-09-252-991A-28054	Sequence 28054, A	366	6	0.8	224	4	US-09-198-452A-683	Sequence 683, App
294	6	0.8	200	4	US-09-489-039A-7536	Sequence 7526, Ap	367	6	0.8	224	4	US-08-630-915A-221	Sequence 221, App
295	6	0.8	201	4	US-08-679-493A-190	Sequence 190, App	368	6	0.8	230	4	US-09-516-143A-6	Sequence 6, Appli
296	6	0.8	202	4	US-09-252-991A-26505	Sequence 26505, A	369	6	0.8	231	4	US-09-543-681A-6357	Sequence 6357, Ap
297	6	0.8	202	4	US-09-252-991A-27017	Sequence 27017, A	370	6	0.8	233	4	US-09-069-023-36	Sequence 36, Appl
298	6	0.8	203	2	US-08-284-391B-31	Sequence 31, Appl	371	6	0.8	234	3	US-08-861-774E-52	Sequence 52, Appl
299	6	0.8	203	3	US-09-218-950-31	Sequence 31, Appl	372	6	0.8	235	1	US-08-287-959-8	Sequence 8, Appli
300	6	0.8	203	4	US-09-543-681A-4329	Sequence 4329, Ap	373	6	0.8	235	4	US-09-107-532A-6979	Sequence 6979, Ap
301	6	0.8	204	4	US-09-252-991A-29225	Sequence 22225, A	374	6	0.8	236	4	US-09-134-000C-4896	Sequence 4896, Ap
302	6	0.8	204	4	US-09-543-681A-8020	Sequence 8020, Ap	375	6	0.8	237	3	US-08-861-774E-68	Sequence 68, Appl
303	6	0.8	205	4	US-09-134-001C-4766	Sequence 4766, Ap	376	6	0.8	238	4	US-09-252-991A-29406	Sequence 29406, A
304	6	0.8	205	4	US-09-252-991A-29334	Sequence 29334, A	377	6	0.8	239	3	US-09-004-731-44	Sequence 44, Appl
305	6	0.8	205	4	US-09-134-000C-3913	Sequence 3913, Ap	378	6	0.8	239	3	US-08-749-699-44	Sequence 44, Appl
306	6	0.8	206	4	US-08-679-493A-75	Sequence 75, Appl	379	6	0.8	239	4	US-08-679-493A-76	Sequence 76, Appl
307	6	0.8	206	4	US-09-543-681A-4763	Sequence 4763, Ap	380	6	0.8	239	4	US-09-004-729-44	Sequence 44, Appl
308	6	0.8	207	4	US-09-198-452A-1020	Sequence 1020, Ap	381	6	0.8	239	4	US-09-328-352-7328	Sequence 7328, Ap
309	6	0.8	208	1	US-07-935-309-2	Sequence 2, Appli	382	6	0.8	240	4	US-09-328-352-7253	Sequence 7253, Ap
310	6	0.8	208	2	US-08-884-682-1	Sequence 1, Appli	383	6	0.8	242	3	US-09-004-731-41	Sequence 41, Appl
311	6	0.8	208	2	US-08-039-364-2	Sequence 2, Appli	384	6	0.8	242	3	US-09-032-215-47	Sequence 47, Appl
312	6	0.8	208	2	US-08-766-551-9	Sequence 9, Appli	385	6	0.8	242	3	US-08-749-699-41	Sequence 41, Appl
313	6	0.8	208	2	US-08-086-082-1	Sequence 1, Appli	386	6	0.8	242	4	US-09-004-729-41	Sequence 41, Appl
314	6	0.8	208	3	US-08-718-904-5	Sequence 5, Appli	387	6	0.8	242	4	US-09-252-991A-19021	Sequence 19021, A
315	6	0.8	208	3	US-08-718-904-7	Sequence 7, Appli	388	6	0.8	242	4	US-09-107-532A-6244	Sequence 6244, Ap
316	6	0.8	208	3	US-08-612-973-30	Sequence 30, Appl	389	6	0.8	243	4	US-09-543-681A-7356	Sequence 7356, Ap
317	6	0.8	208	3	US-09-181-974-2	Sequence 2, Appli	390	6	0.8	244	4	US-09-461-325-463	Sequence 463, App
318	6	0.8	208	3	US-09-158-710-2	Sequence 2, Appli	391	6	0.8	244	4	US-09-252-991A-29762	Sequence 29762, A
319	6	0.8	208	3	US-08-927-597-30	Sequence 30, Appl	392	6	0.8	244	4	US-10-012-542-463	Sequence 463, App



393	6	0.8	245	4	US-08-956-171B-5222	Sequence 5222, Ap	466	6	0.8	306	2	US-08-560-098A-45	Sequence 45, Appl
394	6	0.8	248	1	US-08-366-451B-2	Sequence 2, Appli	467	6	0.8	306	4	US-09-252-991A-27054	Sequence 27054, A
395	6	0.8	248	2	US-08-748-725-2	Sequence 2, Appli	468	6	0.8	306	4	US-09-328-352-5398	Sequence 5398, Ap
396	6	0.8	248	3	US-08-944-483-71	Sequence 71, Appl	469	6	0.8	307	4	US-09-193-634-53	Sequence 53, Appl
397	6	0.8	248	4	US-09-252-991A-17358	Sequence 17358, A	470	6	0.8	308	4	US-09-107-532A-6023	Sequence 6023, Ap
398	6	0.8	249	3	US-09-010-809-21	Sequence 21, Appl	471	6	0.8	309	2	US-08-849-480A-6	Sequence 6, Appli
399	6	0.8	250	3	US-09-010-809-3	Sequence 3, Appli	472	6	0.8	310	3	US-08-477-460B-6	Sequence 6, Appli
400	6	0.8	251	4	US-08-630-915A-8	Sequence 8, Appli	473	6	0.8	310	3	US-08-379-516-6	Sequence 6, Appli
401	6	0.8	252	3	US-08-944-483-72	Sequence 72, Appl	474	6	0.8	310	3	US-09-329-916-6	Sequence 6, Appli
402	6	0.8	253	2	US-09-027-337-8	Sequence 8, Appli	475	6	0.8	310	3	US-08-485-372A-6	Sequence 6, Appli
403	6	0.8	253	3	US-08-975-762-52	Sequence 52, Appl	476	6	0.8	310	4	US-09-409-006A-6	Sequence 6, Appli
404	6	0.8	253	3	US-08-944-483-73	Sequence 73, Appl	477	6	0.8	310	4	US-08-484-681-6	Sequence 6, Appli
405	6	0.8	253	3	US-09-295-028-52	Sequence 52, Appl	478	6	0.8	310	5	PCT-US93-07422-6	Sequence 6, Appli
406	6	0.8	253	4	US-09-106-582-52	Sequence 52, Appl	479	6	0.8	311	4	US-09-543-681A-5602	Sequence 5602, Ap
407	6	0.8	253	4	US-09-644-600-8	Sequence 8, Appli	480	6	0.8	311	4	US-09-489-039A-13013	Sequence 13013, A
408	6	0.8	253	4	US-09-159-469-52	Sequence 52, Appl	481	6	0.8	312	4	US-09-071-035-70	Sequence 70, Appl
409	6	0.8	253	4	US-09-489-039A-13739	Sequence 13739, A	482	6	0.8	312	4	US-09-351-150A-11	Sequence 11, Appl
410	6	0.8	253	4	US-09-554-600A-8	Sequence 8, Appli	483	6	0.8	312	4	US-09-599-360B-96	Sequence 96, Appl
411	6	0.8	254	2	US-09-593-542-52	Sequence 52, Appl	484	6	0.8	313	4	US-09-148-545-233	Sequence 233, Ap
412	6	0.8	254	2	US-08-560-098A-49	Sequence 49, Appl	485	6	0.8	313	4	US-09-252-991A-25243	Sequence 25243, A
413	6	0.8	255	3	US-09-612-126-1	Sequence 1, Appli	486	6	0.8	318	6	5223394-11	Patent No. 5223394
414	6	0.8	256	3	US-09-230-637-29	Sequence 29, Appl	487	6	0.8	320	4	US-09-134-001C-3522	Sequence 3522, Ap
415	6	0.8	256	4	US-09-489-039A-8774	Sequence 8774, Ap	488	6	0.8	320	4	US-09-134-001C-3823	Sequence 3823, Ap
416	6	0.8	257	2	US-08-467-265-16	Sequence 16, Appl	489	6	0.8	320	4	US-09-489-039A-10349	Sequence 10349, A
417	6	0.8	257	3	US-09-407-891-16	Sequence 16, Appl	490	6	0.8	320	4	US-09-489-039A-13881	Sequence 13881, A
418	6	0.8	257	3	US-09-407-891-16	Sequence 16, Appl	491	6	0.8	320	4	US-09-134-000C-5021	Sequence 5021, Ap
419	6	0.8	257	4	US-09-375-907-5	Sequence 5, Appli	492	6	0.8	322	4	US-09-252-991A-29347	Sequence 29347, A
420	6	0.8	258	4	US-09-227-357-198	Sequence 198, App	493	6	0.8	325	4	US-08-311-731A-249	Sequence 249, App
421	6	0.8	258	4	US-09-252-991A-32929	Sequence 32929, A	494	6	0.8	326	3	US-09-066-046-29	Sequence 29, Appl
422	6	0.8	261	4	US-09-252-991A-29007	Sequence 29007, A	495	6	0.8	326	4	US-09-066-047-15	Sequence 15, Appl
423	6	0.8	264	2	US-08-484-905-120	Sequence 120, App	496	6	0.8	326	4	US-09-411-977-3	Sequence 3, Appli
424	6	0.8	264	3	US-08-481-985B-120	Sequence 120, App	497	6	0.8	326	4	US-09-543-681A-7709	Sequence 7709, Ap
425	6	0.8	264	3	US-08-370-476-120	Sequence 120, App	498	6	0.8	327	4	US-09-252-991A-33067	Sequence 33067, A
426	6	0.8	272	4	US-09-252-991A-27911	Sequence 27911, A	499	6	0.8	331	2	US-08-560-098A-46	Sequence 46, Appl
427	6	0.8	276	3	US-08-953-326-18	Sequence 18, Appl	500	6	0.8	332	4	US-09-134-001C-4323	Sequence 4323, Ap
428	6	0.8	276	4	US-09-553-662-18	Sequence 18, Appl	501	6	0.8	333	4	US-09-328-352-7516	Sequence 7516, Ap
429	6	0.8	276	4	US-10-062-994-18	Sequence 18, Appl	502	6	0.8	334	4	US-09-218-363-11	Sequence 11, Appl
430	6	0.8	277	4	US-09-252-991A-17567	Sequence 17567, A	503	6	0.8	336	1	US-07-904-073-2	Sequence 2, Appli
431	6	0.8	278	4	US-09-252-991A-28712	Sequence 28712, A	504	6	0.8	336	1	US-07-904-071-2	Sequence 2, Appli
432	6	0.8	278	4	US-09-328-352-5824	Sequence 5824, Ap	505	6	0.8	336	1	US-08-442-043A-16	Sequence 16, Appl
433	6	0.8	280	4	US-09-107-532A-6088	Sequence 6088, Ap	506	6	0.8	336	4	US-08-441-893A-16	Sequence 16, Appl
434	6	0.8	281	4	US-09-660-587-9	Sequence 9, Appli	507	6	0.8	337	4	US-09-252-991A-26757	Sequence 26757, A
435	6	0.8	281	4	US-09-261-358A-9	Sequence 9, Appli	508	6	0.8	337	4	US-09-252-991A-30261	Sequence 30261, A
436	6	0.8	281	4	US-09-201-458-5	Sequence 5, Appli	509	6	0.8	338	4	US-09-107-532A-5819	Sequence 5819, Ap
437	6	0.8	281	4	US-09-314-701-2	Sequence 2, Appli	510	6	0.8	340	4	US-09-543-681A-7850	Sequence 7850, Ap
438	6	0.8	281	4	US-09-811-007A-9	Sequence 9, Appli	511	6	0.8	341	4	US-09-543-681A-4713	Sequence 4713, Ap
439	6	0.8	282	4	US-09-252-991A-25948	Sequence 25948, A	512	6	0.8	342	4	US-09-252-991A-30257	Sequence 30257, A
440	6	0.8	284	4	US-08-976-063B-2	Sequence 2, Appli	513	6	0.8	343	4	US-09-252-991A-22307	Sequence 22307, A
441	6	0.8	285	3	US-09-027-137-3	Sequence 3, Appli	514	6	0.8	345	3	US-09-027-900-11	Sequence 11, Appl
442	6	0.8	285	4	US-09-344-441-3	Sequence 3, Appli	515	6	0.8	345	4	US-09-489-039A-10740	Sequence 10740, A
443	6	0.8	287	3	US-08-549-515-10	Sequence 10, Appl	516	6	0.8	346	4	US-09-252-991A-21487	Sequence 21487, A
444	6	0.8	288	4	US-09-489-039A-8919	Sequence 8919, Ap	517	6	0.8	347	2	US-08-811-949-1	Sequence 1, Appli
445	6	0.8	289	4	US-09-071-035-72	Sequence 72, Appl	518	6	0.8	347	4	US-09-636-215-590	Sequence 590, App
446	6	0.8	289	4	US-09-252-991A-22483	Sequence 22483, A	519	6	0.8	347	4	US-09-685-166A-590	Sequence 590, App
447	6	0.8	292	3	US-09-027-137-1	Sequence 1, Appli	520	6	0.8	348	4	US-09-360-376-13	Sequence 13, Appl
448	6	0.8	292	4	US-09-344-441-1	Sequence 1, Appli	521	6	0.8	349	4	US-09-489-039A-7582	Sequence 7582, Ap
449	6	0.8	292	4	US-09-328-352-6642	Sequence 6642, Ap	522	6	0.8	351	1	US-08-324-483-2	Sequence 2, Appli
450	6	0.8	292	4	US-09-543-681A-7918	Sequence 7918, Ap	523	6	0.8	354	2	US-08-811-949-61	Sequence 61, Appl
451	6	0.8	295	4	US-09-134-000C-3737	Sequence 3737, Ap	524	6	0.8	355	1	US-08-137-116-1	Sequence 1, Appli
452	6	0.8	295	6	5223394-9	Patent No. 5223394	525	6	0.8	355	1	US-08-217-618-1	Sequence 1, Appli
453	6	0.8	296	4	US-09-252-991A-17385	Sequence 17385, A	526	6	0.8	355	1	US-08-427-640-2	Sequence 2, Appli
454	6	0.8	297	4	US-09-543-681A-7800	Sequence 7800, Ap	527	6	0.8	355	1	US-08-427-640-6	Sequence 6, Appli
455	6	0.8	298	4	US-09-252-991A-25360	Sequence 25360, A	528	6	0.8	355	1	US-08-217-617A-1	Sequence 1, Appli
456	6	0.8	300	1	US-08-148-910-1	Sequence 1, Appli	529	6	0.8	355	2	US-08-217-616-1	Sequence 1, Appli
457	6	0.8	300	1	US-08-448-937A-1	Sequence 1, Appli	530	6	0.8	355	2	US-08-811-949-45	Sequence 45, Appl
458	6	0.8	300	4	US-09-252-991A-20115	Sequence 20115, A	531	6	0.8	355	2	US-08-811-949-47	Sequence 47, Appl
459	6	0.8	301	4	US-09-252-991A-25396	Sequence 25396, A	532	6	0.8	355	2	US-08-811-949-53	Sequence 53, Appl
460	6	0.8	301	4	US-09-134-000C-6014	Sequence 6014, Ap	533	6	0.8	355	2	US-08-811-949-59	Sequence 59, Appl
461	6	0.8	302	4	US-09-232-991A-21231	Sequence 21231, A	534	6	0.8	355	3	US-08-794-528-1	Sequence 1, Appli
462	6	0.8	302	4	US-09-328-352-4508	Sequence 4508, Ap	535	6	0.8	355	4	US-09-252-991A-22326	Sequence 22326, A
463	6	0.8	302	4	US-09-540-236-2119	Sequence 2119, Ap	536	6	0.8	355	6	US-09-198-452A-871	Sequence 871, App
464	6	0.8	303	4	US-09-107-532A-5585	Sequence 5585, Ap	537	6	0.8	355	6	5223256-1	Patent No. 5223256
465	6	0.8	304	4	US-09-489-039A-9424	Sequence 9424, Ap	538	6	0.8	356	1	US-08-427-640-4	Sequence 4, Appli

539	6	0.8	356	1	US-08-427-640-8	Sequence 8, Appli	612	6	0.8	401	4	US-09-252-991A-17090	Sequence 17090, A
540	6	0.8	356	4	US-09-252-991A-30030	Sequence 30030, A	613	6	0.8	402	1	US-08-236-311-1	Sequence 1, Appli
541	6	0.8	362	4	US-09-252-991A-18494	Sequence 18494, A	614	6	0.8	402	3	US-08-457-918-1	Sequence 1, Appli
542	6	0.8	364	4	US-09-252-991A-19037	Sequence 19037, A	615	6	0.8	403	4	US-09-802-213-5	Sequence 5, Appli
543	6	0.8	365	1	US-08-093-741-83	Sequence 83, Appli	616	6	0.8	405	4	US-09-144-914-5	Sequence 5, Appli
544	6	0.8	365	1	US-08-720-012-83	Sequence 83, Appli	617	6	0.8	405	4	US-09-252-991A-23838	Sequence 23838, A
545	6	0.8	365	3	US-09-231-529-3	Sequence 3, Appli	618	6	0.8	405	4	US-09-134-000C-5465	Sequence 5465, Ap
546	6	0.8	365	3	US-08-977-816-3	Sequence 3, Appli	619	6	0.8	408	4	US-09-252-991A-21303	Sequence 21303, A
547	6	0.8	366	4	US-09-252-991A-24466	Sequence 24466, A	620	6	0.8	408	4	US-09-198-452A-141	Sequence 141, App
548	6	0.8	367	3	US-08-895-707-6	Sequence 6, Appli	621	6	0.8	410	1	US-08-792-283A-9	Sequence 9, Appli
549	6	0.8	367	4	US-09-252-991A-17240	Sequence 17240, A	622	6	0.8	410	2	US-09-105-908-9	Sequence 9, Appli
550	6	0.8	367	4	US-09-328-352-7662	Sequence 7662, Ap	623	6	0.8	410	3	US-08-630-172-17	Sequence 17, Appli
551	6	0.8	372	4	US-09-252-991A-28586	Sequence 28586, A	624	6	0.8	410	3	US-09-271-713-9	Sequence 9, Appli
552	6	0.8	372	4	US-09-973-963-4	Sequence 4, Appli	625	6	0.8	410	3	US-09-375-419-17	Sequence 17, Appli
553	6	0.8	373	4	US-09-404-296B-4	Sequence 4, Appli	626	6	0.8	410	4	US-09-252-991A-25812	Sequence 25812, A
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555	6	0.8	374	3	US-09-055-699-25	Sequence 25, Appli	628	6	0.8	410	4	US-09-489-039A-10283	Sequence 10283, A
556	6	0.8	374	3	US-09-273-555-25	Sequence 25, Appli	629	6	0.8	411	1	US-08-087-163-1	Sequence 1, Appli
557	6	0.8	374	4	US-09-565-538-25	Sequence 25, Appli	630	6	0.8	411	1	US-08-286-748B-18	Sequence 18, Appli
558	6	0.8	374	4	US-09-661-468-25	Sequence 25, Appli	631	6	0.8	411	1	US-08-153-799-18	Sequence 18, Appli
559	6	0.8	374	4	US-09-976-165-25	Sequence 25, Appli	632	6	0.8	411	2	US-08-560-098A-48	Sequence 48, Appli
560	6	0.8	374	4	US-09-227-853A-2	Sequence 2, Appli	633	6	0.8	411	3	US-09-376-689-2	Sequence 2, Appli
561	6	0.8	374	4	US-09-540-236-2230	Sequence 2230, Ap	634	6	0.8	411	3	US-09-181-816-1	Sequence 1, Appli
562	6	0.8	374	5	PCT-US95-06385-2	Sequence 3, Appli	635	6	0.8	411	4	US-09-403-736-2	Sequence 2, Appli
563	6	0.8	375	3	US-08-872-979-3	Sequence 3, Appli	636	6	0.8	414	4	US-09-252-991A-27828	Sequence 27828, A
564	6	0.8	375	4	US-09-328-352-6191	Sequence 6191, Ap	637	6	0.8	415	1	US-08-110-286A-6	Sequence 6, Appli
565	6	0.8	375	4	US-09-489-039A-11560	Sequence 11560, A	638	6	0.8	415	3	US-08-981-189B-10	Sequence 10, Appli
566	6	0.8	377	4	US-09-679-279-3	Sequence 3, Appli	639	6	0.8	415	4	US-08-482-746-6	Sequence 6, Appli
567	6	0.8	377	4	US-09-489-039A-12546	Sequence 12546, A	640	6	0.8	415	4	US-09-180-109A-9	Sequence 9, Appli
568	6	0.8	378	4	US-09-553-498-10	Sequence 10, Appli	641	6	0.8	415	4	US-09-180-109A-12	Sequence 12, Appli
569	6	0.8	378	4	US-09-618-869-10	Sequence 10, Appli	642	6	0.8	415	4	US-09-580-734-6	Sequence 6, Appli
570	6	0.8	378	4	US-09-673-395A-618	Sequence 618, App	643	6	0.8	415	4	US-08-374-009-6	Sequence 6, Appli
571	6	0.8	379	4	US-09-252-991A-17472	Sequence 17472, A	644	6	0.8	415	4	US-09-191-724-6	Sequence 6, Appli
572	6	0.8	381	4	US-09-673-395A-441	Sequence 441, App	645	6	0.8	415	4	US-09-799-978-16	Sequence 16, Appli
573	6	0.8	383	1	US-08-486-037B-2	Sequence 2, Appli	646	6	0.8	420	4	US-09-252-991A-17500	Sequence 17500, A
574	6	0.8	383	2	US-08-558-269-6	Sequence 6, Appli	647	6	0.8	422	4	US-09-489-847-357	Sequence 357, App
575	6	0.8	383	3	US-09-410-882-6	Sequence 6, Appli	648	6	0.8	424	4	US-09-134-001C-5009	Sequence 5009, Ap
576	6	0.8	385	3	US-09-071-224-19	Sequence 19, Appli	649	6	0.8	424	4	US-09-173-300-45	Sequence 45, Appli
577	6	0.8	386	3	US-08-895-707-7	Sequence 7, Appli	650	6	0.8	424	4	US-09-107-532A-5459	Sequence 5459, Ap
578	6	0.8	386	3	US-09-045-284A-2	Sequence 2, Appli	651	6	0.8	425	3	US-09-071-224-6	Sequence 6, Appli
579	6	0.8	386	4	US-09-190-911-1	Sequence 1, Appli	652	6	0.8	425	4	US-09-134-001C-5619	Sequence 5619, Ap
580	6	0.8	386	4	US-09-786-240-11	Sequence 11, Appli	653	6	0.8	425	4	US-09-540-236-3466	Sequence 3466, Ap
581	6	0.8	386	4	US-09-489-039A-7410	Sequence 7410, Ap	654	6	0.8	426	4	US-09-252-991A-25192	Sequence 25192, A
582	6	0.8	389	2	US-08-811-949-67	Sequence 67, Appli	655	6	0.8	427	4	US-09-198-452A-31	Sequence 31, Appli
583	6	0.8	389	3	US-09-071-224-27	Sequence 27, Appli	656	6	0.8	427	4	US-09-328-352-5205	Sequence 5205, Ap
584	6	0.8	389	4	US-09-107-532A-6185	Sequence 6185, Ap	657	6	0.8	428	1	US-08-570-157-5	Sequence 5, Appli
585	6	0.8	390	4	US-09-252-991A-26543	Sequence 26543, A	658	6	0.8	428	3	US-08-029-170-31	Sequence 31, Appli
586	6	0.8	391	4	US-09-543-681A-7029	Sequence 7029, Ap	659	6	0.8	428	4	US-08-403-797-2	Sequence 2, Appli
587	6	0.8	392	1	US-08-706-539-9	Sequence 9, Appli	660	6	0.8	428	4	US-09-076-510-5	Sequence 5, Appli
588	6	0.8	392	3	US-09-027-007-9	Sequence 9, Appli	661	6	0.8	428	4	US-09-004-349-5	Sequence 5, Appli
589	6	0.8	393	2	US-08-560-098A-44	Sequence 44, Appli	662	6	0.8	429	4	US-09-252-991A-28788	Sequence 28788, A
590	6	0.8	393	3	US-08-967-024C-24	Sequence 24, Appli	663	6	0.8	430	6	US-07-942-157A-3	Sequence 3, Appli
591	6	0.8	393	3	US-08-967-024C-25	Sequence 25, Appli	664	6	0.8	430	6	5219569-2	Patent No. 5219569
592	6	0.8	394	3	US-08-466-368-2	Sequence 2, Appli	665	6	0.8	431	3	US-09-376-689-4	Sequence 4, Appli
593	6	0.8	394	4	US-09-144-914-4	Sequence 4, Appli	666	6	0.8	431	3	US-09-101-272G-1	Sequence 1, Appli
594	6	0.8	394	4	US-09-252-991A-18502	Sequence 18502, A	667	6	0.8	431	4	US-09-540-236-5536	Sequence 3536, Ap
595	6	0.8	394	4	US-08-328-500-2	Sequence 2, Appli	668	6	0.8	431	4	5188829-1	Patent No. 5188829
596	6	0.8	394	6	5233418-2	Patent No. 5233418	669	6	0.8	432	2	US-08-560-098A-47	Sequence 47, Appli
597	6	0.8	395	1	US-08-485-859-2	Sequence 2, Appli	670	6	0.8	432	3	US-08-477-460B-2	Sequence 2, Appli
598	6	0.8	395	1	US-08-706-539-11	Sequence 11, Appli	671	6	0.8	432	3	US-08-379-516-2	Sequence 2, Appli
599	6	0.8	395	1	US-08-522-166-2	Sequence 2, Appli	672	6	0.8	432	3	US-09-329-916-2	Sequence 2, Appli
600	6	0.8	395	1	US-08-488-382A-2	Sequence 2, Appli	673	6	0.8	432	3	US-08-485-372A-2	Sequence 2, Appli
601	6	0.8	395	2	US-08-480-912-2	Sequence 2, Appli	674	6	0.8	432	4	US-09-409-006A-2	Sequence 2, Appli
602	6	0.8	395	3	US-09-027-007-11	Sequence 11, Appli	675	6	0.8	432	4	US-08-484-681-2	Sequence 2, Appli
603	6	0.8	396	4	US-09-252-991A-18619	Sequence 18619, A	676	6	0.8	432	5	PCT-US93-07422-2	Sequence 2, Appli
604	6	0.8	397	1	US-08-647-928-8	Sequence 8, Appli	677	6	0.8	433	2	US-08-867-149-1	Sequence 1, Appli
605	6	0.8	397	4	US-09-489-039A-13498	Sequence 13498, A	678	6	0.8	433	2	US-08-808-374-1	Sequence 1, Appli
606	6	0.8	398	2	US-08-284-331B-29	Sequence 29, Appli	679	6	0.8	433	3	US-09-100-409A-1	Sequence 1, Appli
607	6	0.8	398	3	US-09-218-950-29	Sequence 29, Appli	680	6	0.8	433	4	US-09-364-230-14	Sequence 14, Appli
608	6	0.8	399	4	US-09-489-039A-8859	Sequence 8859, Ap	681	6	0.8	433	6	5171838-13	Patent No. 5171838
609	6	0.8	400	4	US-09-134-001C-4785	Sequence 4785, Ap	682	6	0.8	434	1	US-08-236-311-4	Sequence 4, Appli
610	6	0.8	400	4	US-09-252-991A-31296	Sequence 31296, A	683	6	0.8	434	3	US-08-457-918-4	Sequence 4, Appli
611	6	0.8	401	4	US-09-489-847-202	Sequence 202, App	684	6	0.8	434	4	US-09-252-991A-23131	Sequence 23131, A

685 6 0.8 434 4 US-09-543-681A-7154 Sequence 7154, Ap  
686 6 0.8 437 2 US-08-811-949-49 Sequence 49, Appl  
687 6 0.8 437 2 US-08-811-949-51 Sequence 51, Appl  
688 6 0.8 437 2 US-08-811-949-55 Sequence 55, Appl  
689 6 0.8 437 2 US-08-811-949-57 Sequence 57, Appl  
690 6 0.8 438 4 US-09-252-991A-28398 Sequence 28398, A  
691 6 0.8 438 4 US-09-489-039A-8464 Sequence 8464, Ap  
692 6 0.8 439 2 US-08-959-638-9 Sequence 9, Appl  
693 6 0.8 439 4 US-09-543-681A-7293 Sequence 7293, Ap  
694 6 0.8 440 4 US-09-489-039A-10782 Sequence 10782, A  
695 6 0.8 441 3 US-09-457-046B-54 Sequence 54, Appl  
696 6 0.8 441 4 US-09-297-937C-11 Sequence 11, Appl  
697 6 0.8 443 1 US-08-570-157-6 Sequence 6, Appl  
698 6 0.8 443 4 US-09-076-510-6 Sequence 6, Appl  
699 6 0.8 443 4 US-09-004-349-6 Sequence 6, Appl  
700 6 0.8 444 1 US-07-937-609-14 Sequence 14, Appl

## ALIGNMENTS

## RESULT 1

US-09-374-135-4  
; Sequence 4, Application US/09374135  
; Patent No. 6277972  
; GENERAL INFORMATION:  
; APPLICANT: Afar, Daniel E.  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Leong, Kahan  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Saffran, Douglas C.  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: BPC-1: A SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED AND  
; FILE REFERENCE: 1703-017.US1  
; CURRENT APPLICATION NUMBER: US/09/374.135  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: 60/095.982  
; PRIOR FILING DATE: 1998-08-10  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 101  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-374-135-4

Query Match 1.2%; Score 9; DB 3; Length 101;  
Best Local Similarity 100.0%; Pred. No. 0.42;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187  
Db 47 YDYVEVRDG 55

## RESULT 2

US-09-341-461-28  
; Sequence 28, Application US/09341461  
; Patent No. 6586389  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, Timothy G.  
; APPLICANT: Verroust, Pierre J.  
; TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin  
; FILE REFERENCE: D6148  
; CURRENT APPLICATION NUMBER: US/09/341.461  
; CURRENT FILING DATE: 2000-07-20  
; PRIOR APPLICATION NUMBER: PCT/US99/01259  
; PRIOR FILING DATE: 1999-01-21  
; NUMBER OF SEQ ID NOS: 40  
; SEQ ID NO 28  
; LENGTH: 110

; TYPE: PRT  
; ORGANISM: human  
; FEATURE:  
; OTHER INFORMATION: amino acid sequence of Bmp-1 CUB1 domain  
US-09-341-461-28

Query Match 1.2%; Score 9; DB 4; Length 110;  
Best Local Similarity 100.0%; Pred. No. 0.46;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187  
Db 56 YDYVEVRDG 64

## RESULT 3

US-08-872-757-2  
; Sequence 2, Application US/08872757  
; Patent No. 6258584  
; GENERAL INFORMATION:  
; APPLICANT: Prockop, Darwin J.  
; APPLICANT: Hqjima, Yoshio  
; APPLICANT: Li, Shi-Wu  
; APPLICANT: Sieron, Aleksander  
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND  
; TITLE OF INVENTION: PROCESSES, METHODS AND USES THEREOF  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/872,757  
; FILING DATE: 10-JUN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/609,187  
; FILING DATE: 01-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 8389-028-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-3660  
; TELEFAX: 415-854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 730 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-872-757-2

Query Match 1.2%; Score 9; DB 3; Length 730;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187  
Db 377 YDYVEVRDG 385

## RESULT 4

US-09-850-048A-2

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; Sequence 2, Application US/09850048A
; Patent No. 6562613
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
;              Hojima, Yoshio
;              Li, Shi-Wu
;              Sieron, Aleksander
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
;                   PROCESSES, METHODS AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/850,048A
; FILING DATE: 07-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,187
; FILING DATE: 1996-03-01
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-028-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-850-048A-2

Query Match 1.2%; Score 9; DB 4; Length 730;
Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 179 YDYVEVRDG 187
Db 377 YDYVEVRDG 385

RESULT 5
US-08-572-225-1
; Sequence 1, Application US/08572225
; Patent No. 5807981
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Hojima, Yoshio
; APPLICANT: Li, Shi-Wu
; APPLICANT: Sieron, Aleksander
; APPLICANT: Brenner, Mitch
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND ITS USE FOR
; TITLE OF INVENTION: DRUG DEVELOPMENT FOR THE TREATMENT OF DISEASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York

```

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; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/572,225
; FILING DATE: 13-DEC-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 788 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-572-225-1

Query Match 1.2%; Score 9; DB 1; Length 788;
Best Local Similarity 100.0%; Pred. No. 2.7; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 179 YDYVEVRDG 187
Db 179 YDYVEVRDG 187

RESULT 6
US-09-285-385C-19
; Sequence 19, Application US/09285385C
; Patent No. 6579702
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S.
; APPLICANT: Scott, Ian C.
; APPLICANT: Thomas, Christina L.
; TITLE OF INVENTION: MAMMALIAN TOLLOID-LIKE GENE AND PROTEIN
; FILE REFERENCE: 960296.96111
; CURRENT APPLICATION NUMBER: US/09/285,385C
; CURRENT FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/111873
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 60/080550
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 986
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-285-385C-19

Query Match 1.2%; Score 9; DB 4; Length 986;
Best Local Similarity 100.0%; Pred. No. 3.3; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 179 YDYVEVRDG 187
Db 377 YDYVEVRDG 385

RESULT 7
US-09-285-385C-2
; Sequence 2, Application US/09285385C

```

; Patent No. 6579702  
; GENERAL INFORMATION:  
; APPLICANT: Greenspan, Daniel S.  
; APPLICANT: Scott, Ian C.  
; APPLICANT: Thomas, Christina L.  
; TITLE OF INVENTION: MAMMALIAN TOLLOID-LIKE GENE AND PROTEIN  
; FILE REFERENCE: 960296.96111  
; CURRENT APPLICATION NUMBER: US/09/285.385C  
; CURRENT FILING DATE: 1999-04-02  
; PRIOR APPLICATION NUMBER: 60/111873  
; PRIOR FILING DATE: 1998-12-11  
; PRIOR APPLICATION NUMBER: 60/080550  
; PRIOR FILING DATE: 1998-04-03  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1015  
; TYPE: PRT  
; ORGANISM: human  
US-09-285-385C-2

Query Match 1.2%; Score 9; DB 4; Length 1015;  
Best Local Similarity 100.0%; Pred. No. 3.4;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 179 YDYVEVRDG 187  
DB 406 YDYVEVRDG 414

RESULT 8  
US-09-188-930-342  
; Sequence 342, Application US/09188930A  
; Patent No. 6150502  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Murison, James Greg  
; TITLE OF INVENTION: Compositions Isolated From Skin Cells  
; FILE REFERENCE: 11000.1011c1  
; CURRENT APPLICATION NUMBER: US/09/188.930A  
; CURRENT FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 348  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 342  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-188-930-342

Query Match 1.1%; Score 8; DB 3; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 265 GYTQRC 272  
DB 36 GYTQRC 43

RESULT 9  
US-09-312-283C-342  
; Sequence 342, Application US/09312283C  
; Patent No. 6573095  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Murison, James G.  
; APPLICANT: Kumble, Krishanand D.

; TITLE OF INVENTION: Compositions Isolated from Skin Cells  
; FILE REFERENCE: 11000.1011c2  
; CURRENT APPLICATION NUMBER: US/09/312.283C  
; CURRENT FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 425  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 342  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-312-283C-342

Query Match 1.1%; Score 8; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 265 GYTQRC 272  
DB 36 GYTQRC 43

RESULT 10  
US-09-472-087-99  
; Sequence 99, Application US/09472087  
; Patent No. 6682736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, ELLEN E.  
; APPLICANT: HANKE, JEFFREY H.  
; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOFFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PFI  
; CURRENT APPLICATION NUMBER: US/09/472.087  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/113.647  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 99  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-472-087-99

Query Match 1.1%; Score 8; DB 4; Length 96;  
Best Local Similarity 100.0%; Pred. No. 4.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 208 QSIGSLH 215  
DB 27 QSIGSLH 34

RESULT 11  
US-09-188-930-187  
; Sequence 187, Application US/09188930A  
; Patent No. 6150502  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Murison, James Greg  
; TITLE OF INVENTION: Compositions Isolated From Skin Cells  
; FILE REFERENCE: 11000.1011c1  
; CURRENT APPLICATION NUMBER: US/09/188.930A  
; CURRENT FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 348

SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 187  
 LENGTH: 152  
 TYPE: PRT  
 ORGANISM: mouse  
 US-09-188-930-187

Query Match 1.1%; Score 8; DB 3; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 6.4;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 265 GYTGQRC 272  
 Db 88 GYTGQRC 95

RESULT 12

US-09-312-283C-187  
 Sequence 187, Application US/09312283C  
 Patent No. 6573095  
 GENERAL INFORMATION:  
 APPLICANT: Watson, James D.  
 APPLICANT: Strachan, Lorna  
 APPLICANT: Sleeman, Matthew  
 APPLICANT: Onrust, Rene  
 APPLICANT: Murison, James G.  
 APPLICANT: Kumble, Krishanand D.  
 TITLE OF INVENTION: Compositions Isolated from Skin Cells  
 TITLE OF INVENTION: and Methods for Their Use  
 FILE REFERENCE: 11000.1011C2  
 CURRENT APPLICATION NUMBER: US/09/312,283C  
 CURRENT FILING DATE: 1999-05-14  
 NUMBER OF SEQ ID NOS: 425  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 187  
 LENGTH: 152  
 TYPE: PRT  
 ORGANISM: Mouse  
 US-09-312-283C-187

Query Match 1.1%; Score 8; DB 4; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 6.4;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 265 GYTGQRC 272  
 Db 88 GYTGQRC 95

RESULT 13

US-09-472-087-20  
 Sequence 20, Application US/09472087  
 Patent No. 6682736  
 GENERAL INFORMATION:  
 APPLICANT: HANSON, DOUGLAS C.  
 APPLICANT: NEVEU, MARK J.  
 APPLICANT: MUELLER, EILLEN E.  
 APPLICANT: HANKE, JEFFREY H.  
 APPLICANT: GILMAN, STEVEN C.  
 APPLICANT: DAVIS, C. GEOFFREY  
 APPLICANT: CORVALAN, JOSE R.  
 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
 FILE REFERENCE: ABX-PF1  
 CURRENT APPLICATION NUMBER: US/09/472,087  
 CURRENT FILING DATE: 1999-12-23  
 PRIOR APPLICATION NUMBER: 60/113,647  
 PRIOR FILING DATE: 1998-12-23  
 NUMBER OF SEQ ID NOS: 147  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 20  
 LENGTH: 155  
 TYPE: PRT  
 ORGANISM: Homo sapiens

US-09-472-087-20

Query Match 1.1%; Score 8; DB 4; Length 155;  
 Best Local Similarity 100.0%; Pred. No. 6.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 208 QSIGSSSLH 215  
 Db 21 QSIGSSSLH 28

RESULT 14

US-09-472-087-112  
 Sequence 112, Application US/09472087  
 Patent No. 6682736  
 GENERAL INFORMATION:  
 APPLICANT: HANSON, DOUGLAS C.  
 APPLICANT: NEVEU, MARK J.  
 APPLICANT: MUELLER, EILLEN E.  
 APPLICANT: HANKE, JEFFREY H.  
 APPLICANT: GILMAN, STEVEN C.  
 APPLICANT: DAVIS, C. GEOFFREY  
 APPLICANT: CORVALAN, JOSE R.  
 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
 FILE REFERENCE: ABX-PF1  
 CURRENT APPLICATION NUMBER: US/09/472,087  
 CURRENT FILING DATE: 1999-12-23  
 PRIOR APPLICATION NUMBER: 60/113,647  
 PRIOR FILING DATE: 1998-12-23  
 NUMBER OF SEQ ID NOS: 147  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 112  
 LENGTH: 155  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-472-087-112

Query Match 1.1%; Score 8; DB 4; Length 155;  
 Best Local Similarity 100.0%; Pred. No. 6.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 208 QSIGSSSLH 215  
 Db 21 QSIGSSSLH 28

RESULT 15

US-08-296-014A-4  
 Sequence 4, Application US/08296014A  
 Patent No. 5716834  
 GENERAL INFORMATION:  
 APPLICANT: Ding, Jeak Ling  
 APPLICANT: Ho, Bow  
 TITLE OF INVENTION: The Cloned Factor C cDNA of the  
 TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius  
 TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Birch, Stewart, Kolasch & Birch  
 STREET: 8110 Gatehouse Road, Suite 500 East  
 CITY: Falls Church  
 STATE: Virginia  
 COUNTRY: USA  
 ZIP: 22042  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/296,014A  
 FILING DATE:  
 CLASSIFICATION: 435

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; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1019 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-296-014A-4

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Query Match      1.1%; Score 8; DB 1; Length 1019;
Best Local Similarity 100.0%; Pred.No.36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      574 TRVQPICL 581
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Db      879 TRVQPICL 886

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Job time : 21 secs



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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:26:05 ; Search time 13 Seconds  
(without alignments)  
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Title: US-10-063-546-38

Perfect score: 720

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Gapop 60.0 , Gapext 60.0

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Post-processing: Listing first 700 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	9	1.2	639	1	BMPH_STRPU
3	9	1.2	986	1	BMP1_HUMAN
4	9	1.2	991	1	BMP1_MOUSE
5	8	1.1	158	1	Y260 AQUAE
6	8	1.1	350	1	MTSB_LACLC
7	8	1.1	395	1	VIBC_VIBCH
8	8	1.1	407	1	PA7_EOVIN
9	8	1.1	486	1	YDBH_SCHPO
10	8	1.1	740	1	CATB_STRRE
11	8	1.1	1019	1	LFC_CARRO
12	8	1.1	1019	1	LFC_TACTR
13	7	1.0	167	1	YPA3_ASCIM
14	7	1.0	193	1	Y377_MYCGE
15	7	1.0	196	1	CRBD_CHICK
16	7	1.0	201	1	ABPI_MAIZE
17	7	1.0	209	1	NODS_BRAJA
18	7	1.0	212	1	OMPW_ECOLI
19	7	1.0	212	1	OMPW_SALT1
20	7	1.0	212	1	OMPW_SALT2
21	7	1.0	255	1	V29K_PERSV
22	7	1.0	260	1	COLI_RANRI
23	7	1.0	263	1	COLI_RANCA
24	7	1.0	291	1	PCAR_PSEPU
25	7	1.0	295	1	PEPW_MYTED
26	7	1.0	303	1	LPXC_XANAC
27	7	1.0	305	1	T2RC_MOUSE
28	7	1.0	308	1	Y001_CAVUR
29	7	1.0	315	1	RTCA_PYRAE
30	7	1.0	348	1	Y001_CAVUR
31	7	1.0	351	1	MSS2_YEAST
32	7	1.0	359	1	MANR_PSEPU
33	7	1.0	360	1	AKOB_EUCAP
34	7	1.0	374	1	TGT_ANASP
35	7	1.0	389	1	PYRC_SULTO
36	7	1.0	420	1	O63A_DRONE
37	7	1.0	463	1	FNWL_HUMAN
38	7	1.0	475	1	GID_BRAJA
39	7	1.0	489	1	MEP3_YEAST
40	7	1.0	492	1	MEP1_YEAST
41	7	1.0	493	1	CAMA_CHICK
42	7	1.0	494	1	CD5_MOUSE
43	7	1.0	504	1	SPAS_MOUSE
44	7	1.0	505	1	GPMI_MYCPU
45	7	1.0	505	1	GPMI_MYCPU
46	7	1.0	507	1	MATK_SPIOL
47	7	1.0	510	1	MATK_BROHE
48	7	1.0	521	1	MATK_GRAHR
49	7	1.0	521	1	GMI2_METAC
50	7	1.0	542	1	GPMI_METWA
51	7	1.0	556	1	MODU_DROME
52	7	1.0	581	1	NU2M_PODAN
53	7	1.0	616	1	YD15_SCHPO
54	7	1.0	617	1	SPAS_HUMAN
55	7	1.0	617	1	THRB_RAT
56	7	1.0	618	1	THRB_MOUSE
57	7	1.0	622	1	THRB_HUMAN
58	7	1.0	625	1	THRB_BOVIN
59	7	1.0	629	1	THIC_PSESM
60	7	1.0	707	1	BMP1_XENLA
61	7	1.0	783	1	YX11_PSEAE
62	7	1.0	790	1	CADI_HUMAN
63	7	1.0	841	1	TRK1_SCHPO
64	7	1.0	859	1	ALR1_YEAST
65	7	1.0	995	1	YPD1_CAEEL
66	7	1.0	1022	1	TLD_BRARE
67	7	1.0	1522	1	DNA2_YEAST
68	7	1.0	1822	1	SC72_SCHPO
69	7	1.0	2907	1	FBN2_MOUSE
70	7	1.0	2911	1	FBN2_HUMAN
71	6	0.8	3564	1	CSM1_MOUSE
72	6	0.8	27	1	ANF_ANGJA
73	6	0.8	55	1	FER_CLOAC
74	6	0.8	62	1	CX51_CONIM
75	6	0.8	70	1	RL31_ECOLI
76	6	0.8	75	1	YOR4_SMYEA
77	6	0.8	77	1	YCXB_CVAPA
78	6	0.8	78	1	YVFB_VACCC
79	6	0.8	79	1	Y476_ARCFU
80	6	0.8	80	1	NUSM_CERCA
81	6	0.8	82	1	VPU_HVIBN
82	6	0.8	85	1	RS17_MYCGE
83	6	0.8	86	1	DINZ_ECOLI
84	6	0.8	92	1	YLXP_BACSU
85	6	0.8	99	1	YQJ2_CABEL
86	6	0.8	107	1	RL21_CHLTR
87	6	0.8	108	1	PT05_STYPL
88	6	0.8	109	1	TCMI_STRGA
89	6	0.8	112	1	PT17_STYPL
90	6	0.8	115	1	CTE9_MOUSE
91	6	0.8	122	1	RLI4_MYCPN
92	6	0.8	123	1	NEF_HVIB1
93	6	0.8	123	1	NEF_HVIB2
94	6	0.8	124	1	VNSI_IATKR
95	6	0.8	126	1	NUAG_BUCAP
96	6	0.8	126	1	U235_HUMAN
97	6	0.8	127	1	U235_MOUSE
98	6	0.8	127	1	CR1_HORVU
99	6	0.8	128	1	WN13_XENLA
100	6	0.8	129	1	RL32_ARCFU
101	6	0.8	132	1	RL7B_SCHPO
102	6	0.8	133	1	Y034_CHLMO
103	6	0.8	134	1	RUXX_HELPJ
104	6	0.8	134	1	SPH1_ASRPE
105	6	0.8	135	1	Y40A_TREPA
106	6	0.8	135	1	Y40A_TREPA

Q8yvt9 anabaena sp  
Q970x5 sulfolobus  
Q9vzw8 drosophila  
Q95466 homo sapien  
Q89121 bradyrhizob  
P53390 saccharomyc  
P40260 saccharomyc  
P05099 gallus gall  
P13379 mus musculu  
Q9gyv8 mus musculu  
Q98qa7 mycoplasma  
Q9m3n0 spinacia ol  
Q95eas brownia  
Q85ee5 grahamia br  
Q8tiy2 methanosarc  
Q8pyf8 methanosarc  
P13469 drosophila  
P15578 podospora a  
Q10238 schizosacch  
Q9ubp0 homo sapien  
P18292 rattus norv  
P19221 mus musculu  
P00734 homo sapien  
P00735 bos taurus  
Q87vg1 pseudomonas  
P98070 xenopus lae  
Q9myt3 pseudomonas  
P47946 schizosacch  
Q8269 saccharomyc  
Q8053 caenorhabdi  
Q57460 brachydanio  
P38859 saccharomyc  
Q9p7v5 schizosacch  
Q61555 mus musculu  
P35556 homo sapien  
Q92313 mus musculu  
P18144 anguilla ja  
P00198 clostridium  
Q9u625 conus imper  
P02432 escherichia  
Q00848 strawberry  
P48332 cyanophora  
P20560 vaccinia vi  
Q29774 archaeoglob  
Q34052 ceratitidis c  
P12516 human immun  
P47406 mycoplasma  
Q47150 escherichia  
P32730 bacillus su  
P34625 caenorhabdi  
Q84425 chlamydia t  
P28197 styela plic  
P39890 streptomyc  
P28209 styela plic  
Q9c37 mus musculu  
P47407 mycoplasma  
Q50308 mycoplasma  
P03404 human immun  
P04601 human immun  
P08376 influenza a  
Q8k97 buchena ap  
Q8wur7 homo sapien  
Q9cxc3 mus musculu  
P23251 hordeum vul  
P31283 xenopus lae  
Q28371 archaeoglob  
Q9p716 schizosacch  
Q9p716 chlamydia m  
Q9zma5 helicobacte  
Q25101 helicobacte  
Q9yed6 aeropyrum p  
P58007 treponema p

107	1	YAL3	ARCFU	0.8	136	1	O29249	archaeoglob	180	1	HBGF	CERAE	0.8	208	1	Q09118	cercopithec
108	1	POIG	HVEVO	0.8	138	1	P27953	hepatitis c	181	1	HBGF	HUMAN	0.8	208	1	Q99075	homo sapien
109	6	YENG	YEAST	0.8	143	1	P40031	saccharomyc	182	6	HBGF	PIG	0.8	208	1	Q01580	eus scrofa
110	6	CPAA	ORYLA	0.8	145	1	O73919	oryzias lat	183	6	NEF	HVIRH	0.8	208	1	P05858	human immun
111	6	YB80	NETJA	0.8	145	1	Q58580	methanococc	184	6	RS3	METJA	0.8	208	1	P54034	methanococc
112	6	HB82	ANAMI	0.8	146	1	P83273	anarhichas	185	6	LFTF	DEIRA	0.8	210	1	Q92744	deinococcus
113	6	Y328	METWA	0.8	146	1	Q57774	methanococc	186	6	TER7	VIBAN	0.8	210	1	P51560	vibrio angu
114	6	IAA	HORVU	0.8	147	1	P16969	hordeum vul	187	6	MOTA	BPT4	0.8	211	1	P22915	bacterioph
115	6	Y490	UREPA	0.8	155	1	Q99000	ureaplasma	188	6	NEF	YEAST	0.8	211	1	P20886	human immun
116	6	RBFA	STRAW	0.8	157	1	Q82K55	streptomyc	189	6	YBS1	YEAST	0.8	211	1	P38243	saccharomyc
117	6	MP63	MYCTU	0.8	159	1	P97175	mycobacteri	190	6	NEP	HV126	0.8	212	1	P04602	human immun
118	6	SSRP	SALTY	0.8	159	1	P43658	salmonella	191	6	RPV	YEAST	0.8	212	1	P35718	saccharomyc
119	6	SSRP	YERPE	0.8	159	1	Q82N14	yersinia pe	192	6	OSF1	HUMAN	0.8	214	1	Q92882	homo sapien
120	6	FM43	ECOLI	0.8	160	1	Q57254	escherichia	193	6	GTT2	DROME	0.8	215	1	Q9V998	drosophila
121	6	RBPA	STRCO	0.8	160	1	Q94527	streptomyc	194	6	GTT4	DROME	0.8	215	1	Q9V996	drosophila
122	6	SSRP	PHOLL	0.8	160	1	Q79101	photorhabd	195	6	OSF1	MOUSE	0.8	215	1	P51560	vibrio angu
123	6	REG4	PVRAB	0.8	162	1	Q9V029	pyrococcus	196	6	THIE	YERPE	0.8	215	1	P20886	human immun
124	6	REG4	PYRHO	0.8	162	1	O58741	pyrococcus	197	6	FUCA	HASIN	0.8	216	1	P38243	saccharomyc
125	6	ATPA	CHNE	0.8	163	1	Q4608	ochrosphaer	198	6	GTT5	DROME	0.8	216	1	P04602	human immun
126	6	LEUD	CLOAB	0.8	163	1	Q97ee1	clostridium	199	6	OMPW	VIBCH	0.8	217	1	P35718	saccharomyc
127	6	T2DA	XENLA	0.8	164	1	Q91858	xenopus lae	200	6	YBGJ	ECOLI	0.8	218	1	Q92882	homo sapien
128	6	SPAT	SALTY	0.8	165	1	P40703	salmonella	201	6	1433	SPIOL	0.8	220	1	Q9V998	drosophila
129	6	DPS	ECOLI	0.8	166	1	P27430	escherichia	202	6	PURQ	CAMJE	0.8	223	1	Q9V996	drosophila
130	6	NUSM	BRALA	0.8	167	1	O79423	branchiost	203	6	TRKA	STRCO	0.8	223	1	Q53949	atreptomyc
131	6	NABP	ALCEU	0.8	169	1	P39186	alcaligenes	204	6	RL1	SPIOL	0.8	224	1	P31184	spinacia ol
132	6	Y52L	SYNY3	0.8	171	1	Q55911	synechocyst	205	6	RL4	CHLPN	0.8	224	1	Q92748	chlamydia p
133	6	SYT8	HUMAN	0.8	172	1	Q8nbv8	homo sapien	206	6	COX2	BURDE	0.8	226	1	P33120	corynebacte
134	6	Y856	PYRHO	0.8	173	1	O58586	pyrococcus	207	6	COX2	ASTPE	0.8	229	1	P50678	bubalus dep
135	6	RL9	BORBU	0.8	173	1	O51139	borrelia bu	208	6	COX2	ASTPE	0.8	229	1	Q37411	asterina pe
136	6	GRPE	METHH	0.8	174	1	O27350	methanobact	209	6	KCX2	PISOC	0.8	229	1	P50678	bubalus dep
137	6	SP	LYCES	0.8	175	1	O82088	lycopersico	210	6	KCY	MYCTU	0.8	230	1	P25002	piasaater oc
138	6	NUDH	SALTY	0.8	176	1	Q8XG03	salmonella	211	6	VNS1	IADA2	0.8	230	1	Q33211	mycobacteri
139	6	YBN2	YEAST	0.8	177	1	P38218	saccharomyc	212	6	VNS1	IAMA6	0.8	230	1	P03501	influenza a
140	6	BDH	BOVIN	0.8	178	1	Q02337	bos taurus	213	6	VNS1	IAP11	0.8	230	1	P13137	influenza a
141	6	ATPD	STAAH	0.8	179	1	Q99af2	staphylococ	214	6	VNS1	IAP13	0.8	230	1	P13141	influenza a
142	6	NEF	HV1MN	0.8	182	1	P05856	human immun	215	6	VNS1	IATKB	0.8	230	1	P13143	influenza a
143	6	REC6	SCHPO	0.8	182	1	P40385	schizosacch	216	6	VNS1	IATKC	0.8	230	1	P30910	influenza a
144	6	YEG2	ARCFU	0.8	183	1	O28810	archaeoglob	217	6	VNS1	IATRT	0.8	230	1	P30911	influenza a
145	6	UPK2	HUMAN	0.8	184	1	O00526	homo sapien	218	6	GPHP	ALCEU	0.8	231	1	P30912	influenza a
146	6	UPK2	MOUSE	0.8	184	1	P38575	mus musculu	219	6	YKNW	BACSU	0.8	231	1	P40853	alcaligenes
147	6	FLAV	AQUAE	0.8	185	1	O67866	aquifex aeo	220	6	YB46	PASMU	0.8	240	1	O31709	bacillus su
148	6	RL25	CHLMU	0.8	185	1	O9plc2	chlamydia m	221	6	H1	NEUCR	0.8	236	1	Q95999	b cell ly
149	6	RL25	CHLTR	0.8	185	1	O84805	chlamydia t	222	6	NOQ	AGRT5	0.8	236	1	O810u2	neurospora
150	6	RRF	BUCAP	0.8	185	1	Q8X988	buchnera ap	223	6	OPE2	NPVOP	0.8	236	1	P35118	agrobacteri
151	6	UPK2	BOVIN	0.8	185	1	O08537	bos taurus	224	6	APH1	DROME	0.8	239	1	P89029	orygia pseu
152	6	NOS1	SHEEP	0.8	186	1	Q29498	ovis aries	225	6	NEP	HV1SC	0.8	239	1	Q9V992	drosophila
153	6	RL18	YEAST	0.8	186	1	P07279	saccharomyc	226	6	M4A7	HUMAN	0.8	240	1	Q92972	ulex europe
154	6	Y552	VIBVU	0.8	186	1	Q8dcg8	vibrio vuln	227	6	LEC1	ULREU	0.8	243	1	P57911	pasteurella
155	6	Y418	VIBCH	0.8	187	1	Q9kuu7	vibrio chol	228	6	LEC1	ULREU	0.8	243	1	Q29972	ulex europe
156	6	YH16	PYRAB	0.8	187	1	Q9uxz1	pyrococcus	229	6	CYSQ	ECOS7	0.8	246	1	Q8XG56	escherichia
157	6	PAAD	RICPR	0.8	189	1	Q9zd09	rickettsia	230	6	CYSQ	ECOL6	0.8	246	1	Q8XG56	escherichia
158	6	UBIX	ECOLI	0.8	189	1	P09550	escherichia	231	6	CYSQ	ECOLI	0.8	246	1	Q8XG56	escherichia
159	6	UBIX	SALTY	0.8	189	1	P40787	salmonella	232	6	CYSQ	SALTY	0.8	246	1	Q82153	salmonella
160	6	YQ88	VIBPA	0.8	189	1	Q871c4	vibrio para	233	6	CYSQ	SALTY	0.8	246	1	P59735	shigella fl
161	6	PAAD	CHLPN	0.8	192	1	Q92884	chlamydia p	234	6	CYSQ	SHIFL	0.8	246	1	P26264	salmonella
162	6	ASC2	HUMAN	0.8	193	1	Q99929	homo sapien	235	6	HBM4	CHLVI	0.8	246	1	Q59335	chilobium
163	6	DCD	BUCBP	0.8	193	1	P59464	buchnera ap	236	6	NEP	SULSO	0.8	247	1	Q97VX5	maftoglobus
164	6	H10	HUMAN	0.8	193	1	P07305	homo sapien	237	6	PGY2	MASLA	0.8	247	1	P29732	mastigoclad
165	6	GSFH	VIBCH	0.8	194	1	P45774	vibrio chol	238	6	1436	ARATH	0.8	248	1	P48349	arabidopsis
166	6	PAAD	THAAR	0.8	194	1	P57767	thauera aro	239	6	H12	DROVI	0.8	250	1	Q45555	drosophila
167	6	LPR1	MYCTU	0.8	197	1	O10785	mycobacteri	240	6	MTR3	YEAST	0.8	250	1	P48240	saccharomyc
168	6	RG9	ARATH	0.8	197	1	P25864	arabidopsis	241	6	DISA	DICDI	0.8	253	1	P02886	dictyosteli
169	6	GTT3	DROME	0.8	199	1	Q9V997	drosophila	242	6	DISC	DICDI	0.8	253	1	P02887	dictyosteli
170	6	PAAD	BACPF	0.8	200	1	P94300	bacillus ps	243	6	YD10	HASIN	0.8	253	1	P44158	haemophilus
171	6	SOEE	ONCVO	0.8	201	1	Q07449	onchocerca	244	6	1432	LYCES	0.8	254	1	P33208	lycopersico
172	6	QOX3	BACSU	0.8	204	1	P34958	bacillus su	245	6	1434	SOLUT	0.8	254	1	Q43643	solanum tub
173	6	YNGF	ECOLI	0.8	204	1	P77313	escherichia	246	6	1435	LYCES	0.8	255	1	P93210	lycopersico
174	6	NEF	HV1S3	0.8	205	1	P19545	human immun	247	6	143A	TOBAC	0.8	255	1	P93342	nicotiana t
175	6	TENT	BACSU	0.8	205	1	P25053	bacillus su	248	6	143B	TOBAC	0.8	255	1	Q93995	nicotiana t
176	6	HPI	DROME	0.8	206	1	P05205	drosophila	249	6	TRYA	MANSE	0.8	256	1	P35045	manduca sex
177	6	NEF	HV112	0.8	206	1	P04324	human immun	250	6	TRYB	MANSE	0.8	256	1	P35046	manduca sex
178	6	NEF	HV1BR	0.8	206	1	P03406	human immun	251	6	YL99	YERPE	0.8	256	1	Q8zeh4	yersinia pe
179	6	NEF	HV1PV	0.8	206	1	P03405	human immun	252	6	AP1B	HUMAN	0.8	257	1	Q8ww43	homo sapien

253	6	0.8	257	1	PDX3_MOUSE	P20108	mus musculus	326	6	0.8	304	1	HTPX_BACHD	Q9k9e6	bacillus ha
254	6	0.8	258	1	1435_SOLTU	P93784	solanum tub	327	6	0.8	305	1	SOHB_BUCSC	Q44600	buchnera ap
255	6	0.8	259	1	1436_LVCES	P93211	lycopersico	328	6	0.8	307	1	T2RA_HUMAN	Q9nyw0	homo sapien
256	6	0.8	258	1	1437_TOBAC	O49998	nicotiana t	329	6	0.8	308	1	ARGC_RHILLO	Q982x3	rhizobium l
257	6	0.8	258	1	UBIE_RHIME	Q928k7	rhizobium m	330	6	0.8	308	1	PVRB_BACCL	P41008	bacillus ca
258	6	0.8	259	1	1432_ARATH	Q01525	arabidopsis	331	6	0.8	310	1	ARGC_BRUME	Q8ygi8	brucella me
259	6	0.8	259	1	1433_LILLO	Q9sp07	lilium long	332	6	0.8	310	1	ARGC_BRUSU	P59314	brucella su
260	6	0.8	259	1	RB34_MOUSE	Q64008	mus musculus	333	6	0.8	310	1	ARGC_RHIME	Q92qr7	rhizobium m
261	6	0.8	259	1	UBIE_AGR5T	Q8uih5	agrobacteri	334	6	0.8	310	1	FAH1_BACAA	Q81j90	bacillus an
262	6	0.8	260	1	1433_LVCES	P93209	lycopersico	335	6	0.8	310	1	FAH1_BACCR	Q81gm0	bacillus ce
263	6	0.8	260	1	1433_OENHO	P29307	oenothera h	336	6	0.8	311	1	KHSE_SULSO	Q97w70	sulfolobus
264	6	0.8	260	1	1433_ORISA	Q06967	oryza sativ	337	6	0.8	311	1	RUVB_UREPA	Q9pq42	ureaplasma
265	6	0.8	260	1	1433_PEA	P46266	pisum sativ	338	6	0.8	313	1	MRWA_ECOL6	Q8f168	escherichia
266	6	0.8	260	1	143C_TOBAC	P93343	nicotiana t	339	6	0.8	313	1	ZS11_HUMAN	Q9y6i9	homo sapien
267	6	0.8	261	1	143A_VICFA	P42653	vicia faba	340	6	0.8	315	1	Y209_AQUAE	Q68403	aquifex aeo
268	6	0.8	261	1	SPRE_MOUSE	Q64105	mus musculus	341	6	0.8	320	1	Y013_NPVOP	P65361	orgyia pseu
269	6	0.8	261	1	YRBE_HAEIN	P45030	haemophilus	342	6	0.8	322	1	Y348_MYCGE	P47590	mycoplasma
270	6	0.8	262	1	143A_HORVU	P29305	hordeum vul	343	6	0.8	323	1	FLIM_PSEAE	Q51465	pseudomonas
271	6	0.8	262	1	143B_HORVU	Q43470	hordeum vul	344	6	0.8	325	1	HMGL_HUMAN	P35914	homo sapien
272	6	0.8	262	1	COX3_BRALA	O47425	branchiosto	345	6	0.8	325	1	HMGL_MOUSE	P38060	mus musculus
273	6	0.8	264	1	HB21_MOUSE	P04230	mus musculus	346	6	0.8	325	1	HMGL_RAT	P97519	rattus norv
274	6	0.8	264	1	HB22_MOUSE	P01915	mus musculus	347	6	0.8	326	1	FSTL_ARATH	P52839	arabidopsis
275	6	0.8	264	1	HB24_MOUSE	P20040	mus musculus	348	6	0.8	326	1	PER1_ORISA	P37834	oryza sativ
276	6	0.8	264	1	Y547_METJA	Q57967	methanococc	349	6	0.8	326	1	RLUC_PASMU	Q9cm51	pasteurella
277	6	0.8	265	1	NUSM_ANOQN	Q31696	anopheles g	350	6	0.8	326	1	YIE1_YEAST	P40531	saccharomyc
278	6	0.8	266	1	ELH1_ACICA	Q59093	acinetobact	351	6	0.8	330	1	LRD2_STAEP	Q8cn22	staphylococ
279	6	0.8	267	1	1431_ARATH	P42643	arabidopsis	352	6	0.8	330	1	PRC2_PORGI	P33437	porphyromon
280	6	0.8	267	1	143A_ARATH	P46077	arabidopsis	353	6	0.8	331	1	FRH4_HUMAN	Q92496	homo sapien
281	6	0.8	267	1	PPN1_OCRH	Q8er99	oceanobacil	354	6	0.8	333	1	Y808_METJA	Q58218	methanococc
282	6	0.8	267	1	TRY7_ANOGA	P35041	anopheles g	355	6	0.8	334	1	PRC1_PORGI	P59916	porphyromon
283	6	0.8	268	1	ET1B_XENIA	P18756	xenopus lae	356	6	0.8	334	1	SIR6_MOUSE	P59941	mus musculus
284	6	0.8	268	1	TRPA_HAEIN	P43759	haemophilus	357	6	0.8	335	1	GCP_AQUAE	Q66986	aquifex aeo
285	6	0.8	269	1	IL1B_TRIVU	P43759	haemophilus	358	6	0.8	335	1	OXA4_BIFLO	Q896j6	bifidobacte
286	6	0.8	269	1	UBIE_BRUME	Q9xe77	trichosurus	359	6	0.8	335	1	YJ89_PYRHO	O57713	pyrococcus
287	6	0.8	269	1	UBIE_BRUSU	Q8ufz3	brucella su	360	6	0.8	337	1	RFAT_SALTY	P19816	salmonella
288	6	0.8	270	1	Y166_LISMO	Q8v634	listeria mo	361	6	0.8	339	1	GPDA_YERPE	Q8zjm6	versinia pe
289	6	0.8	270	1	YJ80_LISMO	Q92ae2	listeria in	362	6	0.8	339	1	YH96_CIOAB	Q97157	clostridium
290	6	0.8	271	1	YLBF_ECOLI	P77518	escherichia	363	6	0.8	340	1	GPDA_SERMA	Q8km1	serratia ma
291	6	0.8	272	1	RR2_NEPOL	Q9t103	nephroselimi	364	6	0.8	340	1	EFTS_LACLA	Q9cd5	lactococcus
292	6	0.8	274	1	UPK1_BACHD	Q9kf15	bacillus ha	365	6	0.8	344	1	DHAS_CORFL	P41400	corynebacte
293	6	0.8	275	1	BPHB_PSEPS	Q9k694	p cis-2,3-d	366	6	0.8	344	1	DHAS_CORFL	P26511	corynebacte
294	6	0.8	275	1	TRY3_ANOGA	P35037	anopheles g	367	6	0.8	344	1	MURB_BUCAP	Q8ka63	buchnera ap
295	6	0.8	275	1	TRY4_ANOGA	P35038	anopheles g	368	6	0.8	345	1	AMIE_RHOER	Q01360	rhodococcus
296	6	0.8	277	1	ZWIN_HUMAN	Q95229	homo sapien	369	6	0.8	345	1	YE38_MYCPN	P75340	mycoplasma
297	6	0.8	278	1	KDUI_YERPE	Q8zfh8	versinia pe	370	6	0.8	346	1	EFTS_STRJ3	Q8e389	streptococc
298	6	0.8	278	1	PHAZ_PSEFL	Q51718	pseudomonas	371	6	0.8	346	1	EFTS_STRP3	P53383	synecocyst
299	6	0.8	279	1	DAPF_AQUAE	Q67693	aquifex aeo	372	6	0.8	346	1	EFTS_STRP8	Q8nz43	streptococc
300	6	0.8	279	1	MURI_SYNY3	P73737	synecocyst	373	6	0.8	346	1	EFTS_STRPY	Q99xq7	streptococc
301	6	0.8	280	1	MDCB_PSEPU	Q9z452	pseudomonas	374	6	0.8	346	1	PRJ2_USTMA	P31303	ustilago ma
302	6	0.8	281	1	AAC9_MICCH	P29810	micromonosop	375	6	0.8	352	1	PAS_ANSAN	P36189	anser anser
303	6	0.8	285	1	CNO7_HUMAN	Q9uivi	homo sapien	376	6	0.8	352	1	NADA_PSEAE	Q9i4w9	pseudomonas
304	6	0.8	285	1	CNO7_MOUSE	Q60809	mus musculus	377	6	0.8	353	1	MRP_SYNY3	P53383	synecocyst
305	6	0.8	285	1	LPXC_SYNEL	Q8di02	synecococc	378	6	0.8	356	1	MURB_BUCAI	P57153	buchnera ap
306	6	0.8	286	1	TRUA_MYCLE	Q9x796	mycobacteri	379	6	0.8	356	1	TORS_CABEL	Q95nu5	caenorhabdi
307	6	0.8	286	1	YO18_PSEAE	Q9i163	pseudomonas	380	6	0.8	357	1	LEU3_XANAC	Q8ph05	xanthomonas
308	6	0.8	286	1	YTFG_ECOLI	P39315	escherichia	381	6	0.8	357	1	LEU3_XANCP	Q8p511	xanthomonas
309	6	0.8	287	1	DMSC_ECOLI	P18777	escherichia	382	6	0.8	357	1	Y303_MYCGE	P47545	mycoplasma
310	6	0.8	287	1	YICC_ECOLI	P23839	escherichia	383	6	0.8	360	1	AROC_ECOLI	Q8xcq4	escherichia
311	6	0.8	288	1	CDSA_HAEIN	P44937	h phosphati	384	6	0.8	360	1	AROC_ECOLI	P12808	escherichia
312	6	0.8	288	1	VP30_EBOZM	Q05323	ebola virus	385	6	0.8	360	1	AROC_SALTI	P16280	salmonella
313	6	0.8	288	1	BCHL_RHORU	Q91855	rhodospiril	386	6	0.8	360	1	AROC_SALTY	P58729	salmonella
314	6	0.8	291	1	FSBO_CHLRE	P12815	chlamydomon	387	6	0.8	360	1	LEU3_AZOVI	P96197	azotobacter
315	6	0.8	292	1	CNT8_HUMAN	Q9uif9	homo sapien	388	6	0.8	360	1	LEU3_PSEAE	Q51375	pseudomonas
316	6	0.8	292	1	RM07_YEAST	P36519	saccharomyc	389	6	0.8	360	1	LEU3_PSEPK	Q881e5	pseudomonas
317	6	0.8	293	1	VU26_HSVJ7	P52445	human herpe	390	6	0.8	360	1	NUIC_ARATH	Q37165	arabidopsis
318	6	0.8	297	1	NLPD_PSEAE	P45682	pseudomonas	391	6	0.8	361	1	AROC_VIBAN	P39198	vibrio angu
319	6	0.8	297	1	TRUA_MYCTU	Q06322	mycobacteri	392	6	0.8	361	1	AROC_VIBCH	Q9kq85	vibrio chol
320	6	0.8	298	1	YIHV_ECOLI	P32143	escherichia	393	6	0.8	361	1	AROC_VIBPA	Q87mm9	vibrio para
321	6	0.8	299	1	YE05_YEAST	P32643	saccharomyc	394	6	0.8	361	1	AROC_VIEBU	Q8db42	vibrio vuln
322	6	0.8	300	1	VLE3_VIBPA	Q87fd6	vibrio para	395	6	0.8	361	1	BMP_TREPA	P29725	treponema p
323	6	0.8	303	1	LIP2_SYNY3	P73572	synecocyst	396	6	0.8	363	1	NUIC_LOTJA	Q9bbn9	lotus japon
324	6	0.8	304	1	CYSD_XYLFA	Q9pd79	xyella fas	397	6	0.8	364	1	YM28_MYCTU	Q10512	mycobacteri
325	6	0.8	304	1	CYSD_XYLFT	Q87d98	xyella fas	398	6	0.8	365	1	PENR_MESCR	P41343	mesembryant

399	6	0.8	365	1	NUIC_SPIOL	Q9m316	spinacia ol	472	6	0.8	411	1	CIW3_RAT	O54912	rattus norv
400	6	0.8	365	1	RECA_SPIPL	P48293	spirulina p	473	6	0.8	412	1	CISY_RICBE	Q59734	rickettsia
401	6	0.8	366	1	RF2_BACSU	P28367	bacillus su	474	6	0.8	412	1	PGK_MYCTU	O06821	mycobacteri
402	6	0.8	366	1	TORY_ECO57	P58361	escherichia	475	6	0.8	413	1	ALMM_TAMSI	O54757	tamias sibi
403	6	0.8	366	1	TORY_ECOLI	P2005	escherichia	476	6	0.8	413	1	ALMS_TAMSI	O54758	tamias sibi
404	6	0.8	367	1	MK12_MOUSE	O08911	mus musculus	477	6	0.8	413	1	ALST_TAMSI	O54760	tamias sibi
405	6	0.8	367	1	MK12_RAT	Q63538	rattus norv	478	6	0.8	413	1	ALST_TAMSI	O54759	tamias sibi
406	6	0.8	368	1	YBHR_ECOLI	P75774	escherichia	479	6	0.8	413	1	HP55_TAMSI	Q09055	tamias sibi
407	6	0.8	369	1	CYCH_BRAJA	P45399	bradyrhizob	480	6	0.8	413	1	LOLC_XYLFA	Q87ef5	xyella fas
408	6	0.8	369	1	PENR_SPIOL	P00455	spinacia ol	481	6	0.8	413	1	LOLC_XYLFA	Q87ef5	xyella fas
409	6	0.8	370	1	CYB_EPIC	Q48043	epicrates c	482	6	0.8	415	1	CRP1_RAT	P35353	rattus norv
410	6	0.8	370	1	EGSI_ARPEE	Q9yer2	aeropyrum p	483	6	0.8	415	1	LOLC_NEIMA	P57061	neisseria m
411	6	0.8	370	1	RECP_LISMO	Q8yav8	listeria mo	484	6	0.8	415	1	LOLC_NEIMA	P57062	neisseria m
412	6	0.8	371	1	CYB_BOACO	P92848	boa constr	485	6	0.8	415	1	TRSA_STRAM	Q07197	streptomyce
413	6	0.8	371	1	MNCP_OXYFA	P15798	oxytricha f	486	6	0.8	416	1	CHTC_MOUSE	P14211	mus musculus
414	6	0.8	371	1	MNCP_OXYTR	Q27151	oxytricha t	487	6	0.8	416	1	SYT_TREPA	O03806	treponema p
415	6	0.8	375	1	ADHA_KLULA	P49385	kluveromyc	488	6	0.8	419	1	ARGJ_SYNY3	P74122	s arginine
416	6	0.8	375	1	HIS7_XYLFA	Q9pbc7	xyella fas	489	6	0.8	419	1	PSG7_HUMAN	Q13046	homo sapien
417	6	0.8	375	1	ISCS_BACHD	Q9kdj6	bacillus ha	490	6	0.8	421	1	SYTC_HUMAN	Q81v01	homo sapien
418	6	0.8	375	1	LEUI_BUCTS	Q31287	buchnera ap	491	6	0.8	421	1	SYTC_MOUSE	Q920n7	mus musculus
419	6	0.8	375	1	YBHF_ECO57	Q8x6g5	escherichia	492	6	0.8	421	1	SYTC_RAT	P97610	rattus norv
420	6	0.8	375	1	YBHF_ECOLI	P75817	escherichia	493	6	0.8	424	1	LE22_METYA	P81291	methanococc
421	6	0.8	377	1	DNAL_BRAJA	P94319	bradyrhizob	494	6	0.8	426	1	ALFA_BACSU	P71006	bacillus su
422	6	0.8	377	1	DNAL_BROSP	Q08356	rhodospseudo	495	6	0.8	427	1	ALFB_BACSU	Q87kh2	bacillus su
423	6	0.8	380	1	AGLG_RHIME	Q923r7	rhizobium m	496	6	0.8	427	1	HISK_LEPIN	Q8f393	leptospira
424	6	0.8	380	1	OPRK_CAVPO	P41144	cavia porce	497	6	0.8	427	1	YF05_METTH	O27549	methanobact
425	6	0.8	381	1	CYB_MYOME	Q35038	myoictis me	498	6	0.8	428	1	CKKR_HUMAN	P32238	homo sapien
426	6	0.8	381	1	RSAL_YEAST	Q06758	zymomonas m	499	6	0.8	428	1	ELK1_HUMAN	P19419	homo sapien
427	6	0.8	382	1	ADH2_ZYMO	P06758	zymomonas m	500	6	0.8	428	1	FIXC_ECOLI	P31575	escherichia
428	6	0.8	382	1	SPCN_MOUSE	P16546	mus musculus	501	6	0.8	428	1	GLYA_AQUAE	O66776	aquifex aeo
429	6	0.8	382	1	YAMF_CABEL	Q10058	schizosacch	502	6	0.8	429	1	ELK1_MOUSE	P41969	mus musculus
430	6	0.8	382	1	YSYF_CABEL	Q8ta81	caenorhabdi	503	6	0.8	429	1	PURK_MYCTU	P96881	mycobacteri
431	6	0.8	384	1	NUSM_ANOAR	P51899	anopheles a	504	6	0.8	431	1	NORF_CHLCV	Q821q3	chlamydophi
432	6	0.8	386	1	RB87_DROME	P48810	drosophila	505	6	0.8	431	1	PELL_ARATH	Q940q1	arabidopsis
433	6	0.8	387	1	CEAN_ECOLI	P08083	escherichia	506	6	0.8	431	1	UROK_HUMAN	P00749	homo sapien
434	6	0.8	387	1	RT05_SCHPO	Q10234	schizosacch	507	6	0.8	431	1	URTB_DESRO	P98121	desmodus ro
435	6	0.8	388	1	ALR_EACHD	Q9kif9	bacillus ha	508	6	0.8	433	1	UROK_BOVIN	Q05589	bos taurus
436	6	0.8	388	1	CUS5_HUMAN	Q9nx36	homo sapien	509	6	0.8	433	1	UROK_PAPCY	P18227	papio cynoc
437	6	0.8	389	1	AL44_PSEAE	Q9hy69	pseudomonas	510	6	0.8	435	1	PNCB_VIBCH	Q9kn67	vibrio chol
438	6	0.8	389	1	WN2B_MOUSE	O70283	mus musculus	511	6	0.8	436	1	CKKR_MOUSE	O08786	mus musculus
439	6	0.8	391	1	WN2B_HUMAN	Q93097	homo sapien	512	6	0.8	436	1	NPT3_HUMAN	O00624	homo sapien
440	6	0.8	392	1	HIS2_LISIN	Q92882	listeria in	513	6	0.8	436	1	YIN5_YEAST	P40463	saccharomyc
441	6	0.8	393	1	HIS2_LISMO	Q8y9f9	listeria mo	514	6	0.8	437	1	KLCM_MOUSE	P08730	mus musculus
442	6	0.8	394	1	AV71_ACAVI	Q17107	acanthocheil	515	6	0.8	438	1	ETIA_XENLA	P18755	xenopus lae
443	6	0.8	394	1	CIW3_HUMAN	O14649	homo sapien	516	6	0.8	438	1	MYC_CALJA	P49032	callichrix
444	6	0.8	394	1	URTG_DESRO	P19450	desmodus ro	517	6	0.8	439	1	ENO_RHOB	Q870b9	rhodotorula
445	6	0.8	394	1	YWFF_BACSU	P19642	bacillus su	518	6	0.8	439	1	MYC_CANFA	Q28350	canis fami
446	6	0.8	395	1	FLD2_RHIME	Q52942	rhizobium m	519	6	0.8	439	1	MYC_PELCA	P06877	felis silve
447	6	0.8	395	1	YHAC_ECOLI	P11864	escherichia	520	6	0.8	439	1	MYC_MARMO	P22555	marmota mon
448	6	0.8	396	1	NASR_KLEOX	Q48468	klebsiella	521	6	0.8	439	1	MYC_MOUSE	P01108	mus musculus
449	6	0.8	397	1	ACKA_OCEIH	Q8epb9	oceanobacil	522	6	0.8	439	1	MYC_SHEEP	Q28566	ovis aries
450	6	0.8	399	1	LHX5_BRARE	P52889	brachydanio	523	6	0.8	439	1	NH97_CAEEL	Q9bjk5	caenorhabdi
451	6	0.8	400	1	AFC3_ARATH	P51568	arabidopsis	524	6	0.8	440	1	BRNQ_BACSU	P94499	bacillus su
452	6	0.8	400	1	DFP_HAETN	P44953	haemophilus	525	6	0.8	440	1	ENO_CLAHE	P42040	cladosporiu
453	6	0.8	401	1	FLDI_RHIME	P58330	rhizobium m	526	6	0.8	440	1	ETSI_MOUSE	P27577	mus musculus
454	6	0.8	402	1	ILV5_NEUCR	P38674	neurospora	527	6	0.8	440	1	YDUN_HAETN	P47097	saccharomyc
455	6	0.8	402	1	OFU1_DROME	Q9v6x7	drosophila	528	6	0.8	440	1	YJZ6_YEAST	P47099	saccharomyc
456	6	0.8	403	1	K1CS_MOUSE	P19001	mus musculus	529	6	0.8	440	1	YJZ8_YEAST	Q04706	saccharomyc
457	6	0.8	403	1	LHX1_XENLA	P29674	xenopus lae	530	6	0.8	440	1	YME5_YEAST	Q12331	saccharomyc
458	6	0.8	403	1	MGLB_TREPA	Q08255	treponema p	531	6	0.8	440	1	YVU1_YEAST	Q08405	saccharomyc
459	6	0.8	403	1	P37_MYCHR	P15363	mycoplasma	532	6	0.8	440	1	YVU1_YEAST	P08405	saccharomyc
460	6	0.8	404	1	ILV5_SCHPO	P78827	schizosacch	533	6	0.8	441	1	DENT_TAXCA	Q81169	taxus canad
461	6	0.8	404	1	LHX1_HUMAN	P48742	homo sapien	534	6	0.8	441	1	ETSI_HUMAN	P14921	homo sapien
462	6	0.8	404	1	PEX9_YARLI	P45817	yarrowia li	535	6	0.8	441	1	ETSI_RAT	P11556	rattus norv
463	6	0.8	406	1	LHX1_CHICK	P53411	gallus gall	536	6	0.8	441	1	ETSA_CHICK	P13474	gallus gall
464	6	0.8	406	1	LHX1_MOUSE	P36199	mus musculus	537	6	0.8	442	1	LEU2_BUCHH	Q9evh7	buchnera ap
465	6	0.8	406	1	SEPR_THESR	P80146	thermus sp.	538	6	0.8	442	1	UROK_PIG	P04185	sus scrofa
466	6	0.8	409	1	CIW3_MOUSE	Q35111	mus musculus	539	6	0.8	443	1	AMTA_AERHY	P41131	aeromonas h
467	6	0.8	410	1	ASSY_PYRFU	Q8u484	pyrococcus	540	6	0.8	444	1	CKKR_RAT	P30551	rattus norv
468	6	0.8	410	1	CGE1_HUMAN	P24864	homo sapien	541	6	0.8	444	1	YK43_CABEL	P34255	caenorhabdi
469	6	0.8	410	1	SAHH_THEAC	Q9hkk4	thermoplasma	542	6	0.8	451	1	PTKC_ECOLI	P37189	escherichia
470	6	0.8	410	1	YCF1_MESVI	Q9mm0	mesocistima	543	6	0.8	452	1	K1CO_MOUSE	Q61414	mus musculus
471	6	0.8	411	1	CISV_RICTY	P51043	rickettsia	544	6	0.8	453	1	Y081_METWA	Q8q0q5	methanosaarc

545	6	0.8	454	1	Y856 METTH	O26944	methanobact	618	1	NRFL_BRARE	Q90x44	brachydanio
546	6	0.8	455	1	YMS5 MOUSE	Q9er04	mus musculus	619	1	ATPA_SYN6	P08449	synecococc
547	6	0.8	456	1	YNU6 YEAST	P40161	saccharomyc	620	1	MOT6_HUMAN	O15375	homo sapien
548	6	0.8	457	1	KICO_HUMAN	P19012	homo sapien	621	1	ATPA_ANASP	P12405	anabaena sp
549	6	0.8	458	1	MPLA YEAST	P53050	saccharomyc	622	1	CPY7_MOUSE	P27786	mus musculus
550	6	0.8	459	1	MGAL_ECOLI	P37773	escherichia	623	1	TDT_XENLA	P42118	xenopus lae
551	6	0.8	460	1	YMS5_HUMAN	Q9h383	homo sapien	624	1	COBI_MYCTU	Q10677	mycobacteri
552	6	0.8	461	1	CD4_CERAE	Q08338	cercopithe	625	1	HUTH_BACSU	P10944	bacillus su
553	6	0.8	462	1	CD4_HUMAN	P01730	homo sapien	626	1	MATK_SCHTR	Q95e84	schlumberge
554	6	0.8	463	1	CD4_MACFA	P79185	macaca fasc	627	1	PR12_HUMAN	P49643	homo sapien
555	6	0.8	464	1	CD4_WACFU	P79184	macaca fusc	628	1	D7A1_HUMAN	P49419	homo sapien
556	6	0.8	465	1	CD4_MACWU	P16003	macaca mula	629	1	D7A1_MOUSE	Q9d5f1	mus musculus
557	6	0.8	466	1	CD4_MACNE	Q08340	macaca neme	630	1	ACCD_TOBAC	P12219	nicotiana t
558	6	0.8	467	1	CD4_PANTR	P16004	pan troglod	631	1	ATPA_RHOBL	P05439	rhodopseudo
559	6	0.8	468	1	NU4M_STRCA	O21406	struthio ca	632	1	ZRF1_MOUSE	P54103	mus musculus
560	6	0.8	469	1	NU4M_CHICK	P18939	gallus gall	633	1	CP11_PAGMA	P98181	pagrus majo
561	6	0.8	470	1	NU4M_FELCA	P48916	felis silve	634	1	LEUI_BUCDN	O85070	buchnera ap
562	6	0.8	471	1	NU4M_RH1UN	Q96088	rhinoceros	635	1	ATPA_MYCGE	P47641	mycoplasma
563	6	0.8	472	1	TRME_STAAN	Q91161	staphylococ	636	1	LEUI_CANBP	Q7VQ16	candidatus
564	6	0.8	473	1	TRME_STAAN	Q99qt3	staphylococ	637	1	SYH_FUGRU	P70076	fugu rubrip
565	6	0.8	474	1	TRME_STAEP	Q8cmu5	staphylococ	638	1	CP11_LIZSAU	O42231	liza aurata
566	6	0.8	475	1	LIP8_CANAL	Q9p8v9	candida alb	639	1	CP11_LIZSAU	Q9w683	liza salien
567	6	0.8	476	1	HGD_ARATH	Q9zra2	arabidopsis	640	1	CP11_ONCMY	Q92110	oncorhynch
568	6	0.8	477	1	KRM2_MOUSE	Q8k157	mus musculus	641	1	GUAR_CORGL	Q92109	oncorhynch
569	6	0.8	478	1	KWFR_SCHPO	O42941	schizosacch	642	1	RORA_MOUSE	Q8nsr1	corynebacte
570	6	0.8	479	1	YG91_METAC	Q8tq61	methanobact	643	1	GUAA_CORAM	P51448	mus musculus
571	6	0.8	480	1	YD63_HELPY	P56176	helicobacte	644	1	ATLI_HUMAN	O52831	corynebacte
572	6	0.8	481	1	BAES_ECOLI	P30847	escherichia	645	1	GUAA_MYCTU	Q8n6g6	homo sapien
573	6	0.8	482	1	CG51_HUMAN	Q9y512	homo sapien	646	1	YU87_TREPA	O50729	mycobacteri
574	6	0.8	483	1	NOLX_RH1FR	P33213	rhizobium f	647	1	GUAA_STRCO	O83500	treponema p
575	6	0.8	484	1	UTG3_FLEPL	Q91280	pleuronecte	648	1	PUR9_BUCAP	Q910h2	streptomyc
576	6	0.8	485	1	T115_CLOPE	Q05309	clostridium	649	1	PUR9_NEIMB	Q8ka70	bifunctio
577	6	0.8	486	1	YV33_MYCLE	P37391	mycobacteri	650	1	GUAA_MYCLE	Q9jzm7	n bifunctio
578	6	0.8	487	1	LEU2_XYLFA	O06250	mycobacteri	651	1	LNT_RHILO	P46810	mycobacteri
579	6	0.8	488	1	LEU2_XYLFA	Q9pax0	xylella fas	652	1	PGPL_MOUSE	Q98b16	rhizobium l
580	6	0.8	489	1	LEU2_XYLFA	Q87bp9	xylella fas	653	1	PUR9_NEIMA	Q8vca0	mus musculus
581	6	0.8	490	1	PYR5_ARATH	Q42586	arabidopsis	654	1	NABI_RALSO	Q9ju88	n bifunctio
582	6	0.8	491	1	TIL1_HUMAN	O75674	homo sapien	655	1	NAD8_YERPE	Q8xwm7	raistonia s
583	6	0.8	492	1	URT1_DESRO	P98119	desmodus ro	656	1	PUR9_PSESM	Q8zd80	yerisinia pe
584	6	0.8	493	1	URT2_DESRO	P15638	desmodus ro	657	1	NAD8_VIBCH	P57828	p bifunctio
585	6	0.8	494	1	BFTU_TOBAC	P41342	nicotiana t	658	1	SCD2_SCHPO	P40936	schizosacch
586	6	0.8	495	1	NIFE_METTM	O06491	bacillus su	659	1	NAD8_ECOLI	P40936	schizosacch
587	6	0.8	496	1	LBP_RABIT	Q87893	vibrio para	660	1	NAD8_ECOLI	P10922	escherichia
588	6	0.8	497	1	UXAB_ECOLI	Q8kpg8	vibrio chol	661	1	NAD8_SALTY	Q8z4k0	salmonella
589	6	0.8	498	1	ETSB_SHIFL	Q8del1	vibrio vuln	662	1	CH60_COREQ	Q8zmx9	salmonella
590	6	0.8	499	1	UXAB_SHIFL	Q8z1e8	yerisinia pe	663	1	CH60_NOCFA	Q93q12	corynebacte
591	6	0.8	500	1	GATA_BACSU	P07729	oryza sativ	664	1	CH60_MOUSE	O9afae	nocardia fa
592	6	0.8	501	1	MURC_VIRPA	P09481	gallus gall	665	1	LCTP_BAGSU	Q8ci33	mus musculus
593	6	0.8	502	1	MURC_VIRCH	Q9fh66	arabidopsis	666	1	CH60_NOCAS	P55910	bacillus su
594	6	0.8	503	1	MURC_VIRVU	Q9p197	chlamydia m	667	1	CH60_NOCAS	Q9afes	nocardia as
595	6	0.8	504	1	MURC_YERPE	P17972	drosophila	668	1	CH60_NOCAS	Q04584	gallus gall
596	6	0.8	505	1	ACH3_BOVIN	P04757	rattus norv	669	1	CH60_NOCAS	P47924	arabidopsis
597	6	0.8	506	1	GUL2_ORYSA	P35962	human immun	670	1	TCPH_MOUSE	Q98312	homo sapien
598	6	0.8	507	1	ACH3_CHICK	P07729	oryza sativ	671	1	TCPA_SCHMA	P08019	saccharomyc
599	6	0.8	508	1	ACH3_CHICK	P09481	gallus gall	672	1	YQ44_CAEEL	P21186	mumps virus
600	6	0.8	509	1	DEGP_CHLMU	Q9fh66	arabidopsis	673	1	TCPA_SCHMA	P42943	saccharomyc
601	6	0.8	510	1	CIKX_DROME	Q9p197	chlamydia m	674	1	YQ44_CAEEL	P40877	escherichia
602	6	0.8	511	1	ACH3_RAT	P17972	drosophila	675	1	TCPH_MOUSE	Q8x4d9	escherichia
603	6	0.8	512	1	GAG_HV1Y2	P04757	rattus norv	676	1	TCPA_SCHMA	P33221	escherichia
604	6	0.8	513	1	GUL1_ORYSA	P35962	human immun	677	1	TCPA_SCHMA	P28904	escherichia
605	6	0.8	514	1	NIFD_RHOCA	P07729	oryza sativ	678	1	TCPA_SCHMA	Q58310	methanococc
606	6	0.8	515	1	PPPS_MOUSE	P30441	homo sapien	679	1	TCPA_SCHMA	Q9v6d6	drosophila
607	6	0.8	516	1	PPPS_MOUSE	P30441	homo sapien	680	1	TCPA_SCHMA	P21277	mumps virus
608	6	0.8	517	1	PPPS_MOUSE	P30441	homo sapien	681	1	TCPA_SCHMA	Q43135	eorghum bic
609	6	0.8	518	1	GGPS_SYN2	P53042	rattus norv	682	1	TCPA_SCHMA		
610	6	0.8	519	1	TRPE_RHOSH	P95645	rhodobacter	683	1	TCPA_SCHMA		
611	6	0.8	520	1	CP2B_RAT	O35132	r 25-hydrox	684	1	TCPA_SCHMA		
612	6	0.8	521	1	LEUI_BUCUN	Q9ev18	buchnera ap	685	1	TCPA_SCHMA		
613	6	0.8	522	1	LPLA_BACSU	P37966	bacillus su	686	1	TCPA_SCHMA		
614	6	0.8	523	1	ACH3_HUMAN	P32297	homo sapien	687	1	TCPA_SCHMA		
615	6	0.8	524	1	LEUI_BUCUM	Q9evh0	buchnera ap	688	1	TCPA_SCHMA		
616	6	0.8	525	1	NRFL_HUMAN	Q16656	homo sapien	689	1	TCPA_SCHMA		
617	6	0.8	526	1	NRFL_MOUSE	Q9wu00	mus musculus	690	1	TCPA_SCHMA		

691 6 0.8 557 1 MERA SHEPU Q54465 shewanella  
692 6 0.8 558 1 Y561\_CHLMU Q9pka6 chlamydia m  
693 6 0.8 559 1 TPA\_MOUSE P11214 mus musculus  
694 6 0.8 559 1 TPA\_RAT P19637 rattus norv  
695 6 0.8 560 1 EFS\_MOUSE Q64355 mus musculu  
696 6 0.8 560 1 HCYG\_SEPOF P58626 sepiia offic  
697 6 0.8 560 1 POTA\_MYCPN P75059 mycoplasma  
698 6 0.8 560 1 YECO\_YEAST P39994 saccharomyc  
699 6 0.8 561 1 EFS\_HUMAN O43281 homo sapien  
700 6 0.8 562 1 TPA\_HUMAN P00750 homo sapien

# ALIGNMENTS

RESULT 1  
Y836\_AQUAE STANDARD; PRT; 232 AA.  
AC O67008;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE Hypothetical protein AQ\_836.  
GN AQ\_836.  
OS Aquifox acolicus.  
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.  
OX NCBI\_TaxID=63363;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VF5;  
RX MEDLINE=98196666; PubMed=9537320;  
RA Dockert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,  
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;  
RT "The complete genome of the hyperthermophilic bacterium Aquifex  
RT acolicus";  
RL Nature 392:353-358(1998).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; A5000709; AAC06970.1; -  
CC PIR; E70372; E70372.  
KW Hypothetical protein; Transmembrane; Complete proteome.  
FT TRANSMEM 4 24 POTENTIAL.  
FT TRANSMEM 42 62 POTENTIAL.  
FT TRANSMEM 100 120 POTENTIAL.  
FT TRANSMEM 145 165 POTENTIAL.  
FT TRANSMEM 171 191 POTENTIAL.  
SQ SEQUENCE 232 AA; 26317 MW; B934B56FEA35B183 CRC64;

Query Match 1.2%; Score 9; DB 1; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 88 FENCKSCRN 96  
|||||  
DB 23 FENCKSCRN 31

RESULT 2  
BMPH\_STRPU STANDARD; PRT; 639 AA.  
AC P98069;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Bone morphogenetic protein 1 homolog precursor (EC 3.4.24.-) (SUBMP).  
OS Strongylocentrotus purpuratus (Purple sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;  
OC Strongylocentrotus.  
OX NCBI\_TaxID=7668;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=94215496; PubMed=8162855;  
RA Hwang S.P.L., Partin J.S., Lennarz W.J.;  
RT "Characterization of a homolog of human bone morphogenetic protein 1  
RT in the embryo of the sea urchin, Strongylocentrotus purpuratus.";  
RL Development 120:559-568(1994).  
CC -1- TISSUE SPECIFICITY: Ectodermal and primary mesenchym cells in  
CC hatched blastula.  
CC -1- DEVELOPMENTAL STAGE: Embryo; highest level before spiculogenesis.  
CC -1- SIMILARITY: Belongs to peptidase family M12A.  
CC -1- SIMILARITY: Contains 1 EGF-like domain.  
CC -1- SIMILARITY: Contains 2 CUB domains.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; L23838; AAA30081.1; -  
CC HSP; P00736; 1APQ.  
DR MEROPS; M12.005; -  
DR InterPro; IPR000152; Asx\_hydroxyl\_1.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro; IPR006026; Peptidase\_M.  
DR InterPro; IPR001506; Peptidase\_M12A.  
DR Pfam; PF01400; Astacin; 1.  
DR Pfam; PF00431; CUB; 2.  
DR Pfam; PF00008; EGF; 1.  
DR PRINTS; PR00480; ASTACIN.  
DR SMART; SM00042; CUB; 2.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00235; ZnMG; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS01180; CUB; 2.  
DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS50026; EGF\_3; 1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW Developmental protein; Repeat; Hydrolase; Protease; Zinc; Embryo;  
KW Metalloprotease; EGF-like domain; Calcium; Signal.  
FT SIGNAL 1 23 POTENTIAL.  
FT PROPEP 24 109 POTENTIAL.  
FT CHAIN 110 639 BONE MORPHOGENETIC PROTEIN 1 HOMOLOG.  
FT DOMAIN 110 306 METALLOPROTEASE.  
FT DOMAIN 307 419 CUB 1.  
FT DOMAIN 420 531 CUB 2.  
FT DOMAIN 532 573 EGF-LIKE, CALCIUM-BINDING (POTENTIAL).  
FT METAL 137 197 ZINC (CATALYTIC) (BY SIMILARITY).  
FT ACT\_SITE 198 198 ZINC (CATALYTIC) (BY SIMILARITY).  
FT METAL 201 201 ZINC (CATALYTIC) (BY SIMILARITY).  
FT METAL 207 207 ZINC (CATALYTIC) (BY SIMILARITY).  
FT DISULFID 536 548 BY SIMILARITY.  
FT DISULFID 544 557 BY SIMILARITY.  
FT DISULFID 559 572 BY SIMILARITY.  
FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).





FT	CHAIN	121	986	BONE MORPHOGENETIC PROTEIN 1.
FT	DOMAIN	121	321	METALLOPROTEINASE.
FT	DOMAIN	322	434	CUB 1.
FT	DOMAIN	435	546	CUB 2.
FT	DOMAIN	547	588	EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	591	703	CUB 3.
FT	DOMAIN	704	743	EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	747	859	CUB 4.
FT	DOMAIN	860	976	CUB 5.
FT	METAL	213	213	ZINC (CATALYTIC) (BY SIMILARITY).
FT	ACT SITE	214	214	BY SIMILARITY.
FT	METAL	217	217	ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL	223	223	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISULFID	183	186	BY SIMILARITY.
FT	DISULFID	322	348	BY SIMILARITY.
FT	DISULFID	375	397	BY SIMILARITY.
FT	DISULFID	435	461	BY SIMILARITY.
FT	DISULFID	488	510	BY SIMILARITY.
FT	DISULFID	551	563	BY SIMILARITY.
FT	DISULFID	559	572	BY SIMILARITY.
FT	DISULFID	574	587	BY SIMILARITY.
FT	DISULFID	591	617	BY SIMILARITY.
FT	DISULFID	644	666	BY SIMILARITY.
FT	DISULFID	707	718	BY SIMILARITY.
FT	DISULFID	714	727	BY SIMILARITY.
FT	DISULFID	729	742	BY SIMILARITY.
FT	CARBOHYD	91	91	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	142	142	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	332	332	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	363	363	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	599	599	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	703	730	DKDCSKDNGCGQDCQVNTGSEYECOCR -> EKBPALQPP
FT				RGRPHQKFRVQRNRTPQ (in isoform BMP1-1).
FT				Missing (in isoform BMP1-1).
FT	VARSPLIC	731	986	/FTid=VSP_005461.
FT	VARSPLIC	245	302	Missing (in isoform BMP1-1).
FT				/FTid=VSP_005462.
FT				QVNFLEWQVEVESIGETVDFDSIMHYARNTSRGIFLDT
FT				IKPVYGVKPTIGOR -> VLSHSLILSCSRNGASFP
FT				CSLESSTHQLCTWGLFLRSPSPFRPLAAPTILAGV
FT				(in isoform BMP1-4).
FT				/FTid=VSP_005463.
FT				Missing (in isoform BMP1-4).
FT	VARSPLIC	303	986	/FTid=VSP_005464.
FT	VARSPLIC	589	622	AACGGPLTKNGITSPGWPKEVPPNKNICWLV -> GCY
FT				DLQVKEFLMDRUCFRSTHGPMLGTALRG (in
FT				isoform BMP1-5).
FT				/FTid=VSP_005465.
FT	VARSPLIC	623	986	Missing (in isoform BMP1-5).
FT				/FTid=VSP_005466.
FT	VARSPLIC	703	717	DKDCSKDNGCGQDCQ -> GGELFGLLGHPPRP (in
FT				isoform BMP1-6).
FT				/FTid=VSP_005467.
FT	VARSPLIC	718	986	Missing (in isoform BMP1-6).
FT				/FTid=VSP_005468.
FT	VARSPLIC	703	823	DKDCSKDNGCGQDCQVNTGSEYECOCRSQFVLNKHDKCK
FT				EGCDHKVTSSTISITSPNWDKVPKCKETWALSTPGRH
FT				VKLTFMWDIESQPECAYDLEVPDGRDAXAPVLGRFCG
FT				-> VLEGADRHSLSGLLELLCHALVDTPAPPALHGD
FT				THARTHTVHTFCIAQCTCGPPLGASRLSPQPGHLTLA
FT				PQEGSYLDFTDTRGDKPRRRRSLTKTFLSLTPATFRGIWA
FT				L (in isoform BMP1-7).
FT				/FTid=VSP_005469.
FT	VARSPLIC	824	986	Missing (in isoform BMP1-7).
FT				/FTid=VSP_005470.
FT	CONFLICT	748	748	D -> N (IN REF. 4).
FT	CONFLICT	934	934	R -> S (IN REF. 4).
FT	SEQUENCE	986 AA;	111248 MW;	F89201913AC3CBEA CRC64;

Query Match 1.2%; Score 9; DB 1; Length 986;  
Best Local Similarity 100.0%; Pred. No. 0.83;  
Matches 9; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
179 YDYVEVRDG 187

Db	377 YDYVEVRDG 385
RESULT 4	
BMP1_MOUSE	
ID_BMP1_MOUSE	STANDARD; PRT; 991 AA.
AC	P98063;
DT	01-FEB-1996 (Rel. 33, Created)
DT	01-FEB-1996 (Rel. 33, Last sequence update)
DT	15-MAR-2004 (Rel. 43, Last annotation update)
DE	Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
DE	(procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mtld).
GN	BMP1.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CS7BL/6; TISSUE=Embryo;
RX	MEDLINE=94229342; PubMed=8174772;
RA	Fukagawa M., Noboru S., Hogan B.L.M., Jones C.M.;
RT	"Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1),
RT	which is related to the Drosophila dorsoventral gene tolloid and
RT	encodes a putative astacin metalloendopeptidase.";
RT	Dev. Biol. 163:175-183(1994).
CC	-!- FUNCTION: Cleaves the C-terminal propeptides of procollagen I, II
CC	and III. Induces cartilage and bone formation.
CC	-!- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at
CC	Ala- -Asp in type I and II procollagens and at Arg- -Asp in type
CC	III.
CC	-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC	-!- ENZYME REGULATION: Activity is increased by the procollagen C-
CC	endopeptidase enhancer protein.
CC	-!- TISSUE SPECIFICITY: At high levels in embryonic maternal deciduum
CC	and floor plate region of the neural tube. Less in developing
CC	membranous and endochondral bone, submucosa of intestine, dermis
CC	of skin and the mesenchyme of spleen and lung.
CC	-!- SIMILARITY: Belongs to peptidase family M12A.
CC	-!- SIMILARITY: Contains 2 EGF-like domains.
CC	-!- SIMILARITY: Contains 5 CUB domains.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; L24755; AAA37306.1; -.
DR	PIR; I49540; I49540.
DR	HSSP; P00736; IAPQ.
DR	MEROPS; M12.005; -.
DR	MGI; 88176; Bmp1.
DR	InterPro; IPR00152; Asx_hydroxyl_s.
DR	InterPro; IPR000859; CUB.
DR	InterPro; IPR001881; EGF_Ca.
DR	InterPro; IPR006209; EGF_like.
DR	InterPro; IPR006025; Pept_M_Zn_BS.
DR	InterPro; IPR006026; Peptidase_M.
DR	InterPro; IPR001506; Peptidase_M12A.
DR	Pfam; PF01400; Astacin; 1.
DR	Pfam; PF00431; CUB; 5.
DR	Pfam; PF00008; EGF; 2.
DR	PRINTS; PR00480; ASTACIN.
DR	SMART; SM00042; CUB; 5.
DR	SMART; SM00179; EGF_CA; 2.
DR	SMART; SM00235; ZmC; 1.
DR	PROSITE; PS00010; ASX_HYDROXYL; 2.
DR	PROSITE; PS01180; CUB; 5.
DR	PROSITE; PS00022; EGF_1; FALSE_NEG.

DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS00026; EGF\_3; 2.  
DR PROSITE; PS01187; EGF\_CA; 2.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW Growth factor; Cytokine; Repeat; Osteogenesis; Chondrogenesis;  
KW Hydrolyase; Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;  
KW Glycoprotein; Zymogen.  
FT SIGNAL 1 25  
FT PROPEP 26 125  
FT CHAIN 126 991  
FT DOMAIN 126 326  
FT DOMAIN 327 439  
FT DOMAIN 440 551  
FT DOMAIN 552 593  
FT DOMAIN 596 707  
FT DOMAIN 708 748  
FT DOMAIN 752 864  
FT DOMAIN 865 981  
FT METAL 218 218  
FT ACT\_SITE 219 219  
FT METAL 222 222  
FT METAL 228 228  
FT METAL 228 228  
FT DISULFID 188 191  
FT DISULFID 327 353  
FT DISULFID 380 402  
FT DISULFID 440 466  
FT DISULFID 493 515  
FT DISULFID 556 568  
FT DISULFID 564 577  
FT DISULFID 579 592  
FT DISULFID 596 622  
FT DISULFID 649 671  
FT DISULFID 712 723  
FT DISULFID 719 732  
FT DISULFID 734 747  
FT CARBOHYD 96 96  
FT CARBOHYD 147 147  
FT CARBOHYD 337 337  
FT CARBOHYD 368 368  
FT CARBOHYD 604 604  
SQ SEQUENCE 991 AA; 111607 MW; 68A1847783A0BB9E CRC64;  
Query Match 1.2%; Score 9; DB 1; Length 991;  
Best Local Similarity 100.0%; Pred. No. 0.83;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 179 YDVEVRDG 187  
DB 382 YDVEVRDG 390  
RESULT 5  
ID Y260 AQUAE STANDARD; PRT; 158 AA.  
AC Q6619;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypothetical UPF0090 protein AQ\_260.  
GN AQ\_260.  
OS Aquifex aeolicus.  
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.  
OX NCBI\_TaxID=63363;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VF5;  
RX MEDLINE=98196666; PubMed=9537320;  
RA Dockert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Anjay M., Huber R.,  
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;  
RT "The complete genome of the hyperthermophilic bacterium Aquifex  
aeolicus";  
RL Nature 392:353-358 (1998).

CC -!- SIMILARITY: Belongs to the UPF0090 family.  
CC -----  
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CC -----  
CC EMBL; AE000681; AAC06588.1; -;  
DR PIR; G70323; G70323.  
DR HAMAP; MF\_01077; -; 1.  
DR InterPro; IPR003728; DUF150.  
DR Pfam; PF02576; DUF150; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 158 AA; 18147 MW; 6F9869AB382FE734 CRC64;  
Query Match 1.1%; Score 8; DB 1; Length 158;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 57 GKREVVGY 64  
DB 114 GKREVVGY 121  
RESULT 6  
ID WTSB LACLC STANDARD; PRT; 360 AA.  
AC P34878;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Modification methylase ScrFIB (EC 2.1.1.73) (Cytosine-specific  
DE methyltransferase ScrFIB) (M.ScrFIB) (M.ScrFIB-B).  
GN SCRFBM.  
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.  
OX NCBI\_TaxID=1359;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UC503;  
RA Twomey D.P., Davis R., Daly C., Fitzgerald G.F.;  
RT "Sequence of the gene encoding a second ScrFI m5C methyltransferase  
of Lactococcus lactis.";  
RL Gene 136:205-209 (1993).  
CC -!- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE  
CC CCNGG. CAUSES SPECIFIC METHYLATION ON C-2 ON BOTH STRANDS, AND  
CC PROTECTS THE DNA FROM CLEAVAGE BY THE SCRFI ENDONUCLEASE.  
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA cytosine = S-  
CC adenosyl-L-homocysteine + DNA 5-methylcytosine.  
CC -!- SIMILARITY: Belongs to the C5-methyltransferase family.  
CC -----  
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CC -----  
CC EMBL; LI2227; AAA16838.1; -;  
DR EMBL; U89998; AAB66694.1; -;  
DR HSSP; P05102; 6MHT.  
DR REBASE; 3682; M.ScrFIB.  
DR InterPro; IPR001525; C5\_DNA\_meth.  
DR Pfam; PF00145; DNA\_methylase; 1.  
DR PRINTS; PR00105; C5METTRFRASE.  
DR TIGRFAMs; TIGR00675; dcm; 1.  
DR PROSITE; PS00094; C5\_MTASE\_1; 1.  
DR PROSITE; PS00095; C5\_MTASE\_2; 1.  
DR Transferase; Methyltransferase; Restriction system.  
KW

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FT ACT_SITE 127 127 BY SIMILARITY.
SQ SEQUENCE 360 AA; 41844 MW; B51D60F72A22A7D7 CRC64;

Query Match 1.1%; Score 8; DB 1; Length 360;
Best Local Similarity 100.0%; Pred.No. 4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 ENLLEARN 279
DB 46 ENLLEARN 53

RESULT 7
VIBC_VIBC STANDARD; PRT; 395 AA.
AC 007898; Q9JQ09;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vibriobactin-specific isochorismate synthase (EC 5.4.99.6)
DE (isochorismate mutase).
GN VIBC OR VC0773.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E1 Tor Lou15;
RX MEDLINE=98037504; PubMed=9371453;
RA Wyckoff E.E., Stoeckner J.A., Reed K.E., Payne S.M.;
RT "Cloning of a Vibrio cholerae vibriobactin gene cluster:
RT identification of genes required for early steps in siderophore
RT biosynthesis."
RL J. Bacteriol. 179:7055-7062 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=E1 Tor N16961 / Serotype O1;
RX MEDLINE=20406933; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483 (2000).
CC -!- CATALYTIC ACTIVITY: Chorismate = isochorismate.
CC -!- PATHWAY: Vibriobactin biosynthesis.
CC -!- SIMILARITY: Belongs to the isochorismate synthase family.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-3 is the initiator.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U52150; AAC45925.1; -.
CC DR EMBL; A8004162; AAF93938.1; -.
CC DR F1R; A82283; A82283.
CC DR TIGR; VC0773; -.
CC DR InterPro; IPR005801; Anth synth chor.
CC DR InterPro; IPR004561; Isochor synth.
CC DR Pfam; PF00425; chorismate bind; 1.
CC DR ProDom; PD000779; Anth synth chor; 1.
CC DR TIGRFAMs; TIGR00543; isochor_syn; 1.
CC DR Iron transport; Isomerase; Complete proteome.
CC SQ SEQUENCE 395 AA; 43594 MW; 2FFAF87DD948C78B CRC64;

Query Match 1.1%; Score 8; DB 1; Length 395;
Best Local Similarity 100.0%; Pred.No. 4.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 KREVVGYT 65
DB 4 KREVVGYT 11

RESULT 8
FA7_BOVIN STANDARD; PRT; 407 AA.
AC F22457;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion
DE accelerator).
GN F7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=89008362; PubMed=3049594;
RA Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,
RA Iwanaga S.;
RT "Bovine factor VII. Its purification and complete amino acid
RT sequence."
RL J. Biol. Chem. 263:14868-14877 (1988).
RN [2]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=89213999; PubMed=3149637;
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
RA Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in bovine
RT blood coagulation factors VII and IX."
RL J. Biochem. 104:867-868 (1988).
RN [3]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein 2."
RL Adv. Exp. Med. Biol. 281:121-131 (1990).
CC -!- FUNCTION: Circulates in the blood in a zymogen form. Factor VII is
CC converted to factor VIIa by factor Xa, factor XIIa, factor IXa, or
CC thrombin by minor proteolysis. In the presence of tissue factor
CC and calcium ions, factor VIIa then converts factor X to factor Xa
CC by limited proteolysis. Factor VIIa will also convert factor IX to
CC factor IXa in the presence of tissue factor and calcium.
CC -!- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -!- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by
CC a disulfide bond.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some
CC glutamate residues allows the modified protein to bind calcium.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC F1R; A31979; KFB07.
CC HSP; P08709; IBF9.
CC DR MEROPS; S01.215; -.
CC DR InterPro; IPR00152; Asx hydroxyl S.
CC DR InterPro; IPR009003; Cys_Ser_tryptain.
CC DR InterPro; IPR000742; EGF_2.
CC DR InterPro; IPR001881; EGF_Ca.
CC DR InterPro; IPR001438; EGF_II.
CC DR InterPro; IPR006209; EGF like.
CC DR InterPro; IPR002383; GLA_blood.

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DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHMOTRYPSIN.
DR PRINTS; PR00010; EGFLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Src; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00022; EGF_2; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat.
FT CHAIN 1 152
FT CHAIN 153 407
FT DOMAIN 6 35
FT DOMAIN 46 82
FT DOMAIN 87 128
FT DOMAIN 153 407
FT SITE 152 153
FT ACT SITE 193
FT ACT SITE 242
FT ACT SITE 344
FT BINDING 338 338
FT BINDING 17 22
FT DISULFID 50 61
FT DISULFID 55 70
FT DISULFID 72 81
FT DISULFID 91 102
FT DISULFID 98 112
FT DISULFID 114 127
FT DISULFID 135 262
FT DISULFID 159 164
FT DISULFID 178 194
FT DISULFID 310 329
FT DISULFID 340 368
FT MOD_RES 6 6
FT MOD_RES 7 7
FT MOD_RES 14 14
FT MOD_RES 16 16
FT MOD_RES 19 19
FT MOD_RES 20 20
FT MOD_RES 25 25
FT MOD_RES 26 26
FT MOD_RES 29 29
FT MOD_RES 35 35
FT MOD_RES 52 52
FT CARBOHYD 145 145
FT CARBOHYD 203 203
FT CARBOHYD 407 407
FT SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;

Query Match 1.1%; Score 8; DB 1; Length 407;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 643 VTDNMFCA 650
Db 323 VTDNMFCA 330

RESULT 9

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YDBH SCHPO STANDARD; PRT; 486 AA.
ID YDBH SCHPO
AC Q10367;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C22E12.17c in chromosome I.
GN SPAC22E12.17C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidaigo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
RA Welter J., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves J.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dega R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Uesery D., Barrell B.G., Nurse P.;
RA "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -!- FUNCTION: GTPase-activating protein for the ADP ribosylation
CC factor family (potential).
CC -!- SIMILARITY: Contains 1 Arf-GAP domain.
CC -----
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CC -----
CC EMBL; Z70043; CAA93904.1; -.
CC PIR; T38174; T38174.
CC GeneDB Spombe; SPAC22E12.17c; -.
CC InterPro; IPR001164; hRIP_like.
CC Pfam; PF01412; ArfGAP; 1.
CC PRINTS; PR00405; REVINTRACTNG.
CC SMART; SM00105; ArfGAP; 1.
CC PROSITE; PS00115; ArfGAP; 1.
KW Hypothetical protein; GTPase activation; Zinc-finger.
FT DOMAIN 9 131
FT ZN_FING 24 47
FT SEQUENCE 486 AA; 53000 MW; 3A6ED366C04F8105 CRC64;

Query Match 1.1%; Score 8; DB 1; Length 486;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 386 SAPTKKPA 393

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Db          279 SAKTKPA 286
|||||
RESULT 10
CATB_STRRE  STANDARD;      PRT;    740 AA.
AC          087864;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
GN CPB.
OS Streptomyces reticuli.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1926;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tu45;
RX MEDLINE=99231840; PubMed=10217488;
RA Zou F., Borovok I., Ortiz de Orue Lucana D., Muller D., Schrempf H.;
RT "The mycelium-associated Streptomyces reticuli catalase-peroxidase,
its gene and regulation by Furs.";
RL Microbiology 145:549-559(1999).
CC -!- FUNCTION: Bifunctional, exhibiting both a catalase and broad-
spectrum peroxidase activities (By similarity).
CC -!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
CC -!- COFACTOR: Binds 1 heme B (iron-protophyrin IX) group per
dimer (By similarity).
CC -!- SIMILARITY: Belongs to the peroxidase family. Bacterial
peroxidase/catalase subfamily.
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CC -----
CC EMBL; Y14317; CAA74698.1; -.
CC HSSP; P00431; 1CCA.
CC InterPro; IPR000763; Bac_ctase/prase.
CC InterPro; IPR02016; Peroxidase.
CC Pfam; PF00141; peroxidase; 1.
CC PRINTS; PR00458; PEROXIDASE.
CC TIGRfam; TIGR00198; cat_per HPI; 1.
CC PROSITE; PS00435; PEROXIDASE_1; 1.
CC PROSITE; PS00436; PEROXIDASE_2; 1.
CC PROSITE; PS00873; PEROXIDASE_4; 1.
CC Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
KW ACT SITE 105 105 BY SIMILARITY.
FT ACT SITE 109 109 BY SIMILARITY.
FT METAL 272 272 IRON (HEME AXIAL LIGAND).
SQ SEQUENCE 740 AA; 81345 MW; E21860AEE4B4A0E CRC64;

Query Match 1.1%; Score 8; DB 1; Length 740;
Best Local Similarity 100.0%; Pred.No. 7.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 558 DADIATLK 565
DB 453 DADIATLK 460
|||||
RESULT 11
LFC_CARRO
ID LFC_CARRO STANDARD;      PRT;    1019 AA.
AC Q26422;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

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DE Limulus clotting factor C precursor (EC 3.4.21.84) (FC).
OS Carinoscorpius rotundicauda (Southeast Asian horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Carinoscorpius.
OX NCBI_TaxID=6848;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95268506; PubMed=7538401;
RA Ding J.L., Navas M.A. III, Ho B.;
RT "Molecular cloning and sequence analysis of factor C cDNA from the
Singapore horseshoe crab, Carinoscorpius rotundicauda.";
RL Mol. Mar. Biol. Biotechnol. 4:90-103(1995).
CC -!- FUNCTION: This enzyme is closely associated with an endotoxin-
sensitive hemolymph coagulation system which may play important
roles in both hemostasis and host defense mechanisms. Its active
form catalyzes the activation of factor B.
CC -!- CATALYTIC ACTIVITY: Selective cleavage of 103-Arg-|-Ser-104 and
124-Ile-|-Ile-125 bonds in Limulus clotting factor B to form
activated factor B. Cleavage of Pro-Arg-|-Xaa bonds in synthetic
substrates.
CC -!- ENZYME REGULATION: Activated by Gram-negative bacterial
lipopolysaccharides and chymotrypsin (By similarity).
CC -!- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by
a disulfide bond (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 LCCL domain.
CC -!- SIMILARITY: Contains 5 Sushi (SCR) domains.
CC -----
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CC -----
CC EMBL; S77063; AAB34361.1; -.
CC HSSP; P00763; LDPO.
CC MEROPS; S01.219; -.
CC InterPro; IPR009003; Cys Ser trypsin.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR004043; LCCL_dom.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF03815; LCCL; 1.
CC Pfam; PF00059; lectin_C; 1.
CC Pfam; PF00084; sushi; 5.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC SMART; SM00032; CCP; 5.
CC SMART; SM00034; CLECT; 1.
CC SMART; SM00181; EGF; 1.
CC SMART; SM00603; LCCL; 1.
CC SMART; SM00020; TRYPSIN; 1.
CC PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
CC PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; FALSE_NEG.
CC PROSITE; PS00026; EGF_3; 1.
CC PROSITE; PS00820; LCCL; 1.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Signal; Lectin; Hemolymph clotting;
KW Glycoprotein; Cell adhesion; EGF-like domain; Sushi; Repeat.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 1019 LIMULUS CLOTTING FACTOR C.

```

```
FT CHAIN 26 690 LIMULUS CLOTTING FACTOR C, HEAVY CHAIN.
FT CHAIN 691 1019 LIMULUS CLOTTING FACTOR C, LIGHT CHAIN.
FT CHAIN 691 762 LIMULUS CLOTTING FACTOR C, A CHAIN.
FT CHAIN 763 1019 LIMULUS CLOTTING FACTOR C, B CHAIN.
FT DOMAIN 102 137 EGF-LIKE.
FT DOMAIN 142 195 SUSHI 1.
FT DOMAIN 200 254 SUSHI 2.
FT DOMAIN 260 321 SUSHI 3.
FT DOMAIN 325 421 LCCL.
FT DOMAIN 436 568 SUSHI 4.
FT DOMAIN 576 634 SUSHI 5.
FT DOMAIN 683 1019 SERINE PROTEASE.
FT ACT SITE 809 809 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 865 865 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 966 966 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT BINDING 960 960 SUBSTRATE (BY SIMILARITY).
FT DOMAIN 643 689 PRO-RICH.
FT DISULFID 106 118 BY SIMILARITY.
FT DISULFID 112 125 BY SIMILARITY.
FT DISULFID 127 136 BY SIMILARITY.
FT DISULFID 436 447 BY SIMILARITY.
FT DISULFID 464 564 BY SIMILARITY.
FT DISULFID 538 556 BY SIMILARITY.
FT DISULFID 794 810 BY SIMILARITY.
FT DISULFID 932 951 BY SIMILARITY.
FT DISULFID 962 996 BY SIMILARITY.
FT CARBOHYD 523 523 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 534 534 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 740 767 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 912 912 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1019 AA; 112429 NW; 918A1ED8B817B6C3 CRC64;

Query Match 1.1%; Score 8; DB 1; Length 1019;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 574 TRVQPICL 581
DB 879 TRVQPICL 886

RESULT 12
LPC_TACTR STANDARD; PRT; 1019 AA.
AC P28175;1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DS Limulus clotting factor C precursor (EC 3.4.21.84) (FC).
OS Tachyplesus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachyplesus.
OX NCBI_TaxID=6853;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND PARTIAL SEQUENCE.
RX MEDLINE=91177916; PubMed=2007602;
RA Muta T., Miyata T., Misumi Y., Tokunaga F., Nakamura T., Toh Y.,
RA Ikehara Y., Iwanaga S.;
RT "Limulus factor C. An endotoxin-sensitive serine protease zymogen
with a mosaic structure of complement-like, epidermal growth
factor-like, and lectin-like domains."
RL J. Biol. Chem. 266:6554-6561(1991).
CC -|- FUNCTION: This enzyme is closely associated with an endotoxin-
sensitive hemolymph coagulation system which may play important
roles in both hemostasis and host defense mechanisms. Its active
form catalyzes the activation of factor B.
CC -|- CATALYTIC ACTIVITY: Selective cleavage of 103-Arg-Ser-104 and
124-Ile-Ile-125 bonds in Limulus clotting factor B to form
activated factor B. Cleavage of Pro-Arg-Xaa bonds in synthetic
substrates.
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CC -|- ENZYME REGULATION: Activated by Gram-negative bacterial
lipopolysaccharides and chymotrypsin.
CC -|- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by
a disulfide bond.
CC -|- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=Long;
IsoId=P28175-1; Sequence=Displayed;
Name=Short;
IsoId=P28175-2; Sequence=VSP_005413, VSP_005414;
CC -|- SIMILARITY: Belongs to peptidase family S1_
-|- SIMILARITY: Contains 1 C-type lectin family domain.
CC -|- SIMILARITY: Contains 1 EGF-like domain.
CC -|- SIMILARITY: Contains 1 LCCL domain.
CC -|- SIMILARITY: Contains 5 Sushi (SCR) domains.
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entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D90271; BAA14315.1; -
CC EMBL; D90272; BAA14316.1; -
CC PIR; A38738; A38738.
CC HSPSP; P00763; IDPO.
CC MEROPS; S01.219; -.
CC InterPro; IPR009003; Cys Ser trypsin.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR006210; EGF.
CC InterPro; IPR004043; LCCL dom.
CC InterPro; IPR001304; Lectin C.
CC InterPro; IPR001254; Peptidase S1.
CC InterPro; IPR001314; Peptidase S1A.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF03815; LCCL; 1.
CC Pfam; PF00059; lectin_c; 1.
CC Pfam; PF00084; sushi; 5.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC SMART; SM00032; CCF; 5.
CC SMART; SM00034; CLECT; 1.
CC SMART; SM00181; EGF; 1.
CC SMART; SM00603; LCCL; 1.
CC SMART; SM00020; Tryp_SPC; 1.
CC PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
CC PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; FALSE_NEG.
CC PROSITE; PS50026; EGF_3; 1.
CC PROSITE; PS50820; LCCL; 1.
CC PROSITE; PS50240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Hydrolase; Serine protease; Signal; Alternative splicing; Lectin;
KW Hemolymph clotting; Glycoprotein; Cell adhesion; EGF-like domain;
KW Sushi; Repeat.
FT SIGNAL 1 25
FT CHAIN 26 1019 LIMULUS CLOTTING FACTOR C.
FT CHAIN 26 690 LIMULUS CLOTTING FACTOR C, HEAVY CHAIN.
FT CHAIN 691 1019 LIMULUS CLOTTING FACTOR C, LIGHT CHAIN.
FT CHAIN 691 762 LIMULUS CLOTTING FACTOR C, A CHAIN.
FT CHAIN 763 1019 LIMULUS CLOTTING FACTOR C, B CHAIN.
FT DOMAIN 102 137 EGF-LIKE.
FT DOMAIN 142 195 SUSHI 1.
FT DOMAIN 200 254 SUSHI 2.
FT DOMAIN 260 321 SUSHI 3.
FT DOMAIN 325 421 LCCL.
FT DOMAIN 436 568 C-TYPE LECTIN.
FT DOMAIN 576 634 SUSHI 4.
FT DOMAIN 685 748 SUSHI 5.
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```
FT DOMAIN 763 1019 SERINE PROTEASE.
FT ACT_SITE 809 865 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 865 965 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 965 965 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT BINDING 960 960 SUBSTRATE (BY SIMILARITY).
FT BINDING 960 960 PRO-RICH.
FT DOMAIN 643 689 BY SIMILARITY.
FT DISULFID 106 118 BY SIMILARITY.
FT DISULFID 112 125 BY SIMILARITY.
FT DISULFID 127 136 BY SIMILARITY.
FT DISULFID 436 447 BY SIMILARITY.
FT DISULFID 464 564 BY SIMILARITY.
FT DISULFID 538 556 BY SIMILARITY.
FT DISULFID 794 810 BY SIMILARITY.
FT DISULFID 932 951 BY SIMILARITY.
FT DISULFID 962 996 BY SIMILARITY.
FT CARBOHYD 523 523 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 534 534 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 740 740 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 767 767 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 912 912 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 492 498 LTTWTG -> TDNVAT (in isoform Short).
FT VARSPLIC /FTId=VSP 005413.
FT VARSPLIC Missing (in isoform Short).
FT VARSPLIC /FTId=VSP 005414.
FT SEQUENCE 1019 AA; 112346 MW; 58C2864C6715289B CRC64;
SQ SEQUENCE 1.1%; Score 8; DB 1; Length 1019;
Query Match 1.1%; Score 8; DB 1; Length 1019;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 574 TRVQICL 581
DB 879 TRVQICL 886

RESULT 13
YPA2_ASCIM STANDARD; PRT; 167 AA.
AC P2375;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 19.7 kDa protein (ORF2).
OS Ascobolus immersus.
OG Mitochondrion.
CG Plasmid pA12.
CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Pezizomycetes;
CC Pezizales; Ascobolaceae; Ascobolus.
CC NCBI_TaxID=5191;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2/I;
RX MEDLINE=90066356; PubMed=2573821;
RA Kompen F., Meinhardt F., Esser K.;
RA "In organello replication and viral affinity of linear,
RT extrachromosomal DNA of the ascomycete Ascobolus immersus."
RL Mol. Gen. Genet. 218:523-530(1989).
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CC -----
CC EMBL; X15982; CAA34107.1; --
CC STRAIN=2/I;
CC MEDLINE=90066356; PubMed=2573821;
CC Kompen F., Meinhardt F., Esser K.;
CC "In organello replication and viral affinity of linear,
RT extrachromosomal DNA of the ascomycete Ascobolus immersus."
RL Mol. Gen. Genet. 218:523-530(1989).
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CC -----
CC EMBL; X15982; CAA34107.1; --
CC PIR; S05364; S05364.
KW Hypothetical protein; Plasmid; Mitochondrion.
SQ SEQUENCE 167 AA; 19762 MW; 2A6EC8ADD91E8D93 CRC64;
Query Match 1.0%; Score 7; DB 1; Length 167;
```

```
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLISSL 22
DB 106 LLLISSL 112

RESULT 14
Y377_MYCGE STANDARD; PRT; 193 AA.
AC P47617;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG377.
GN MG377.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RA "The minimal gene complement of Mycoplasma genitalium."
RL Science 270:397-403(1995).
CC -----
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CC -----
CC EMBL; U39719; AAC71604.1; --
CC PIR; G64241; G64241.
CC TIGR; MG377; --.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 193 AA; 22649 MW; A85E543B6D281DF CRC64;
Query Match 1.0%; Score 7; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 534 DEKTIQS 540
DB 102 DEKTIQS 108

RESULT 15
CRBD_CHICK STANDARD; PRT; 196 AA.
AC P49152;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta crystallin A4.
GN CRBA4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Lens;
```



```

RX MEDLINE=96032342; PubMed=7557428;
RA Duncan M.K., Haynes J.I. II, Piatigorsky J.;
RT "The chicken beta A4- and beta B1-crystallin-encoding genes are
RT tightly linked";
RL Gene 162:189-196(1995).
CC -!- FUNCTION: Crystallins are the dominant structural components of
CC the vertebrate eye lens.
CC -!- SUBUNIT: Homo/heterodimer, or complexes of higher order. The
CC structure of beta-crystallin oligomers seems to be stabilized
CC through interactions between the N-terminal arms (By similarity).
CC -!- DOMAIN: Has a two-domain beta-structure, folded into four very
CC similar greek key motifs.
CC -!- SIMILARITY: Belongs to the beta/gamma-crystallin family.
CC -!- SIMILARITY: Contains 4 beta/gamma crystallin 'greek key' domains.
CC -----
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CC -----
DR EMBL; U18261; AAB60607.1; -.
DR EMBL; U18260; AAB62669.1; -.
DR HSSP; P02522; 2BB2.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF00030; crystall; 2.
DR PRINTS; PR01367; HGCYSTALLIN.
DR SMART; SM00247; XTALbg; 2.
DR PROSITE; PS50915; CRYSTALLIN_BETAGAMMA; 4.
KW Eyo lens protein; Repeat.
FT DOMAIN 1 11 N-TERMINAL ARM.
FT DOMAIN 12 51 BETA/GAMMA CRYSTALLIN 'GREEK KEY' 1.
FT DOMAIN 52 98 BETA/GAMMA CRYSTALLIN 'GREEK KEY' 2.
FT DOMAIN 99 104 CONNECTING PEPTIDE.
FT DOMAIN 105 146 BETA/GAMMA CRYSTALLIN 'GREEK KEY' 3.
FT DOMAIN 147 195 BETA/GAMMA CRYSTALLIN 'GREEK KEY' 4.
FT VARIANT 103 103 G -> R.
SQ SEQUENCE 196 AA; 22416 MW; BC0787DC8FCBC8D5 CRC64;

Query Match 1.0%; Score 7; DB 1; Length 196;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 486 FLVCSGA 492
Db 142 FLVCSGA 148
|||||

```

Search completed: August 18, 2004, 16:32:40  
Job time : 24 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:17:08 ; Search time 57 Seconds  
(without alignments)  
3569.021 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945

Sequence: 1 MELGCWTGLTFLQLLLS.....LSTFTKVLVLPKDWIERNMK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 700 summaries

Database : A\_Geneseq\_23Jan04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3945	100.0	720	3	Aay66695 Membrane-
2	3945	100.0	720	4	Aau29108 Human PRO
3	3945	100.0	720	4	Aab87544 Human PRO
4	3945	100.0	720	4	Aab65218 Human PRO
5	3945	100.0	720	5	Abg95869 Human sec
6	3945	100.0	720	6	Abu58484 Human PRO
7	3945	100.0	720	6	Abu88032 Novel hum
8	3945	100.0	720	6	Abu84347 Human sec
9	3945	100.0	720	6	AbR66221 Human sec
10	3945	100.0	720	6	AbR65611 Human sec
11	3945	100.0	720	6	Abu599551 Human sec
12	3945	100.0	720	6	Abu58033 Human PRO
13	3945	100.0	720	6	Abu59111 Novel hum
14	3945	100.0	720	6	Abu82623 Human sec
15	3945	100.0	720	6	Abu82790 Human PRO
16	3945	100.0	720	6	Abu89911 Novel hum
17	3945	100.0	720	6	AbR68160 Human sec
18	3945	100.0	720	6	Abu60542 Human sec
19	3945	100.0	720	6	Abu96213 Novel hum
20	3945	100.0	720	6	Abu92644 Human sec
21	3945	100.0	720	6	AbO08721 Human sec
22	3945	100.0	720	6	AbO02773 Human sec
23	3945	100.0	720	6	AbR74927 Human sec
24	3945	100.0	720	6	AbR94689 Human sec
25	3945	100.0	720	6	Abu13924 Human PRO

26	3945	100.0	720	6	ABU85662	Human PRO
27	3945	100.0	720	6	ABU98822	Novel hum
28	3945	100.0	720	6	ABU98037	Novel hum
29	3945	100.0	720	6	ABU91743	Novel hum
30	3945	100.0	720	6	ABU89436	Human PRO
31	3945	100.0	720	6	ABU86277	Human sec
32	3945	100.0	720	6	ABU67490	Human sec
33	3945	100.0	720	6	ABU80518	Human PRO
34	3945	100.0	720	6	ABU72509	Novel hum
35	3945	100.0	720	6	ABU90894	Novel hum
36	3945	100.0	720	6	ABO33953	Human sec
37	3945	100.0	720	6	ABR99436	Human sec
38	3945	100.0	720	6	ABR98826	Human sec
39	3945	100.0	720	6	ABO16349	Human sec
40	3945	100.0	720	6	ABR92249	Human sec
41	3945	100.0	720	6	ABO18890	Human sec
42	3945	100.0	720	6	ABR78311	Human sec
43	3945	100.0	720	6	ABU71970	Novel hum
44	3945	100.0	720	6	ABU85047	Novel hum
45	3945	100.0	720	6	ABO00186	Novel hum
46	3945	100.0	720	6	ABO11518	Human sec
47	3945	100.0	720	6	ABO02163	Human sec
48	3945	100.0	720	6	ABU88737	Novel hum
49	3945	100.0	720	6	ABU83432	Human sec
50	3945	100.0	720	6	ABO06233	Novel hum
51	3945	100.0	720	6	ABR59269	Human sec
52	3945	100.0	720	6	ABO09331	Human sec
53	3945	100.0	720	6	ABO19195	Novel hum
54	3945	100.0	720	6	ABO11213	Human sec
55	3945	100.0	720	6	ABR66831	Human sec
56	3945	100.0	720	6	ABO16044	Human sec
57	3945	100.0	720	6	ABO13750	Human sec
58	3945	100.0	720	6	ABU71524	Human sec
59	3945	100.0	720	6	ABU65653	Human sec
60	3945	100.0	720	6	ABO07501	Human PRO
61	3945	100.0	720	6	ABO03688	Human sec
62	3945	100.0	720	6	ABR67136	Human sec
63	3945	100.0	720	6	ABO15739	Human sec
64	3945	100.0	720	6	ABU56020	Human sec
65	3945	100.0	720	6	ABU72305	Human PRO
66	3945	100.0	720	6	ABU65348	Human PRO
67	3945	100.0	720	6	ABU95293	Novel hum
68	3945	100.0	720	6	ABU71196	Human PRO
69	3945	100.0	720	6	ABO07806	Human PRO
70	3945	100.0	720	6	ABR70047	Human sec
71	3945	100.0	720	6	ABR69380	Human sec
72	3945	100.0	720	6	ABO01521	Human PRO
73	3945	100.0	720	6	ABU81323	Human PRO
74	3945	100.0	720	6	ABR60120	Human sec
75	3945	100.0	720	6	ABR90978	Human PRO
76	3945	100.0	720	6	ABR67855	Human sec
77	3945	100.0	720	6	ABR65243	Human sec
78	3945	100.0	720	6	ABR68465	Human sec
79	3945	100.0	720	6	ABR71877	Human sec
80	3945	100.0	720	6	ABU59258	Human sec
81	3945	100.0	720	6	ABU85357	Human PRO
82	3945	100.0	720	6	ABU89047	Human sec
83	3945	100.0	720	6	ABU83127	Human sec
84	3945	100.0	720	6	ABU94983	Novel hum
85	3945	100.0	720	6	ABU90531	Novel hum
86	3945	100.0	720	6	ABU84042	Human sec
87	3945	100.0	720	6	ABU93693	Novel hum
88	3945	100.0	720	6	ABO25955	Human PRO
89	3945	100.0	720	6	ABR64938	Human sec
90	3945	100.0	720	6	ABO27299	Human sec
91	3945	100.0	720	6	ABR68770	Human sec
92	3945	100.0	720	6	ABO06586	Human sec
93	3945	100.0	720	6	ABR99131	Human sec
94	3945	100.0	720	6	ABU57015	Human PRO
95	3945	100.0	720	6	ABU85967	Novel hum
96	3945	100.0	720	6	ABU82254	Novel hum
97	3945	100.0	720	6	ABU87265	Human PRO
98	3945	100.0	720	6	ABU83737	Human sec

99	3945	100.0	720	6	ABO08111	Human PRO	172	3945	100.0	720	6	ABR90334	Human sec
100	3945	100.0	720	6	ABU92494	Human sec	173	3945	100.0	720	6	ABM17248	Human sec
101	3945	100.0	720	6	ABU81822	Novel hum	174	3945	100.0	720	6	ABR94994	Human sec
102	3945	100.0	720	6	ABU65986	Novel hum	175	3945	100.0	720	6	ABR95299	Human sec
103	3945	100.0	720	6	ABU81164	Human sec	176	3945	100.0	720	6	ADB17095	Human tra
104	3945	100.0	720	6	ABR59815	Human sec	177	3945	100.0	720	6	ABO21537	Human sec
105	3945	100.0	720	6	ABU94003	Novel hum	178	3945	100.0	720	6	ABR97801	Human sec
106	3945	100.0	720	6	ABU99856	Novel hum	179	3945	100.0	720	6	ABR87589	Human sec
107	3945	100.0	720	6	ABR66526	Human sec	180	3945	100.0	720	6	ABM77630	Human sec
108	3945	100.0	720	6	ABR90944	Human sec	181	3945	100.0	720	6	ABM7860	Human sec
109	3945	100.0	720	6	ABO53279	Novel hum	182	3945	100.0	720	6	ABM06141	Human sec
110	3945	100.0	720	6	ABU58964	Human sec	183	3945	100.0	720	6	ABM03647	Human sec
111	3945	100.0	720	6	ABU94371	Human PRO	184	3945	100.0	720	6	ABM35098	Human sec
112	3945	100.0	720	6	ABU79253	Human PRO	185	3945	100.0	720	6	ABM26335	Human sec
113	3945	100.0	720	6	ABU86582	Human sec	186	3945	100.0	720	6	ABO48117	Human sec
114	3945	100.0	720	6	ABU86887	Novel hum	187	3945	100.0	720	6	ABR92859	Human sec
115	3945	100.0	720	6	ABU94676	Human PRO	188	3945	100.0	720	6	ABO24620	Human sec
116	3945	100.0	720	6	ABO04603	Human PRO	189	3945	100.0	720	6	ADA37742	Human sec
117	3945	100.0	720	6	ABR70352	Human sec	190	3945	100.0	720	6	ABM11631	Human sec
118	3945	100.0	720	6	ABU92342	Novel hum	191	3945	100.0	720	6	ABM02732	Human sec
119	3945	100.0	720	6	ABU98517	Human PRO	192	3945	100.0	720	6	ABM16028	Human sec
120	3945	100.0	720	6	ABR65916	Human sec	193	3945	100.0	720	6	ABO27589	Human sec
121	3945	100.0	720	6	ABR64633	Human sec	194	3945	100.0	720	6	ABM29080	Human sec
122	3945	100.0	720	6	ABU59407	Novel hum	195	3945	100.0	720	6	ABM07056	Human sec
123	3945	100.0	720	6	ABU79558	Human PRO	196	3945	100.0	720	6	ABM21150	Human sec
124	3945	100.0	720	6	ABU92949	Human sec	197	3945	100.0	720	6	ABM09496	Human sec
125	3945	100.0	720	6	ABU95508	Human PRO	198	3945	100.0	720	6	ABO41366	Human sec
126	3945	100.0	720	6	ABU91128	Novel hum	199	3945	100.0	720	6	ABO36181	Human PRO
127	3945	100.0	720	6	ABU90221	Novel hum	200	3945	100.0	720	6	ABO43710	Human PRO
128	3945	100.0	720	6	ABO09636	Human sec	201	3945	100.0	720	6	ABM76410	Human sec
129	3945	100.0	720	6	ABO10908	Human sec	202	3945	100.0	720	6	ABM76106	Human sec
130	3945	100.0	720	6	ABR70962	Human sec	203	3945	100.0	720	6	ABM25725	Human sec
131	3945	100.0	720	6	ABU98281	Novel hum	204	3945	100.0	720	6	ABM26030	Human sec
132	3945	100.0	720	6	ABU87570	Human PRO	205	3945	100.0	720	6	ADA21428	Human sec
133	3945	100.0	720	6	ABU91438	Human PRO	206	3945	100.0	720	6	ABO03383	Human sec
134	3945	100.0	720	6	ABU89286	Novel hum	207	3945	100.0	720	6	ABO02468	Human sec
135	3945	100.0	720	6	ABU84552	Human sec	208	3945	100.0	720	6	ABO44257	Human sec
136	3945	100.0	720	6	ABR69742	Human sec	209	3945	100.0	720	6	ABR90639	Human sec
137	3945	100.0	720	6	ABU80119	Human PRO	210	3945	100.0	720	6	ABR73707	Human sec
138	3945	100.0	720	6	ABU82493	Novel hum	211	3945	100.0	720	6	ABO16959	Human sec
139	3945	100.0	720	6	ABU92173	Novel hum	212	3945	100.0	720	6	ABR94384	Human sec
140	3945	100.0	720	6	ABU93388	Human PRO	213	3945	100.0	720	6	ABR75891	Human sec
141	3945	100.0	720	6	ABO09941	Human sec	214	3945	100.0	720	6	ABR71267	Human sec
142	3945	100.0	720	6	ABO09026	Human sec	215	3945	100.0	720	6	ABR93164	Human sec
143	3945	100.0	720	6	ABU96457	Human PRO	216	3945	100.0	720	6	ABR93469	Human sec
144	3945	100.0	720	6	ABU10879	Human PRO	217	3945	100.0	720	6	ADA10215	Human sec
145	3945	100.0	720	6	ABU10594	Human sec	218	3945	100.0	720	6	ABR87894	Human sec
146	3945	100.0	720	6	ABU81631	Novel hum	219	3945	100.0	720	6	ABO27894	Human sec
147	3945	100.0	720	6	ABU72127	Human PRO	220	3945	100.0	720	6	ABO30029	Human sec
148	3945	100.0	720	6	ABU95603	Human PRO	221	3945	100.0	720	6	ABO33238	Human PRO
149	3945	100.0	720	6	ABU96812	Novel hum	222	3945	100.0	720	6	ABM04926	Human sec
150	3945	100.0	720	6	ABR70657	Human sec	223	3945	100.0	720	6	ABM08886	Human sec
151	3945	100.0	720	6	ABO05008	Novel hum	224	3945	100.0	720	6	ABO36486	Human sec
152	3945	100.0	720	6	ABO08416	Human sec	225	3945	100.0	720	6	ABO35571	Human PRO
153	3945	100.0	720	6	ABU88570	Human sec	226	3945	100.0	720	6	ABO39536	Human sec
154	3945	100.0	720	6	ABO34084	Human PRO	227	3945	100.0	720	6	ABM10411	Human sec
155	3945	100.0	720	6	ABO05623	Human sec	228	3945	100.0	720	6	ABM11936	Human sec
156	3945	100.0	720	6	ABR74012	Human sec	229	3945	100.0	720	6	ABO52082	Human PRO
157	3945	100.0	720	6	ABR95604	Human sec	230	3945	100.0	720	6	ABO52387	Human PRO
158	3945	100.0	720	6	ABR80901	Human sec	231	3945	100.0	720	6	ADA19900	Novel hum
159	3945	100.0	720	6	ABR81206	Human sec	232	3945	100.0	720	6	ADA19900	Novel hum
160	3945	100.0	720	6	ABM00902	Human sec	233	3945	100.0	720	6	ADB17283	Human tra
161	3945	100.0	720	6	ABR88504	Human sec	234	3945	100.0	720	6	ADA17759	Human PRO
162	3945	100.0	720	6	ABM77325	Human sec	235	3945	100.0	720	6	ABR97191	Human sec
163	3945	100.0	720	6	ABO28809	Human sec	236	3945	100.0	720	6	ABR86979	Human sec
164	3945	100.0	720	6	ABO31554	Human sec	237	3945	100.0	720	6	ABM11021	Human sec
165	3945	100.0	720	6	ABM07971	Human sec	238	3945	100.0	720	6	ABM28165	Human sec
166	3945	100.0	720	6	ABO40451	Human sec	239	3945	100.0	720	6	ABO32164	Human sec
167	3945	100.0	720	6	ABO35876	Human PRO	240	3945	100.0	720	6	ABM15291	Human sec
168	3945	100.0	720	6	ABO44015	Human PRO	241	3945	100.0	720	6	ABM06446	Human sec
169	3945	100.0	720	6	ADA77922	Human sec	242	3945	100.0	720	6	ABM04257	Human sec
170	3945	100.0	720	6	ABM24810	Human sec	243	3945	100.0	720	6	ABM22370	Human sec
171	3945	100.0	720	6	ABO03078	Human sec	244	3945	100.0	720	6	ABM07666	Human sec

245	3945	100.0	720	6	ABO40756	Human sec	318	3945	100.0	720	6	ABO37096	Human sec
246	3945	100.0	720	6	ABM35403	Human sec	319	3945	100.0	720	6	ABO41671	Human sec
247	3945	100.0	720	6	ABM33166	Human sec	320	3945	100.0	720	6	ABO35266	Human PRO
248	3945	100.0	720	6	ABO52692	Human PRO	321	3945	100.0	720	6	ABM25115	Human sec
249	3945	100.0	720	6	ABO50252	Human sec	322	3945	100.0	720	6	ABO47507	Human sec
250	3945	100.0	720	6	ABU99246	Human sec	323	3945	100.0	720	6	ABO47812	Human sec
251	3945	100.0	720	6	ABO44298	Human sec	324	3945	100.0	720	6	ABO48422	Human sec
252	3945	100.0	720	6	ABO04528	Human sec	325	3945	100.0	720	6	ABO51472	Human PRO
253	3945	100.0	720	6	ABM18468	Human sec	326	3945	100.0	720	6	ABO51777	Human PRO
254	3945	100.0	720	6	ADA27867	Human sec	327	3945	100.0	720	6	ABO50557	Human sec
255	3945	100.0	720	6	ABR97496	Human sec	328	3945	100.0	720	6	ABR79681	Human sec
256	3945	100.0	720	6	ABR80596	Human sec	329	3945	100.0	720	6	ABM16943	Human sec
257	3945	100.0	720	6	ABM01207	Human sec	330	3945	100.0	720	6	ABO17975	Human sec
258	3945	100.0	720	6	ABR88809	Human sec	331	3945	100.0	720	6	ABO20927	Human sec
259	3945	100.0	720	6	ABM13461	Human sec	332	3945	100.0	720	6	ABR96886	Human sec
260	3945	100.0	720	6	ABM20845	Human sec	333	3945	100.0	720	6	ADA38672	Human sec
261	3945	100.0	720	6	ABO41976	Human sec	334	3945	100.0	720	6	ABM12241	Human sec
262	3945	100.0	720	6	ABO42586	Human sec	335	3945	100.0	720	6	ABM16333	Human sec
263	3945	100.0	720	6	ABM10106	Human sec	336	3945	100.0	720	6	ABM24200	Human sec
264	3945	100.0	720	6	ABO38621	Human sec	337	3945	100.0	720	6	ABM14681	Human sec
265	3945	100.0	720	6	ABM32861	Human sec	338	3945	100.0	720	6	ABM04562	Human sec
266	3945	100.0	720	6	ABM22675	Human sec	339	3945	100.0	720	6	ABM06751	Human sec
267	3945	100.0	720	6	ABM74886	Human sec	340	3945	100.0	720	6	ABM09191	Human sec
268	3945	100.0	720	6	ADA79714	Human sec	341	3945	100.0	720	6	ABO39231	Human sec
269	3945	100.0	720	6	ABR96276	Human sec	342	3945	100.0	720	6	ABM75496	Human sec
270	3945	100.0	720	6	ABM02427	Human sec	343	3945	100.0	720	6	ABM25420	Human sec
271	3945	100.0	720	6	ABR86369	Human sec	344	3945	100.0	720	6	ABM15930	Human sec
272	3945	100.0	720	6	ABR86674	Human sec	345	3945	100.0	720	6	ABO46836	Human PRO
273	3945	100.0	720	6	ABM16638	Human sec	346	3945	100.0	720	6	ABO47141	Human PRO
274	3945	100.0	720	6	ABM29690	Human sec	347	3945	100.0	720	6	ADA83239	Human sec
275	3945	100.0	720	6	ABO29114	Human sec	348	3945	100.0	720	6	ABR71572	Human sec
276	3945	100.0	720	6	ABM23895	Human sec	349	3945	100.0	720	6	ABR72182	Human sec
277	3945	100.0	720	6	ABM23285	Human sec	350	3945	100.0	720	6	ABR98521	Human sec
278	3945	100.0	720	6	ABM22065	Human sec	351	3945	100.0	720	6	ABO06891	Human sec
279	3945	100.0	720	6	ABO37706	Human sec	352	3945	100.0	720	6	ABR84844	Human sec
280	3945	100.0	720	6	ABM28470	Human sec	353	3945	100.0	720	6	ABR73402	Human sec
281	3945	100.0	720	6	ABM28775	Human sec	354	3945	100.0	720	6	ABR76496	Human sec
282	3945	100.0	720	6	ABM66419	Human sec	355	3945	100.0	720	6	ABR73097	Human sec
283	3945	100.0	720	6	ABM75801	Human sec	356	3945	100.0	720	6	ABM18163	Human sec
284	3945	100.0	720	6	ABM34081	Human sec	357	3945	100.0	720	6	ABO20622	Human sec
285	3945	100.0	720	6	ABM34386	Human sec	358	3945	100.0	720	6	ABO25365	Human PRO
286	3945	100.0	720	6	ABO20317	Human sec	359	3945	100.0	720	6	ABO25670	Human PRO
287	3945	100.0	720	6	ABO21232	Human sec	360	3945	100.0	720	6	ABR94079	Human sec
288	3945	100.0	720	6	ABO22147	Human sec	361	3945	100.0	720	6	ADA92793	Human sec
289	3945	100.0	720	6	ADA20072	Novel hum	362	3945	100.0	720	6	ABR79986	Human sec
290	3945	100.0	720	6	ABO34185	Human sec	363	3945	100.0	720	6	ABM11326	Human sec
291	3945	100.0	720	6	ABR96581	Human sec	364	3945	100.0	720	6	ABO32933	Human PRO
292	3945	100.0	720	6	ADA94447	Human sec	365	3945	100.0	720	6	ABO30639	Human sec
293	3945	100.0	720	6	ABR85759	Human sec	366	3945	100.0	720	6	ABO30944	Human sec
294	3945	100.0	720	6	ABR99741	Human sec	367	3945	100.0	720	6	ABM27250	Human sec
295	3945	100.0	720	6	ABM00597	Human sec	368	3945	100.0	720	6	ABM29995	Human sec
296	3945	100.0	720	6	ABM00292	Human sec	369	3945	100.0	720	6	ABM05531	Human sec
297	3945	100.0	720	6	ABO29724	Human sec	370	3945	100.0	720	6	ABM15596	Human sec
298	3945	100.0	720	6	ABM23590	Human sec	371	3945	100.0	720	6	ABM08581	Human sec
299	3945	100.0	720	6	ABM29385	Human sec	372	3945	100.0	720	6	ABO42281	Human sec
300	3945	100.0	720	6	ABO38316	Human sec	373	3945	100.0	720	6	ABO38011	Human sec
301	3945	100.0	720	6	ABO45616	Human sec	374	3945	100.0	720	6	ABO45921	Human PRO
302	3945	100.0	720	6	ABM20540	Human sec	375	3945	100.0	720	6	ABM66724	Human sec
303	3945	100.0	720	6	ADA81441	Human sec	376	3945	100.0	720	6	ABD20282	Human sec
304	3945	100.0	720	6	ABO16654	Human sec	377	3945	100.0	720	6	ABM19625	Human sec
305	3945	100.0	720	6	ABO18280	Human sec	378	3945	100.0	720	6	ABO49337	Human sec
306	3945	100.0	720	6	ABO22707	Human PRO	379	3945	100.0	720	6	ABO49642	Human sec
307	3945	100.0	720	6	ABO23012	Human PRO	380	3945	100.0	720	6	ADA78534	Human sec
308	3945	100.0	720	6	ABR92554	Human sec	381	3945	100.0	720	6	ABR88199	Human sec
309	3945	100.0	720	6	ABR81511	Human sec	382	3945	100.0	720	6	ADA00369	Human sec
310	3945	100.0	720	6	ABM77935	Human sec	383	3945	100.0	720	6	ABM26945	Human sec
311	3945	100.0	720	6	ABR89724	Human sec	384	3945	100.0	720	6	ABM03342	Human sec
312	3945	100.0	720	6	ABM26640	Human sec	385	3945	100.0	720	6	ABO39841	Human sec
313	3945	100.0	720	6	ABM13766	Human sec	386	3945	100.0	720	7	ABO49947	Human sec
314	3945	100.0	720	6	ABO28504	Human sec	387	3945	100.0	720	7	ABO50862	Human sec
315	3945	100.0	720	6	ABO30334	Human sec	388	3945	100.0	720	7	ABO05318	Human sec
316	3945	100.0	720	6	ABM07361	Human sec	389	3945	100.0	720	7	ABR74622	Human sec
317	3945	100.0	720	6	ABM03952	Human sec	390	3945	100.0	720	7	ABR77101	Human sec

391	3945	100.0	720	7	ABM17858	Human sec	464	3945	100.0	720	7	ABM14986	Human sec
392	3945	100.0	720	7	ABR95909	Human sec	465	3945	100.0	720	7	ABO41061	Human sec
393	3945	100.0	720	7	ABO21842	Human sec	466	3945	100.0	720	7	ABO36791	Human sec
394	3945	100.0	720	7	ABO20012	Human sec	467	3945	100.0	720	7	ABO37401	Human sec
395	3945	100.0	720	7	ABO24315	Human sec	468	3945	100.0	720	7	ABM75191	Human sec
396	3945	100.0	720	7	ABR86064	Human sec	469	3945	100.0	720	7	ABM33471	Human sec
397	3945	100.0	720	7	ABM10716	Human sec	470	3945	100.0	720	7	ABO46226	Human sec
398	3945	100.0	720	7	ABM76715	Human sec	471	3945	100.0	720	7	ADA82605	Human sec
399	3945	100.0	720	7	ABR89419	Human sec	472	3945	100.0	720	7	ADB85611	Novel hum
400	3945	100.0	720	7	ABM12546	Human sec	473	3945	100.0	720	7	ADB96239	Human PRO
401	3945	100.0	720	7	ABM05836	Human sec	474	3945	100.0	720	7	ABM31825	Human sec
402	3945	100.0	720	7	ABO34961	Human PRO	475	3945	100.0	720	7	ABM31215	Human sec
403	3945	100.0	720	7	ABM03037	Human sec	476	3945	100.0	720	7	ADB85913	Human sec
404	3945	100.0	720	7	ABM19015	Human sec	477	3945	100.0	720	7	ABM32130	Human sec
405	3945	100.0	720	7	ABM19320	Human sec	478	3945	100.0	720	7	ABM32435	Human sec
406	3945	100.0	720	7	ABO46531	Human PRO	479	3945	100.0	720	7	ADB68290	Human PRO
407	3945	100.0	720	7	ABO49032	Human sec	480	3945	100.0	720	7	ADB68097	Human PRO
408	3945	100.0	720	7	ABR69075	Human sec	481	3945	100.0	720	7	ABM31520	Human sec
409	3945	100.0	720	7	ABR89114	Human sec	482	3945	100.0	720	7	ABM30910	Human sec
410	3945	100.0	720	7	ABR72487	Human sec	483	3945	100.0	720	7	ADB90914	Novel hum
411	3945	100.0	720	7	ABR74317	Human sec	484	3945	100.0	720	7	ADC57711	Human PRO
412	3945	100.0	720	7	ABO18585	Human sec	485	3945	100.0	720	7	ADC55075	Human PRO
413	3945	100.0	720	7	ABR80291	Human sec	486	3945	100.0	720	7	ADC11942	Human sec
414	3945	100.0	720	7	ABM01512	Human sec	487	3945	100.0	720	7	ADC06994	Human PRO
415	3945	100.0	720	7	ABM02122	Human sec	488	3945	100.0	720	7	ADC56364	Human PRO
416	3945	100.0	720	7	ABR87284	Human sec	489	3945	100.0	720	7	ADC17173	Mammalian
417	3945	100.0	720	7	ABM12851	Human sec	490	3945	100.0	720	7	ADC07419	Human sec
418	3945	100.0	720	7	ABM30605	Human sec	491	3945	100.0	720	7	ADC11409	Human sec
419	3945	100.0	720	7	ABM24505	Human sec	492	3945	100.0	720	7	ADC14871	Novel hum
420	3945	100.0	720	7	ABO29419	Human sec	493	3945	100.0	720	7	ADC52366	Novel hum
421	3945	100.0	720	7	ABO31249	Human sec	494	3945	100.0	720	7	ADC14531	Novel hum
422	3945	100.0	720	7	ABM14376	Human sec	495	3945	100.0	720	7	ADC08063	Novel hum
423	3945	100.0	720	7	ABM09801	Human sec	496	3945	100.0	720	7	ADC81888	Human PRO
424	3945	100.0	720	7	ABO38926	Human sec	497	3945	100.0	720	7	ADC07530	Novel hum
425	3945	100.0	720	7	ABM34691	Human sec	498	3945	100.0	720	7	ADC82421	Human PRO
426	3945	100.0	720	7	ABO51167	Human sec	499	3945	100.0	720	7	ADC05643	Human sec
427	3945	100.0	720	7	ABO03993	Human sec	500	3945	100.0	720	7	ADC08601	Novel hum
428	3945	100.0	720	7	ABO10463	Human PRO	501	3945	100.0	720	7	ADC06850	Novel hum
429	3945	100.0	720	7	ABO53170	Human sec	502	3945	100.0	720	7	ADC83097	Human PRO
430	3945	100.0	720	7	ABR77706	Human sec	503	3945	100.0	720	7	ADC55204	Human PRO
431	3945	100.0	720	7	ABR78916	Human sec	504	3945	100.0	720	7	ADC36042	Novel hum
432	3945	100.0	720	7	ABO24010	Human sec	505	3945	100.0	720	7	ADC56162	Human PRO
433	3945	100.0	720	7	ABO37774	Human sec	506	3945	100.0	720	7	ADC54600	Human PRO
434	3945	100.0	720	7	ABM01817	Human sec	507	3945	100.0	720	7	ADC26754	Novel hum
435	3945	100.0	720	7	ABR78240	Human sec	508	3945	100.0	720	7	ADC26221	Novel hum
436	3945	100.0	720	7	ABR90029	Human sec	509	3945	100.0	720	7	ADC52176	Novel hum
437	3945	100.0	720	7	ADA22354	Human sec	510	3945	100.0	720	7	ADC74307	Human sec
438	3945	100.0	720	7	ABM27555	Human sec	511	3945	100.0	720	7	ADC74919	Human sec
439	3945	100.0	720	7	ABM13156	Human sec	512	3945	100.0	720	7	ADC70532	Human PRO
440	3945	100.0	720	7	ABO31859	Human sec	513	3939	99.8	720	4	AAU00401	Human sec
441	3945	100.0	720	7	ABM14071	Human sec	514	3936	99.8	720	3	AAU00401	Human sec
442	3945	100.0	720	7	ABM08276	Human sec	515	3921.5	99.4	737	4	AAU00401	Human sec
443	3945	100.0	720	7	ABO40146	Human sec	516	3921.5	99.4	737	4	AAU00401	Human sec
444	3945	100.0	720	7	ABM74581	Human sec	517	3921.5	99.4	762	4	AAU00401	Human sec
445	3945	100.0	720	7	ABM33776	Human sec	518	3612	91.6	720	4	AAU00401	Human sec
446	3945	100.0	720	7	ABM20235	Human sec	519	3602.5	91.6	719	3	AAU00401	Human sec
447	3945	100.0	720	7	ABO48727	Human sec	520	3500.5	88.7	649	5	AAU00401	Human sec
448	3945	100.0	720	7	ABO22540	Human sec	521	3089.5	78.3	567	4	AAU00401	Human sec
449	3945	100.0	720	7	ABO22540	Human sec	522	2946.5	74.7	570	3	AAU00401	Human sec
450	3945	100.0	720	7	ABO15434	Human sec	523	2577.5	65.3	499	4	AAU00401	Human sec
451	3945	100.0	720	7	ABO15129	Human sec	524	2413	61.2	455	5	AAU00401	Human sec
452	3945	100.0	720	7	ABO15129	Human sec	525	2413	61.2	455	5	AAU00401	Human sec
453	3945	100.0	720	7	ABO17264	Human sec	526	1909	48.4	359	4	AAU00401	Human sec
454	3945	100.0	720	7	ABM17553	Human sec	527	1909	48.4	359	4	AAU00401	Human sec
455	3945	100.0	720	7	ADA06520	Human sec	528	1708.5	43.3	323	5	AAU00401	Human sec
456	3945	100.0	720	7	ADA39213	Human sec	529	1708.5	43.3	323	5	AAU00401	Human sec
457	3945	100.0	720	7	ABR85454	Human sec	530	1175.5	29.8	234	4	AAU00401	Human sec
458	3945	100.0	720	7	ABM77020	Human sec	531	672	17.0	1019	6	AAU00401	Human sec
459	3945	100.0	720	7	ABO28199	Human sec	532	665	16.9	1019	2	AAU00401	Human sec
460	3945	100.0	720	7	ABM22380	Human sec	533	665	16.9	1019	2	AAU00401	Human sec
461	3945	100.0	720	7	ABM30300	Human sec	534	665	16.9	1019	2	AAU00401	Human sec
462	3945	100.0	720	7	ABM21760	Human sec	535	665	16.9	1019	3	AAU00401	Human sec
463	3945	100.0	720	7	ABM21455	Human sec	536	665	16.9	1019	4	AAU00401	Human sec

537	665	16.9	1019	6	ABP72334	Abp72334	Horsehoe	610	315.5	8.0	419	5	AAU99071	Aau99071	Human Pro
538	665	16.9	1083	2	AAW43393	Aaw43393	Singapore	611	315.5	8.0	419	5	AAU99087	Aau99087	Human Pro
539	665	16.9	1083	2	AY05749	Ay05749	Horsehoe	612	315.5	8.0	419	5	AAU99079	Aau99079	Human Pro
540	665	16.9	1083	2	AAW94301	Aaw94301	Horsehoe	613	315.5	8.0	461	2	AAR62653	Aar62653	Human Pro
541	665	16.9	1083	2	AAW94301	Aaw94301	Horsehoe	614	314.5	8.0	419	2	AAR35760	Aar35760	Protein C
542	665	16.9	1083	3	AAW2489	Aaw2489	Horsehoe	615	314.5	8.0	419	5	AAU99053	Aau99053	Human Pro
543	665	16.9	1083	3	AAW2489	Aaw2489	Horsehoe	616	314.5	8.0	419	5	AAU99007	Aau99007	Human Pro
544	665	16.9	1083	6	ABP72333	Abp72333	Horsehoe	617	314.5	8.0	419	5	AAU99077	Aau99077	Human Pro
545	580	14.7	1033	7	AAW11743	Aam11743	Human pol	618	314.5	8.0	419	5	AAU99043	Aau99043	Human Pro
546	476	12.1	699	7	AD877459	Ade877459	Human MBL	619	314	8.0	855	5	AAE23083	Aae23083	Epithin p
547	471	11.9	728	4	AB85060	Ab85060	Human ser	620	313.5	7.9	419	2	AAW72753	Aaw72753	Primary s
548	468	11.9	728	7	AD877461	Ad877461	Human MBL	621	313.5	7.9	419	5	AAU99005	Aau99005	Human Pro
549	461	11.7	728	4	AA847559	Ad847559	Protease	622	313.5	7.9	419	5	AAU99025	Aau99025	Human Pro
550	429	10.9	707	5	AB807556	Ab807556	Murine Cl	623	313.5	7.9	419	5	AAU99065	Aau99065	Human Pro
551	403.5	10.2	705	5	AB850288	Ab850288	Complemen	624	313.5	7.9	419	5	AAU99016	Aau99016	Human Pro
552	401.5	10.2	686	5	AB850288	Ab850288	Complemen	625	313.5	7.9	419	5	AAU99023	Aau99023	Human Pro
553	401.5	10.2	686	5	AB850288	Ab850288	Complemen	626	313	7.9	509	2	AAR13083	Aar13083	PAP-I-Pro
554	401.5	10.2	686	5	AB850288	Ab850288	Complemen	627	312.5	7.9	419	5	AAU99072	Aau99072	Human Pro
555	401.5	10.2	686	5	AB850288	Ab850288	Complemen	628	312.5	7.9	419	5	AAU99072	Aau99072	Human Pro
556	400.5	10.2	686	5	AB850288	Ab850288	Complemen	629	312.5	7.9	419	5	AAU99009	Aau99009	Human Pro
557	400.5	10.2	686	7	AD877460	Ad877460	Human MBL	630	312.5	7.9	419	5	AAU99064	Aau99064	Human Pro
558	398.5	10.1	671	5	AAE14565	Aae14565	Human mat	631	312.5	7.9	419	5	AAU99069	Aau99069	Human Pro
559	340.5	8.6	694	7	AD856422	Ad856422	Rat Prote	632	312.5	7.9	419	5	AAU99082	Aau99082	Human Pro
560	340.5	8.6	694	7	AD856422	Ad856422	Rat Prote	633	312.5	7.9	419	5	AAU99096	Aau99096	Human Pro
561	340.5	8.6	695	7	AD856418	Ad856418	Rat Prote	634	312.5	7.9	419	5	AAU99091	Aau99091	Human Pro
562	340.5	8.6	695	7	AD856418	Ad856418	Rat Prote	635	312.5	7.9	419	5	AAU99024	Aau99024	Human Pro
563	336	8.5	760	3	AA435338	Aab435338	Human can	636	312.5	7.9	419	5	AAU99048	Aau99048	Human Pro
564	334	8.5	688	7	AD856420	Ade56420	Human Pro	637	312.5	7.9	419	5	AAU99067	Aau99067	Human Pro
565	334	8.5	688	7	AD856420	Ade56420	Human Pro	638	312.5	7.9	419	5	AAU99075	Aau99075	Human Pro
566	331.5	8.4	1019	4	AAE06940	Aae06940	Human ent	639	312.5	7.9	419	5	AAU99092	Aau99092	Human Pro
567	331.5	8.4	1019	6	AD883395	Aad83395	Human PRS	640	312.5	7.9	419	5	AAU99011	Aau99011	Human Pro
568	329	8.3	460	2	AAU13623	Aau13623	Human Pro	641	312.5	7.9	419	5	AAU99032	Aau99032	Human Pro
569	328.5	8.3	1274	5	ABG76507	Abg76507	DNA encod	642	312	7.9	419	4	AAAB82677	Aab82677	Human Pro
570	328.5	8.3	1783	5	AAU11815	Aau11815	Cancer an	643	312	7.9	460	2	AAR13537	Aar13537	Human Pro
571	328.5	8.3	1800	5	AAU11812	Aau11812	Cancer an	644	312	7.9	1031	5	ABP60993	Abp60993	Novel hum
572	328.5	8.3	1826	5	AAU11812	Aau11812	Cancer an	645	311.5	7.9	419	5	AAU99008	Aau99008	Human Pro
573	328.5	8.3	2008	5	AAU11814	Aau11814	Cancer an	646	311.5	7.9	419	5	AAU99039	Aau99039	Human Pro
574	328.5	8.3	2306	5	AAU11817	Aau11817	Cancer an	647	311.5	7.9	419	5	AAU99047	Aau99047	Human Pro
575	328.5	8.3	2352	5	AAU11816	Aau11816	Cancer an	648	311.5	7.9	419	5	AAU99070	Aau99070	Human Pro
576	328.5	8.3	683	3	AAU19551	Aab19551	Human mat	649	311.5	7.9	419	5	AAU99017	Aau99017	Human Pro
577	328.5	8.3	762	3	AAU90284	Aay90284	Human pep	650	311.5	7.9	419	5	AAU99044	Aau99044	Human Pro
578	328.5	8.3	851	4	AB811428	Aab811428	Human pro	651	311.5	7.9	419	5	AAU99014	Aau99014	Human Pro
579	328.5	8.3	851	4	AB811428	Aab811428	Human pro	652	311.5	7.9	419	5	AAU99031	Aau99031	Human Pro
580	328.5	8.3	855	3	AAU19552	Aab19552	Human mem	653	311.5	7.9	419	5	AAU99057	Aau99057	Human Pro
581	328.5	8.3	855	3	AAU19552	Aab19552	Human mem	654	311.5	7.9	419	5	AAU99054	Aau99054	Human Pro
582	327.5	8.3	449	3	AAE58274	Aab58274	Lung canc	655	311.5	7.9	419	5	AAU99095	Aau99095	Human Pro
583	327.5	8.3	855	2	AAU96671	Aay96671	Tumour an	656	311.5	7.9	419	5	AAU99015	Aau99015	Human Pro
584	327.5	8.3	855	4	AAU98500	Aab98500	Human TAD	657	311.5	7.9	461	1	AAU81205	Aap81205	Human Pro
585	327.5	8.3	855	4	AAU98500	Aab98500	Human TAD	658	311.5	7.9	461	2	AAR13539	Aar13539	Human Pro
586	327.5	8.3	855	5	AAU98500	Aab98500	Human mem	659	311.5	7.9	461	2	AAR13997	Aar13997	Human Pro
587	327.5	8.3	855	5	AAU98500	Aab98500	Human mem	660	311	7.9	419	4	AAAB82678	Aab82678	Human Pro
588	327.5	8.3	855	6	AAU98500	Aab98500	Human mem	661	311	7.9	419	4	AAAB82675	Aab82675	Human Pro
589	327.5	8.3	855	6	AAU98500	Aab98500	Human mem	662	310.5	7.9	409	7	ADC40013	Adc40013	Human act
590	327.5	8.3	855	6	AAU98500	Aab98500	Human mem	663	310.5	7.9	410	7	ADC40012	Adc40012	Human act
591	327.5	8.3	855	6	AAU98500	Aab98500	Human mem	664	310.5	7.9	415	3	AAU56803	Aay56803	Truncated
592	327.5	8.3	855	7	AD877551	Ad877551	Human MTS	665	310.5	7.9	419	4	AAAB82673	Aab82673	Wild-type
593	324	8.2	3095	5	AAE20788	Aae20788	Rat C3b/C	666	310.5	7.9	419	4	AAAB82673	Aab82673	Wild-type
594	320.5	8.1	3069	5	AAE20788	Aae20788	Rat C3b	667	310.5	7.9	419	4	AAAB82673	Aab82673	Wild-type
595	320.5	8.1	3100	5	AAE20789	Aae20789	Human C3b	668	310.5	7.9	419	5	AAE08625	Aae08625	Human mat
596	319.5	8.1	419	5	AAU99088	Aau99088	Human Pro	669	310.5	7.9	419	5	AAU99063	Aau99063	Human Pro
597	319.5	8.1	419	5	AAU99080	Aau99080	Human Pro	670	310.5	7.9	419	5	AAU99012	Aau99012	Human Pro
598	318.5	8.1	419	5	AAU99078	Aau99078	Human Pro	671	310.5	7.9	419	5	AAU99050	Aau99050	Human Pro
599	318.5	8.1	2669	5	ABG79169	Abg79169	Human cub	672	310.5	7.9	419	5	AAU99010	Aau99010	Human Pro
600	318.5	8.1	3104	5	ABG79168	Abg79168	Human cub	673	310.5	7.9	419	5	AAU99040	Aau99040	Human Pro
601	317.5	8.0	419	5	AAU99006	Aau99006	Human Pro	674	310.5	7.9	419	5	AAU99060	Aau99060	Human Pro
602	317.5	8.0	419	5	AAU99066	Aau99066	Human Pro	675	310.5	7.9	419	5	AAU99055	Aau99055	Human Pro
603	317.5	8.0	788	2	AAR57283	Aar57283	Bovine en	676	310.5	7.9	419	5	AAU99056	Aau99056	Human Pro
604	317.5	8.0	3069	5	AAE20900	Aae20900	Human C3b	677	310.5	7.9	419	5	AAU99059	Aau99059	Human Pro
605	317.5	8.0	3100	5	AAE20901	Aae20901	Human C3b	678	310.5	7.9	419	5	AAU99002	Aau99002	Human Pro
606	316.5	8.0	419	5	AAU99076	Aau99076	Human Pro	679	310.5	7.9	419	5	AAU99051	Aau99051	Human Pro
607	316.5	8.0	419	5	AAU99022	Aau99022	Human Pro	680	310.5	7.9	419	5	AAU99052	Aau99052	Human Pro
608	315.5	8.0	419	5	AAU99026	Aau99026	Human Pro	681	310.5	7.9	419	6	ABR55547	Abx55547	Amino aci
609	315.5	8.0	419	5	AAU99081	Aau99081	Human Pro	682	310.5	7.9	419	7	ADC40014	Adc40014	Human act

683 310.5 7.9 460 1 AAP81104 Sequence  
 684 310.5 7.9 460 2 AA25086 Human pro  
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 698 310 7.9 419 4 AAB82676 Human pro  
 699 310 7.9 419 4 AA08630 Human pro  
 700 310 7.9 460 2 AAP13538 Human pro

## ALIGNMENTS

## RESULT 1

AA166695  
 ID AAY66695 standard; protein; 720 AA.

XX AC AAY66695;  
 XX DT 05-APR-2000 (first entry)  
 XX DE Membrane-bound protein PRO1344.  
 XX KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
 KW pharmacutical; receptor immunoadhesin; gene mapping.  
 XX OS Homo sapiens.

XX PN WO963088-A2.  
 XX PD 09-DEC-1999.

XX PF 02-JUN-1999; 99KO-US012252.  
 XX PR 02-JUN-1998; 98US-0087607P.  
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PR 17-AUG-1998; 98US-0096895P.  
PR 17-AUG-1998; 98US-0096897P.  
PR 18-AUG-1998; 98US-0096949P.  
PR 18-AUG-1998; 98US-0096950P.  
PR 18-AUG-1998; 98US-0096950P.  
PR 18-AUG-1998; 98US-0096959P.  
PR 18-AUG-1998; 98US-0097022P.  
PR 19-AUG-1998; 98US-0097141P.  
PR 20-AUG-1998; 98US-0097218P.  
PR 24-AUG-1998; 98US-0097661P.  
PR 26-AUG-1998; 98US-0097951P.  
PR 26-AUG-1998; 98US-0097952P.  
PR 26-AUG-1998; 98US-0097954P.  
PR 26-AUG-1998; 98US-0097955P.  
PR 26-AUG-1998; 98US-0097971P.  
PR 26-AUG-1998; 98US-0097974P.  
PR 26-AUG-1998; 98US-0097978P.  
PR 26-AUG-1998; 98US-0097979P.  
PR 26-AUG-1998; 98US-0097986P.  
PR 26-AUG-1998; 98US-0098014P.  
PR 31-AUG-1998; 98US-0098525P.  
PR 16-SEP-1998; 98US-0100634P.  
PR 12-JAN-1999; 99US-0115565P.  
XX (GETH ) GENENTECH INC.  
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
PI Wood WI, Yuan J, Yoo J;  
XX WPI; 2000-072883/06.  
DR N-PSDB; AA265034.  
XX  
PT Membrane-bound proteins and related nucleotide sequences.  
XX Claim 12; Fig 159; 822pp; English.  
XX The invention provides membrane-bound PRO polypeptides and  
CC polynucleotides encoding them. The PRO sequences of the invention were  
CC identified based on extracellular domain homology screening. The PRO  
CC sequences have homology with proteins including LDL receptors, TIE  
CC ligands and various enzymes. The membrane-bound proteins and receptor  
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
CC immunoadhesins, for instance, can be used as therapeutic agents to block  
CC receptor-ligand interactions. The membrane-bound proteins can also be  
CC employed for screening of potential peptide or small molecule inhibitors  
CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
CC are useful as hybridization probes, in chromosome and gene mapping and in  
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will  
CC also be useful for the preparation of PRO polypeptides, especially by  
CC recombinant techniques  
XX  
SQ Sequence 720 AA;  
Query Match 100.0%; Score 3945; DB 3; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.2e-204;  
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MELGCWTQLGLTFLQLLISLSPREYTVINEACPGAENIMCECEYDQIECVCPGKRE 60  
DB 1 MELGCWTQLGLTFLQLLISLSPREYTVINEACPGAENIMCECEYDQIECVCPGKRE 60  
QY 61 VVGVTIPCCRNEECDSCLIHPGCTIFENCKSCRNGSWGGLTDDPYVKGFCACRAGW 120

Db 61 VVGVTIPCCRNEECDSCLIHPGCTIFENCKSCRNGSWGGLTDDPYVKGFCACRAGW 120  
QY 121 YGGDCMCGQVLRAPKGOILLESYPLNAHCBSWTTHAKPGFVIQLRFVNLSEFFDMCOYD 180  
Db 121 YGGDCMCGQVLRAPKGOILLESYPLNAHCBSWTTHAKPGFVIQLRFVNLSEFFDMCOYD 180  
QY 181 YVEVRDGDNRDQIIKRVCGNERPAPIQSIGSSLHVLFHSKGNFQGFHAIYEITACS 240  
Db 181 YVEVRDGDNRDQIIKRVCGNERPAPIQSIGSSLHVLFHSKGNFQGFHAIYEITACS 240  
QY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGRCENLEERNCSDPGPNVNGYQKITGGPGLI 300  
Db 241 SSPCFHDGTCVLDKAGSYKACLAGYTGRCENLEERNCSDPGPNVNGYQKITGGPGLI 300  
QY 301 NGRHAKIGTVVSFFCNNSYVLSGNEKTCQNGSWGSKQPICIKACREPKISDLVRRVL 360  
Db 301 NGRHAKIGTVVSFFCNNSYVLSGNEKTCQNGSWGSKQPICIKACREPKISDLVRRVL 360  
QY 361 PMQVQSRETPHLQLYSAAFSKQLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPPYR 420  
Db 361 PMQVQSRETPHLQLYSAAFSKQLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPPYR 420  
QY 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLWPMQAAIYRSTSGVHDGSL 480  
Db 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLWPMQAAIYRSTSGVHDGSL 480  
QY 481 HKGAWFLVCSGALVNERTVVVAACHVCTDLGKVTMIKTADLVKLGKFRDDEKTKTQS 540  
Db 481 HKGAWFLVCSGALVNERTVVVAACHVCTDLGKVTMIKTADLVKLGKFRDDEKTKTQS 540  
QY 541 LQISAILHPNYDPILLDADIAILKLDKARISTRVQPICLAASRDISTSTQESHITVAG 600  
Db 541 LQISAILHPNYDPILLDADIAILKLDKARISTRVQPICLAASRDISTSTQESHITVAG 600  
QY 601 WNVLADVRSPGFKNDTLRSVGVVSDSLCEEQHDHGIPVSVTDNMFCASWEPTAPSDI 660  
Db 601 WNVLADVRSPGFKNDTLRSVGVVSDSLCEEQHDHGIPVSVTDNMFCASWEPTAPSDI 660  
QY 661 CTAETGGIAAVSFFPGRASPEPRWHLMLVSNYSYDKTCSHRLSTAFKVLPFKDWIERNNK 720  
Db 661 CTAETGGIAAVSFFPGRASPEPRWHLMLVSNYSYDKTCSHRLSTAFKVLPFKDWIERNNK 720  
RESULT 2  
AAU29108  
ID AAU29108 standard; protein; 720 AA.  
XX AC AAU29108;  
XX DT 18-DEC-2001 (first entry)  
XX DE Human PRO polypeptide sequence #85.  
XX KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
XX OS Homo sapiens.  
XX PN WO200168848-A2.  
XX PD 20-SEP-2001.  
XX PF 28-FEB-2001; 2001WO-US006520.  
XX PR 01-MAR-2000; 2000WO-US005601.  
XX PR 02-MAR-2000; 2000WO-US005841.  
XX PR 03-MAR-2000; 2000US-0187202P.  
XX PR 06-MAR-2000; 2000US-0186968P.  
XX PR 14-MAR-2000; 2000US-0189320P.  
XX PR 14-MAR-2000; 2000US-0189328P.

PR 15-MAR-2000; 2000WO-US006884.  
 PR 21-MAR-2000; 2000US-0190828P.  
 PR 21-MAR-2000; 2000US-0191007P.  
 PR 21-MAR-2000; 2000US-0191048P.  
 PR 21-MAR-2000; 2000US-0191314P.  
 PR 28-MAR-2000; 2000US-0192655P.  
 PR 29-MAR-2000; 2000US-0193032P.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 04-APR-2000; 2000US-0194449P.  
 PR 04-APR-2000; 2000US-0194647P.  
 PR 11-APR-2000; 2000US-0195975P.  
 PR 11-APR-2000; 2000US-0196000P.  
 PR 11-APR-2000; 2000US-0196187P.  
 PR 11-APR-2000; 2000US-0196690P.  
 PR 11-APR-2000; 2000US-0196820P.  
 PR 18-APR-2000; 2000US-0198121P.  
 PR 18-APR-2000; 2000US-0198585P.  
 PR 25-APR-2000; 2000US-0199397P.  
 PR 25-APR-2000; 2000US-0199550P.  
 PR 25-APR-2000; 2000US-0199654P.  
 PR 03-MAY-2000; 2000US-0201516P.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 05-JUN-2000; 2000US-0209832P.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PA (GETH ) GENENTECH INC.  
 XX Baker KP, Chen J, Deanovers L, Goddard A, Godowski PJ, Gurney AL;  
 XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 XX WPI; 2001-602746/68.  
 DR N-PSDB; AAS46009.  
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumors, such as prostate and breast tumors, in mammals and to  
 PT screen for modulators of the compounds.  
 XX Claim 11; Fig 170; 774pp; English.  
 PS Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
 CC The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumour in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of  
 CC expression in the test sample indicates the presence of a tumour in the  
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
 CC and rabbits but are preferably human. The polypeptides can be used to  
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
 CC when contacted with it. A specific polypeptide can be used to stimulate  
 CC the proliferation or differentiation of chondrocyte cells. The PRO  
 CC proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders  
 XX Sequence 720 AA;  
 Query Match 100.0%; Score 3945; DB 4; Length 720;  
 Match Local Similarity 100.0%; Pred. No. 1.2e-204; Indels 0; Gaps 0;  
 Matches 720; Conservative 0; Mismatches 0;  
 QY 1 MELGCWTQLGLTFLQLLLISSLPREYTVINEACFGAENWIMCRECCEDYDQIECVCPGKRE 60  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 MELGCWTQLGLTFLQLLLISSLPREYTVINEACFGAENWIMCRECCEDYDQIECVCPGKRE 60  
 QY 61 VVGTTIPCCNEENECDSCLIHPGCTIFENCKSCRNGSWGTTLDDFVXKGFYCAECRAGW 120  
 Db 61 VVGTTIPCCNEENECDSCLIHPGCTIFENCKSCRNGSWGTTLDDFVXKGFYCAECRAGW 120  
 QY 121 YGGDCMRGCGVLRAPKQILLESYPINAHCEWTHAKPGFVIQLRFVMLSLEFDYMCQYD 180  
 Db 121 YGGDCMRGCGVLRAPKQILLESYPINAHCEWTHAKPGFVIQLRFVMLSLEFDYMCQYD 180  
 QY 181 YVEVRDGNDRDGOIKRVCGNERPAPIQSGSLHLVLFHSDGSKNFDGPHAIYEETIACS 240  
 Db 181 YVEVRDGNDRDGOIKRVCGNERPAPIQSGSLHLVLFHSDGSKNFDGPHAIYEETIACS 240  
 QY 241 SSPCFHDGTCLVDKAGSYKACIAGYTQRCENLEERNCSDFGPGVNGYQKITGGPGLI 300  
 Db 241 SSPCFHDGTCLVDKAGSYKACIAGYTQRCENLEERNCSDFGPGVNGYQKITGGPGLI 300  
 QY 301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOONGEWSGKQPICIKACREPKISDLVRRVL 360  
 Db 301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOONGEWSGKQPICIKACREPKISDLVRRVL 360  
 QY 361 PMOVQSRRETPHLQYSAAPFSKQLQAPTKKPALPFGDLPMGYOHLHTLQYECISPFYR 420  
 Db 361 PMOVQSRRETPHLQYSAAPFSKQLQAPTKKPALPFGDLPMGYOHLHTLQYECISPFYR 420  
 QY 421 RLGSRRRTCLRTKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL 480  
 Db 421 RLGSRRRTCLRTKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL 480  
 QY 481 HKGAWFLVCSGALVNERTVVAACHVTDLGKVTMIKTADLKVVLGKPYRDDDRDEKTIQS 540  
 Db 481 HKGAWFLVCSGALVNERTVVAACHVTDLGKVTMIKTADLKVVLGKPYRDDDRDEKTIQS 540  
 QY 541 LOISAILHPNYPILLDDADIALKLLDKARISTRVQPICLAASRDLSTSFQESHITVAG 600  
 Db 541 LOISAILHPNYPILLDDADIALKLLDKARISTRVQPICLAASRDLSTSFQESHITVAG 600  
 QY 601 WNVLDVRSFGKNDTLRSQVSVVDSLLCEBQEHEDHIGIPVSVTDNMFCASWEPTAPSDI 660  
 Db 601 WNVLDVRSFGKNDTLRSQVSVVDSLLCEBQEHEDHIGIPVSVTDNMFCASWEPTAPSDI 660  
 QY 661 CTATGTGIAAVSPFGRASPEPRWHLGLVSWSDYDKTCSHRLSTAFTKVLPFKDWIERNMK 720  
 Db 661 CTATGTGIAAVSPFGRASPEPRWHLGLVSWSDYDKTCSHRLSTAFTKVLPFKDWIERNMK 720  
 RESULT 3  
 AAB87544  
 ID AAB87544 standard; protein; 720 AA.  
 XX AC AAB87544;  
 XX DT 15-MAY-2001 (first entry)  
 XX DE Human PRO1344.  
 XX KW Human; PRO protein; mapping.  
 XX OS Homo sapiens.  
 XX PN WO200116318-A2.  
 XX PD 08-MAR-2001.  
 XX PF 24-AUG-2000; 2000WO-US023328.  
 XX PR 01-SEP-1999; 99WO-US020111.  
 XX PR 15-SEP-1999; 99WO-US021090.  
 XX PR 07-DEC-1999; 99US-0169495P.  
 XX PR 09-DEC-1999; 99US-0170262P.  
 XX PR 11-JAN-2000; 2000US-0175481P.  
 XX PR 18-FEB-2000; 2000WO-US004341.

PR 18-FEB-2000; 2000WO-US004342.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 01-MAR-2000; 2000WO-US005601.  
 PR 03-MAR-2000; 2000US-0187202P.  
 PR 21-MAR-2000; 2000US-0191007P.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 25-APR-2000; 2000US-0199397P.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 05-JUN-2000; 2000US-0209832P.  
 XX (GETH ) GENENTECH INC.  
 PA Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
 XX Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;  
 DR N-PSDB; AAP92076.  
 XX WPI; 2001-183260/18.  
 XX Eighty four nucleic acids encoding PRO polypeptides, useful in molecular  
 PT biology, including use as hybridization probes, and in chromosome and  
 PT gene mapping.  
 XX Claim 12; Fig 38; 278pp; English.  
 XX The present sequence is a human PRO polypeptide (secreted and  
 CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or  
 CC anti-PRO antibodies are useful for preparation of a medicament useful in  
 CC the treatment of a condition which is responsive to the PRO protein,  
 CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be  
 CC employed as molecular weight markers for protein electrophoresis. The PRO  
 CC coding sequence has applications in molecular biology, including use as  
 CC hybridisation probes, and in chromosome and gene mapping  
 XX Sequence 720 AA;  
 SQ  
 Query Match 100.0%; Score 3945; DB 4; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-204;  
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MELGCTQLGLTFLQLLLSSLPREYTVINEACPGAENWIMCRECCBYDQIECVCPGRE 60  
 DB 1 MELGCTQLGLTFLQLLLSSLPREYTVINEACPGAENWIMCRECCBYDQIECVCPGRE 60  
 QY 61 VVGTYTPCCNEENECDSCLIHFGCTTFENCKSCRNCSWGGLTDDFVYKGFYCAECRAGW 120  
 DB 61 VVGTYTPCCNEENECDSCLIHFGCTTFENCKSCRNCSWGGLTDDFVYKGFYCAECRAGW 120  
 QY 121 YGGDCMRGQVLRAPKQIILLESYPLNAHCETWTHAKPGFVIOLRFVWLSLEFDYMCQYD 180  
 DB 121 YGGDCMRGQVLRAPKQIILLESYPLNAHCETWTHAKPGFVIOLRFVWLSLEFDYMCQYD 180  
 QY 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSGSLHLVLFHSDGSKNFDGPHAIYEEITACS 240  
 DB 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSGSLHLVLFHSDGSKNFDGPHAIYEEITACS 240  
 QY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGRCENLLEERNCSDPGPGVNGKTTGGPLI 300  
 DB 241 SSPCFHDGTCVLDKAGSYKACLAGYTGRCENLLEERNCSDPGPGVNGKTTGGPLI 300  
 QY 301 NGRHAKITGVVSFFCNNSYVLSGNEKRTCOQNGSWGSKQPICIKACREPKISDLVRRVL 360  
 DB 301 NGRHAKITGVVSFFCNNSYVLSGNEKRTCOQNGSWGSKQPICIKACREPKISDLVRRVL 360  
 QY 361 PMQVQSRETPHLQLYSAFSAKQLQSAPTKKPALPFGDLPMGYOHLTLQYECISPFYR 420  
 DB 361 PMQVQSRETPHLQLYSAFSAKQLQSAPTKKPALPFGDLPMGYOHLTLQYECISPFYR 420  
 QY 421 RLSSRRTRCLRTGKWSGRAPSCPIPCGKIENITAPKTQGLRWPAQAAIYRTSGVHDGSL 480  
 DB 421 RLSSRRTRCLRTGKWSGRAPSCPIPCGKIENITAPKTQGLRWPAQAAIYRTSGVHDGSL 480  
 QY 481 HKGAWFLVCSGALVNERTVVAACHVTDLGKVTMIKTADLKVLGKFPYRDDDRDEKTIQS 540

DB 481 HKGAWFLVCSGALVNERTVVAACHVTDLGKVTMIKTADLKVLGKFPYRDDDRDEKTIQS 540  
 QY 541 LOISAIILHPNYDPILLDADIAILKLLDKARISTRVQVPICLAASRDLSSTFQESHITVAG 600  
 DB 541 LOISAIILHPNYDPILLDADIAILKLLDKARISTRVQVPICLAASRDLSSTFQESHITVAG 600  
 QY 601 WNVLADVRSPGFKNDTLRSQVSVVDSLLCEQHEDHGIPVSVTDNMFCASWEPTAPSDI 660  
 DB 601 WNVLADVRSPGFKNDTLRSQVSVVDSLLCEQHEDHGIPVSVTDNMFCASWEPTAPSDI 660  
 QY 661 CTAETGGIAAASFPGGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLFPFKDWIERNNK 720  
 DB 661 CTAETGGIAAASFPGGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLFPFKDWIERNNK 720  
 RESULT 4  
 AAB65218  
 ID AAB65218 standard; protein; 720 AA.  
 XX AAB65218;  
 AC AAB65218;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX Human PRO1344 (UNQ699) protein sequence SEQ ID NO:231.  
 DE Human; secreted and transmembrane protein; PRO; cytostatic; cell death;  
 XX cancer; chromosomal mapping; Gene mapping; tissue typing;  
 KW diagnostic assay.  
 XX Homo sapiens.  
 OS  
 XX WO200073454-A1.  
 XX  
 PD 07-DEC-2000.  
 XX  
 XX 30-MAR-2000; 2000WO-US008439.  
 PF  
 XX 02-JUN-1999; 99WO-US012252.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 07-JUL-1999; 99US-0143048P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 28-JUL-1999; 99US-0146222P.  
 PR 17-AUG-1999; 99US-0149396P.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 08-OCT-1999; 99US-0158663P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 02-MAR-2000; 2000WO-US005004.  
 PR 15-MAR-2000; 2000WO-US005841.  
 PR 20-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX Ashkenazi AV, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi CJ, Gurney AL, KJavin IJ, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;  
 XX WPI; 2001-032160/04.  
 DR N-PSDB; AAP44180.  
 XX



PR 24-SEP-1998; 98US-0101916P.  
 PR 30-SEP-1998; 98US-0102570P.  
 PR 06-OCT-1998; 98US-0103449P.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 14-MAY-1999; 99WO-US010733.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 22-DEC-1999; 99WO-US021194.  
 PR 18-FEB-2000; 99WO-US030720.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 22-FEB-2000; 2000WO-US004342.  
 PR 01-MAR-2000; 2000WO-US004414.  
 PR 30-MAR-2000; 2000WO-US005601.  
 PR 02-MAY-2000; 2000WO-US008439.  
 PR 22-JUN-2000; 2000WO-US014042.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032378.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 30-MAY-2001; 2001WO-US017443.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 XX  
 PA (GETH ) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
 XX  
 DR WPI; 2002-731348/79.  
 DR N-PSDB; ABS74396.  
 XX

PT New isolated secreted and transmembrane PRO polypeptide useful for  
 PT modulating biological activity of a cell, or for treating sports-related  
 PT joint problems, osteoarthritis or rheumatoid arthritis.  
 XX  
 XX Claim 20; Fig 38; 399pp; English.

XX The invention relates to an isolated secreted and transmembrane PRO  
 CC polypeptide having 80 % sequence identity to a sequence appearing as  
 CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an  
 CC extracellular domain of the proteins with their associated signal peptide  
 CC or lacking its associated signal peptide. Also included are the nucleic  
 CC acids encoding the proteins, vectors, host cells, fusion proteins and  
 CC antibodies which specifically bind to the proteins. The proteins are  
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample  
 CC suspected of containing A, B, C or D polypeptide, by contacting the  
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)  
 CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide  
 CC conjugate in the sample, where the formation of the conjugate is  
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,  
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a  
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801  
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a  
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises  
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,  
 CC H or I polypeptide is labeled with a detectable label or is attached to a  
 CC solid support. The proteins are useful for linking a bioactive molecule  
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,  
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.  
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,  
 CC or I, or antibodies against them are useful for modulating a biological  
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or  
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for  
 CC identifying agonists or antagonists, for the preparation of a medicament  
 CC useful in the treatment of a condition which is responsive to the  
 CC proteins, as molecular weight markers for protein electrophoresis

CC purposes, and as therapeutic agents for treating sports-related joint  
 CC problems, articular cartilage defects, osteoarthritis or rheumatoid  
 CC arthritis. Nucleic acids encoding the proteins are useful as  
 CC hybridisation probes, in chromosome and gene mapping, in the generation  
 CC of anti-sense RNA and DNA, for the preparation of the proteins, to  
 CC generate transgenic or knockout animals which are useful in the  
 CC development and screening of therapeutic useful reagents, for chromosome  
 CC identification, and in gene therapy. The antibody is useful as a  
 CC therapeutic agent, in a diagnostic assay and for affinity purification of  
 CC the protein from recombinant cell culture natural sources. The present  
 CC sequence represents a novel secreted or transmembrane protein of the  
 CC invention  
 XX

SQ Sequence 720 AA;

Query Match	100.0%;	Score 3945;	DB 5;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 1.2e-204;		
Matches 720;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 MELGWTQLGLTFLQLLLISSLPREYTVINACPGAENIMCRECEYDQIECVCPGKRE 60  
 DB 1 MELGWTQLGLTFLQLLLISSLPREYTVINACPGAENIMCRECEYDQIECVCPGKRE 60  
 QY 61 VGYTIPCRNEECDSCLHPGCTIIFENCKSCNWSGGTLDFFYKGFYCAECRAGW 120  
 DB 61 VGYTIPCRNEECDSCLHPGCTIIFENCKSCNWSGGTLDFFYKGFYCAECRAGW 120  
 QY 121 YGGDCMRGQVLRAPKGQILLESYPLNAHCWTTHAKPGFVIQLRFVWMLSEFDMQYD 180  
 DB 121 YGGDCMRGQVLRAPKGQILLESYPLNAHCWTTHAKPGFVIQLRFVWMLSEFDMQYD 180  
 QY 181 YVEVDGDNRDQIIRKVCNRPAPIQISGLSHLVFHSKGNFDFHAIYEITACS 240  
 DB 181 YVEVDGDNRDQIIRKVCNRPAPIQISGLSHLVFHSKGNFDFHAIYEITACS 240  
 QY 241 SSPCFHDTGVLDKAGSYKACLAGYTCORCENLLEENCSDDPGPVNGYQKITGGGLI 300  
 DB 241 SSPCFHDTGVLDKAGSYKACLAGYTCORCENLLEENCSDDPGPVNGYQKITGGGLI 300  
 QY 301 NGRHAKIGTVWSFFCNNSYVLSGNEKRTCCQNGEWSGKQPCIKACREPKISDLVRRVRL 360  
 DB 301 NGRHAKIGTVWSFFCNNSYVLSGNEKRTCCQNGEWSGKQPCIKACREPKISDLVRRVRL 360  
 QY 361 PMQVSRRTPLHQLYSAAFSKQKQLOSAPTKPKPALPFGDLPMGYQHLTQLOVECSPPFR 420  
 DB 361 PMQVSRRTPLHQLYSAAFSKQKQLOSAPTKPKPALPFGDLPMGYQHLTQLOVECSPPFR 420  
 QY 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSL 480  
 DB 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSL 480  
 QY 481 HKGAWFLVCSGALVNERVTWVAACHVTDLGKVTMIKTADLKVLGKPYRDDDDREKTIQS 540  
 DB 481 HKGAWFLVCSGALVNERVTWVAACHVTDLGKVTMIKTADLKVLGKPYRDDDDREKTIQS 540  
 QY 541 LQISAILHPNVDPIILLDADITAILKLLDKARISTRVQPICLAASRDLSSTFQESHITVAG 600  
 DB 541 LQISAILHPNVDPIILLDADITAILKLLDKARISTRVQPICLAASRDLSSTFQESHITVAG 600  
 QY 601 MNVLADVRSPGKNDTLRSVVVVDLSLLCEQHEHDGIPVSVTDNMFCASWEPTAPSDI 660  
 DB 601 MNVLADVRSPGKNDTLRSVVVVDLSLLCEQHEHDGIPVSVTDNMFCASWEPTAPSDI 660  
 QY 661 CTATGGIAAASFPGRASPEPRWHLMLGLVSNYSYDKTCSHRLSTAFTKVLFPFKDWIERNNK 720  
 DB 661 CTATGGIAAASFPGRASPEPRWHLMLGLVSNYSYDKTCSHRLSTAFTKVLFPFKDWIERNNK 720

RESULT 6  
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 ID ABUS8484 standard; protein; 720 AA.  
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 AC ABUS8484;

XX 15-APR-2003 (first entry) 98US-0086486P.  
DT 28-MAY-1998; 98US-0087098P.  
XX 28-MAY-1998; 98US-0087208P.  
DE 02-JUN-1998; 98US-0087609P.  
XX 02-JUN-1998; 98US-0087759P.  
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver; 98US-0087827P.  
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT; 98US-0088025P.  
KW antibody-dependent enzyme mediated prodrug therapy. 98US-0088028P.  
XX 04-JUN-1998; 98US-0088029P.  
OS Homo sapiens. 98US-0088033P.  
XX 04-JUN-1998; 98US-0088326P.  
XX 04-JUN-1998; 98US-0088167P.  
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XX 05-JUN-1998; 98US-0088212P.  
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XX 01-JUL-1998; 98US-0091359P.  
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PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-00168978.
Query Match 100.0%; Score 3945; DB 6; Length 720;		
Best Local Similarity 100.0%; Pred. No. 1.2e-204;		
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0		
QY	1	MELGCWTQLGTLFTLQLLLISSLPREYTVINACPGAENINWCRECEYDQIECVCPGKRE 60
Db	1	MELGCWTQLGTLFTLQLLLISSLPREYTVINACPGAENINWCRECEYDQIECVCPGKRE 60
QY	61	VVGYYTIPCCRNENECDSCLIHPGCTTIFENCKSCRNSWGGLTDDFYVKGIFYCAECRAGW 120
Db	61	VVGYYTIPCCRNENECDSCLIHPGCTTIFENCKSCRNSWGGLTDDFYVKGIFYCAECRAGW 120
QY	121	YGGDCMCGQVLRAPKGGQILLESPLNAHCWTHAKDGFVIOQLRFVMLSLSEFDYMCQYD 180
Db	121	YGGDCMCGQVLRAPKGGQILLESPLNAHCWTHAKDGFVIOQLRFVMLSLSEFDYMCQYD 180
QY	181	YVEVRDGNDRDQIILKRVCGNERPAPIQSIGSSLLHVLPHSDGSKNFDGFHAIYEIITACS 240
Db	181	YVEVRDGNDRDQIILKRVCGNERPAPIQSIGSSLLHVLPHSDGSKNFDGFHAIYEIITACS 240
QY	241	SSPCFHDGTCVLDKAGSYKCAACLAGYTGQRCENLLEENECSDPGGFVNGYQKITGGPGLI 300

Db	241	SSPCFHDTGTCVLDKAGSYKACACIAGTYTGORCENLLEERNCSDPGGPVNGYKLTGPGGLI	300
Qy	301	NGRHAKIGTVVSPFCNNYSVYLSGNEKRTCOQNGESGKQPICIKACREPKISDLVRRRVL	360
Db	301	NGRHAKIGTVVSPFCNNYSVYLSGNEKRTCOQNGESGKQPICIKACREPKISDLVRRRVL	360
Qy	361	PMQVQSRETPLHQIYSAAFSKQKLOSAPTKKPALPGDILPMGYOHLHTOLQYECISPPFYR	420
Db	361	PMQVQSRETPLHQIYSAAFSKQKLOSAPTKKPALPGDILPMGYOHLHTOLQYECISPPFYR	420
Qy	421	RLGSSRTCLRTGKWSGRAPSCPICGKIENITAPKTQGLRWPQAAIYVRTSGVHDGSL	480
Db	421	RLGSSRTCLRTGKWSGRAPSCPICGKIENITAPKTQGLRWPQAAIYVRTSGVHDGSL	480
Qy	481	HKGAWFLVCSGALVNERTVVAACHVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQS	540
Db	481	HKGAWFLVCSGALVNERTVVAACHVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQS	540
Qy	541	LQISAILLHPNYPDILLADAIILKLLDKARISTRVQVOPICLAASRDLSFQESHITVAG	600
Db	541	LQISAILLHPNYPDILLADAIILKLLDKARISTRVQVOPICLAASRDLSFQESHITVAG	600
Qy	601	MNVLADVRSFGKNDTLRSGVSVVDSLLCEEQEDHGIPVSVTDNNFCASWEPTAPSDI	660
Db	601	MNVLADVRSFGKNDTLRSGVSVVDSLLCEEQEDHGIPVSVTDNNFCASWEPTAPSDI	660
Qy	661	CTAETGGIAAVSFFGRASPPRWHLMLGLVSWSDKTCSHRLSTAFTKVLPFKDWIERNMK	720
Db	661	CTAETGGIAAVSFFGRASPPRWHLMLGLVSWSDKTCSHRLSTAFTKVLPFKDWIERNMK	720
RESULT 7			
ABU88032			
ID	ABU88032	standard; protein; 720 AA.	
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AC	ABU88032;		
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DT	DT	07-JUL-2003 (first entry)	
XX	XX		
DE	DE	Novel human secreted and transmembrane protein PRO1344.	
XX	XX		
KW	KW	Human; secreted and transmembrane protein; PRO; gene therapy;	
KW	KW	tumour necrosis factor-alpha release; TNF-alpha release;	
KW	KW	chondrocyte proliferation; chondrocyte differentiation; tumour;	
KW	KW	adrenal tumour; lung tumour; colon tumour; breast tumour;	
KW	KW	prostate tumour; rectal tumour; cervical tumour; liver tumour.	
XX	XX		
OS	OS	Homo sapiens.	
XX	XX		
PN	PN	US2003032127-A1.	
PD	PD	13-FEB-2003.	
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PF	PF	26-JUN-2002; 2002US-00183012.	
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PR	PR	18-SEP-1997; 97US-0059263P.	
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PR	PR	21-OCT-1997; 97US-0063486P.	
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PR	PR	28-OCT-1997; 97US-0063544P.	
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PR 11-DEC-1997; 97US-00693335P.  
PR 12-DEC-1997; 97US-00694252P.  
PR 17-DEC-1997; 97US-00698707P.  
PR 18-DEC-1997; 97US-00680117P.  
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PR 09-APR-1998; 98US-00811959P.  
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PR 10-SEP-1998; 98US-00998129P.  
PR 15-SEP-1998; 98US-01003889P.  
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Query Match		100.0%;	Score 3945;	DB 6;	Length 720;
Best Local Similarity		100.0%;	Pred. No. 1.2e-204;		
Matches 720;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MELGCTQLGLTFLQLLLISLPREYTVINEACPGAENIMCRECCYDQIECVCPGKRE	60		
Db	1	MELGCTQLGLTFLQLLLISLPREYTVINEACPGAENIMCRECCYDQIECVCPGKRE	60		
Qy	61	VVGTYTPCCNEECDSLIHPGCTIFENCKSCRNCSWGGLTDDFVYKGFYCAECRAGW	120		
Db	61	VVGTYTPCCNEECDSLIHPGCTIFENCKSCRNCSWGGLTDDFVYKGFYCAECRAGW	120		
Qy	121	YGGDCMRCGOVLAPKGOILLESYPLNAHCEWTHAKPGFVIQLRFVMLSLEFDYMCQYD	180		
Db	121	YGGDCMRCGOVLAPKGOILLESYPLNAHCEWTHAKPGFVIQLRFVMLSLEFDYMCQYD	180		
Qy	181	YVEVRDGDNRDGOIIRKVCNGNERPAPIQSGSSLSHLVLFHSDGSKNFDGFHAIYEETACS	240		
Db	181	YVEVRDGDNRDGOIIRKVCNGNERPAPIQSGSSLSHLVLFHSDGSKNFDGFHAIYEETACS	240		
Qy	241	SSPCFHDGTCVLKAGSYKACIAGYTGQRCENLLBERNCSDPGPVNGYKQITGGPGLI	300		
Db	241	SSPCFHDGTCVLKAGSYKACIAGYTGQRCENLLBERNCSDPGPVNGYKQITGGPGLI	300		
Qy	301	NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSGKQPIKACREPKISDLVRRRLV	360		
Db	301	NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSGKQPIKACREPKISDLVRRRLV	360		
Qy	361	PMQVQSRTEPLHQLYSAFSAKQLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYR	420		
Db	361	PMQVQSRTEPLHQLYSAFSAKQLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYR	420		
Qy	421	RLGSSRRTCRLTKGWSRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSL	480		
Db	421	RLGSSRRTCRLTKGWSRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSL	480		
Qy	481	HKGAWFLVCSGALVNTVVAAHCVTDLGKVTMIKTADLKVLGKPYRDDDEKTIQS	540		
Db	481	HKGAWFLVCSGALVNTVVAAHCVTDLGKVTMIKTADLKVLGKPYRDDDEKTIQS	540		
Qy	541	LQISAILHPNYDPIILDADIALKLDKARISTRVQPICLAASRDLSTSFQSSHITVAG	600		
Db	541	LQISAILHPNYDPIILDADIALKLDKARISTRVQPICLAASRDLSTSFQSSHITVAG	600		
Qy	601	WNVLVDRSPFGKNDTLRSQVSVSDSLICEQHEHGIPIVSTDNMFCAWFTAPSFI	660		
Db	601	WNVLVDRSPFGKNDTLRSQVSVSDSLICEQHEHGIPIVSTDNMFCAWFTAPSFI	660		
Qy	661	CTAETGGIAAVSPGRASPRVHLMGLVSWSDYDKTCSHRLSTAFKTLVLPFKDWIERNMK	720		
Db	661	CTAETGGIAAVSPGRASPRVHLMGLVSWSDYDKTCSHRLSTAFKTLVLPFKDWIERNMK	720		

RESULT 8  
ABU84347  
ID ABU84347 standard; protein; 720 AA.  
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DT	02-AUG-2003 (first entry)	
XX		
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XX		
KW	Human; secreted and transmembrane protein; PRO; TNF-alpha;	
KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;	
XX	tissue typing.	
OS	Homo sapiens.	
XX		
PN	US2003032112-A1.	
XX		
PD	13-FEB-2003.	
XX		
PF	21-JUN-2002; 2002US-00176756.	
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Query Match		100.0%;	Score 3945;	DB 6;	Length 720;
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Db	1	MELGCTOLGTLFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKRE	60		
QY	61	VVGYTIPCCRNEECDSLIHPGCTIFENCKSCNGSWGCTLDDFYVKGFCACRAGW	120		
Db	61	VVGYTIPCCRNEECDSLIHPGCTIFENCKSCNGSWGCTLDDFYVKGFCACRAGW	120		
QY	121	YGGDCMRCQVLRAPKQILLESYPLNAHCEWTTHAKPGFVIQLRFVMLSLFEDYMCQYD	180		
Db	121	YGGDCMRCQVLRAPKQILLESYPLNAHCEWTTHAKPGFVIQLRFVMLSLFEDYMCQYD	180		
QY	181	YVEVRDGNRDGQIIRKVCNRPAPIQISGSLHLVLFHSDGSKNFDGFHAIYEBITACS	240		
Db	181	YVEVRDGNRDGQIIRKVCNRPAPIQISGSLHLVLFHSDGSKNFDGFHAIYEBITACS	240		

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QY 301 NGRHAKIGTVVSPFCNNSVYLSENEKRTCOONGEWSGKOPICIKACREPKISDLVRRVYL 360  
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QY 361 PMQVQSRRETPHLQYLSAFAFSKQLSAPTKKPPALPFGDLPNGYQHLHTQLQYECISPPFYR 420  
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QY 421 RLGSRRRTCLRTGKSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL 480  
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QY 481 HKGAWFLVCSGALNVNRTVVAAHCVTDLGKVTMIKTADLVKLGKPYRDDRDEKTIOS 540  
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QY 661 CTAETGGIAAVSPFGGRASPEPRWHLGLVSWSDYDKTCSHRLSTAFKVLPPFKDWIERNMK 720  
DB 661 CTAETGGIAAVSPFGGRASPEPRWHLGLVSWSDYDKTCSHRLSTAFKVLPPFKDWIERNMK 720

RESULT 9

ABR66221  
ID ABR66221 standard; protein; 720 AA.

XX AC ABR66221;

XX DT 05-AUG-2003 (first entry)

XX DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

XX KW Human; PRO; secreted protein; transmembrane protein;  
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
KW chondrocyte; proliferation; differentiation; cartilage disorder;  
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
KW antiarthritic; vulnery; gene therapy.

XX OS Homo sapiens.

XX PN US2003027278-A1.

XX PD 06-FEB-2003.

XX PF 21-JUN-2002; 2002US-00176987.

XX PR 18-SEP-1997; 97US-0059263P.

XX PR 18-SEP-1997; 97US-0059266P.

XX PR 17-OCT-1997; 97US-0062250P.

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XX PR 24-OCT-1997; 97US-0063121P.

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Qy	421	RLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRMPQAAIYRRTSGVHDGSL	480	PR	04-JUN-1998;	98US-0088025P.
Db	421	RLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRMPQAAIYRRTSGVHDGSL	480	PR	04-JUN-1998;	98US-0088026P.
Qy	481	HKGAFVLCGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDDEKTIQS	540	PR	04-JUN-1998;	98US-0088028P.
Db	481	HKGAFVLCGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDDEKTIQS	540	PR	04-JUN-1998;	98US-0088029P.
Qy	541	LOISAILHPNDPILLDADIALLKLDKARTSTRVQPICLAASRDLSFQESHITVAG	600	PR	04-JUN-1998;	98US-0088030P.
Db	541	LOISAILHPNDPILLDADIALLKLDKARTSTRVQPICLAASRDLSFQESHITVAG	600	PR	04-JUN-1998;	98US-0088033P.
Qy	601	MNVADVRSPGKNDTLRSQVSVVDSLLCEQHEHDGIPVSVTDNMFCASWEPTAPSDI	660	PR	04-JUN-1998;	98US-0088326P.
Db	601	MNVADVRSPGKNDTLRSQVSVVDSLLCEQHEHDGIPVSVTDNMFCASWEPTAPSDI	660	PR	05-JUN-1998;	98US-0088167P.
Qy	661	CTAETGGIAAVSFPGRASPEPRHMLGVLWSYDKTCSHRLSTAFKVLFPKDWIERNMK	720	PR	05-JUN-1998;	98US-0088212P.
Db	661	CTAETGGIAAVSFPGRASPEPRHMLGVLWSYDKTCSHRLSTAFKVLFPKDWIERNMK	720	PR	05-JUN-1998;	98US-0088217P.
RESULT 13						
ABUS9111	ID ABUS9111 standard; protein; 720 AA.					
XX	AC ABUS9111;					
XX	DT 28-APR-2003 (first entry)					
DE	Novel human secreted or transmembrane protein PRO1344.					
XX	Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;					
KW	cardiac insufficiency disorder; cancer; tumour; immune response;					
KW	adrenal cortical capillary endothelial growth; c-fos induction;					
KW	vascular endothelial growth factor inhibition; VEGF inhibition;					
KW	endothelial cell growth inhibitor; T-lymphocytes stimulation;					
KW	retinal neurons cell survival; rod photoreceptor cell survival;					
KW	retinal disorder; retinitis pigmentosa; kidney disease;					
KW	mammalian kidney mesangial cell proliferation; Berger disease;					
KW	dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;					
XX	chondrocyte redifferentiation; sports injury; arthritis.					
OS	Homo sapiens.					
XX	US2002132252-A1.					
PN	19-SEP-2002.					
PD	14-NOV-2001; 2001US-00990442.					
PP	16-JUN-1997; 97US-0049787P.					
XX	17-OCT-1997; 97US-0062250P.					
PR	05-NOV-1997; 97WO-US020069.					
PR	12-NOV-1997; 97US-0065186P.					
PR	13-NOV-1997; 97US-0065311P.					
PR	24-NOV-1997; 97US-0066770P.					
PR	25-FEB-1998; 98US-0075945P.					
PR	20-MAR-1998; 98US-0078910P.					
PR	28-APR-1998; 98US-0083322P.					

11-AUG-2000; 2000MO-US022031.  
 23-AUG-2000; 2000MO-US023522.  
 24-AUG-2000; 2000MO-US023328.  
 08-NOV-2000; 2000MO-US030952.  
 01-DEC-2000; 2000MO-US032678.  
 28-FEB-2001; 2001MO-US0008520.  
 01-JUN-2001; 2001MO-US017800.  
 20-JUN-2001; 2001MO-US019692.  
 29-JUN-2001; 2001MO-US021066.  
 09-JUL-2001; 2001MO-US021735.  
 28-AUG-2001; 2001US-00941992.  
 (GETH ) GENENTECH INC.  
 Auhonazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;  
 Pi Forrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 Pi Grimaldi JC, Gurney AL, Kijavini TJ, Napier MA, Pan J, Paoni NF;  
 Pi Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 Pi Zhang Z;  
 XX  
 DR WPI; 2003-247083/24.  
 DR N-PSDB; ABX80270.  
 XX  
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 PT are therapeutically useful for enhancing immune response and in cancer  
 PT treatments.  
 XX  
 PS Claim 12; Fig 159; 648pp; English.  
 XX  
 CC The invention describes an isolated human PRO polypeptide. The PRO  
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 CC in modulating at least one biological activity of a cell expressing a PRO  
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1185  
 CC stimulate adrenal cortical capillary endothelial growth, and PRO336,  
 CC PRO943, PRO828, PRO1068 or PRO335, PRO826, PRO819, PRO1126,  
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
 CC useful for treating conditions or disorders where angiogenesis would be  
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
 CC useful for treating cancerous tumours. PRO812 inhibits vascular  
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 CC cells and is thus useful for inhibiting endothelial cell growth in  
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
 CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
 CC rod photoreceptor cells) and therefore are useful for treating retinal  
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD, PRO819, PRO813  
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
 CC and therefore are useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger disease or other  
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
 CC proliferation and/or redifferentiation of chondrocytes in culture and are  
 CC thus useful for treating sports injuries, and arthritis. This is the  
 CC amino acid sequence of a novel human PRO protein  
 XX  
 SQ Sequence 720 AA;

Query Match 100.0%; Score 3945; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-204;  
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 VVGVTTPCCNEENECDSCLHPGCTIFENCKSCRNCSWGGLDLDFFVYKGFYCAECRAGW 120  
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QY 121 YGDCMRCQVLRAPKQQLLESYFLNAHCEWTIIHAKPGFVIQLRFVMLSLEFDYMCQYD 180  
 DB 121 YGDCMRCQVLRAPKQQLLESYFLNAHCEWTIIHAKPGFVIQLRFVMLSLEFDYMCQYD 180  
 QY 181 YVEVRDGNRGOIIRKVCGRNERPAPIOSIGSLHVLHSDGSKNFDGPHAYEEITACS 240  
 DB 181 YVEVRDGNRGOIIRKVCGRNERPAPIOSIGSLHVLHSDGSKNFDGPHAYEEITACS 240  
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 DB 241 SSPCFHDGTCLVDKAGSYKACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGPGGLI 300  
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 DB 301 NGRHAKIGTVVSVFFCNNSVYLSGNEKRTCCQNGESGKQPCIKACREPKISDLVRRVRL 360  
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 DB 361 PMQVOSRETPHLHOLYSAAFSKQKLSAPTKKPKALPGDLPMGVQHLHTLOQECISPFYR 420  
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 DB 481 HGWFLVCSGALVNERVTVVAAHCVTDIGKVTMTADLKVVLGKFPYRDDDRDEKTIQS 540  
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 DB 541 LOISAILHPNYDPIILLDADIALKLLDKARISTRVQPICLAASRDLSSTFQESHITVAG 600  
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 QY 661 CTAETGGIAAASPGRASPEPRWHLMLGLVSWYDKTCSHRLSTAFTKVLPFKDWIERNMK 720  
 DB 661 CTAETGGIAAASPGRASPEPRWHLMLGLVSWYDKTCSHRLSTAFTKVLPFKDWIERNMK 720

RESULT 14  
 ABUS2623  
 ID ABUS2623 standard; protein; 720 AA.  
 XX  
 AC ABUS2623;  
 XX  
 DT 26-JUN-2002 (first entry)  
 XX  
 DE Human secreted/transmembrane protein PRO1344.  
 XX  
 KW Human; PRO; secreted protein; transmembrane protein;  
 KW cardiac insufficiency disorders; angiogenesis; wound healing;  
 KW cancerous tumour; immune response; retinal disorder; sight loss;  
 KW retinitis pigmentosa; age-related macular degeneration; AMD;  
 KW kidney disease; Berger disease; nephropathy; dermatitis; herpeticiformis;  
 KW Crohn's disease; sports injury; arthritis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2003032023-A1.  
 XX  
 PD 13-FEB-2003.  
 XX  
 XX 14-NOV-2001; 2001US-00990711.  
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 XX 17-OCT-1997; 97US-0062250P.  
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 XX 24-NOV-1997; 97US-0066770P.

PR 25-FEB-1998; 98US-0075945P.  
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PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101477P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
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PR 24-SEP-1998; 98US-0101922P.
PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
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PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
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PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
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Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.2e-204;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Qy 181 YVEVRDGDNRDGOIIRKVCNERPAPIQSIGSSHLVLFHSDGSKNFDGFHAIYEEITACS 240  
 Db 181 YVEVRDGDNRDGOIIRKVCNERPAPIQSIGSSHLVLFHSDGSKNFDGFHAIYEEITACS 240  
 Qy 241 SSPCFHDGTCLVDKAGYKACLAGYTGRCENLLEERNCSDPGPGVNGYQKITGGPGLI 300  
 Db 241 SSPCFHDGTCLVDKAGYKACLAGYTGRCENLLEERNCSDPGPGVNGYQKITGGPGLI 300  
 Qy 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOONGEWSGKQICIKACREPKISDLVRRRL 360  
 Db 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOONGEWSGKQICIKACREPKISDLVRRRL 360  
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 Db 361 PMQVQSRETPHLQLYSAAFSKQKLSAPTCKPALPFGDLPMGYQHLHTQLOYECISPFYR 420  
 Qy 421 RLSSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRMPQAAIYVRTSGVHDGSL 480  
 Db 421 RLSSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRMPQAAIYVRTSGVHDGSL 480  
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 Db 481 HKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADLKVLGKFYRDDDRDEKTIQS 540  
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 Db 541 LOISAILHPNYDPILLDADIAILKLDKARISTRVQPICLAASRDISTSFQESHITVAG 600  
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 Db 601 WNLADVRSPGFKNLTLRSVGVSVVDSILCEEHEDHGI PVSVTDNNMFCASWEPTAPSDI 660  
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Search completed: August 18, 2004, 16:23:42  
 Job time : 63 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:16:43 ; Search time 50 Seconds  
(without alignments)  
4520.551 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945

Sequence: 1 MELGCWTGLTFLQLLIS.....LSTAFKVLPPKDWIERNK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 700 summaries

Database : Published Applications AA.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	3945	100.0	720	9	US-09-989-279-231
4	3945	100.0	720	9	US-09-989-727-231
5	3945	100.0	720	9	US-09-989-731-231
6	3945	100.0	720	9	US-09-989-732-231
7	3945	100.0	720	9	US-09-991-073-231
8	3945	100.0	720	9	US-09-990-442-231
9	3945	100.0	720	9	US-09-991-163-231
10	3945	100.0	720	9	US-09-993-604-231
11	3945	100.0	720	9	US-09-990-456-231
12	3945	100.0	720	9	US-09-989-721-231
13	3945	100.0	720	9	US-09-992-598-231
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17	3945	100.0	720	9	US-09-991-181-231	Sequence 231, App
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259	3945	100.0	720	14	US-10-176-916-170	Sequence 170, App	332	3945	100.0	720	14	US-10-201-770-170	Sequence 170, App
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580	3945	100.0	720	14	US-10-175-754-170	Sequence 170, App	653	3945	100.0	720	14	US-10-063-726-38	Sequence 38, Appl
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584	3945	100.0	720	14	US-10-176-755-170	Sequence 170, App	657	3945	100.0	720	14	US-10-063-523-38	Sequence 38, Appl
585	3945	100.0	720	14	US-10-176-759-170	Sequence 170, App	658	3945	100.0	720	14	US-10-063-527-38	Sequence 38, Appl
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597	3945	100.0	720	14	US-10-174-574-170	Sequence 170, App	670	3945	100.0	720	14	US-10-063-640-38	Sequence 38, Appl
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ALIGNMENTS

RESULT 1  
US-09-989-722-231  
Sequence 231, Application US/09989722  
Patent No. US20020072067A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
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APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P27301C63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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Best Local Similarity 100.0%; Pred. No. 0;  
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Qy 61 VVGYYTIPCCRNENECDSCLIHGCTTIFENCKSCRNGSWGGLTDDFYVKGFYCAECRAGW 120  
Db 61 VVGYYTIPCCRNENECDSCLIHGCTTIFENCKSCRNGSWGGLTDDFYVKGFYCAECRAGW 120

Qy 121 YGGDCMRCGOVLRAPKGOILLESYPLNAHCEWTHAKPGVQLRFLVMSLEFDYMCQYD 180  
Db 121 YGGDCMRCGOVLRAPKGOILLESYPLNAHCEWTHAKPGVQLRFLVMSLEFDYMCQYD 180

Qy 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSHLVLFHSDGSKNPDGFHAIYEETACS 240  
Db 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSHLVLFHSDGSKNPDGFHAIYEETACS 240

Qy 241 SSPCFHDGTCVLDKAGSYKACLAGYTGORCENLLBERNCSDPGGPNVGYQKITGPGGLI 300  
Db 241 SSPCFHDGTCVLDKAGSYKACLAGYTGORCENLLBERNCSDPGGPNVGYQKITGPGGLI 300

Qy 301 NGRHAKIGTVVSFFCNNSVVLGNEKRTCOQNGESGKOPICIKACREPKISDLVRRVL 360  
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Qy 361 PMQVQSRETPHLQYSAAFSKQLQSAPTKXKAPLPGDLPMGYQHLHTQLQYECISPFYR 420  
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Qy 421 RLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL 480  
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Qy 481 HKGANFLVCSGALVNERTVVAAHCVTDLGKVTMIKADLVKVLGKPYRDDDEKTIQS 540  
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Qy 541 LQISAILHPNYDPILLDDADIALKLLDKARISTRVQPICLAASRDLSSTFQESHITVAG 600  
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Qy 601 WNVLADVRSPGKNDTLRSQVSVVDSLLCEQHEHDGIPVSVTDNMFCASHEPTAPSDI 660  
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RESULT 2  
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; Sequence 231, Application US/09989723

Patent No. US20020072092A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyors, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC62  
CURRENT APPLICATION NUMBER: US/09/989,723  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR APPLICATION NUMBER: 60/065186  
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 YGGDCMCGQVLRAPKPGQILLESPLNAHCETWTHAKPGFVIQLRFVWLSPEDYMCQYD 180
Db 121 YGGDCMCGQVLRAPKPGQILLESPLNAHCETWTHAKPGFVIQLRFVWLSPEDYMCQYD 180

Qy 181 YVEVRDGNDRDQGIKRVCGNERPAPIQSIGSSHLVLFHSDGSKNFDGFHAIYEITACS 240
Db 181 YVEVRDGNDRDQGIKRVCGNERPAPIQSIGSSHLVLFHSDGSKNFDGFHAIYEITACS 240

241 S S P C F H D G T C V L D K A G S Y K C A C L A G Y T G O R C E N L L E E R N C S D P G P V N G Y Q K I T G P G L I 300
241 S S P C F H D G T C V L D K A G S Y K C A C L A G Y T G O R C E N L L E E R N C S D P G P V N G Y Q K I T G P G L I 300
301 N G R H A K I G T V S F F C N N S V V L S G N E K R T C Q Q N G E W S G K O P I C I K A C R E P K I S D L V R R V L 360
301 N G R H A K I G T V S F F C N N S V V L S G N E K R T C Q Q N G E W S G K O P I C I K A C R E P K I S D L V R R V L 360
361 P M Q V Q S R E T P L H Q L Y S A A F S K Q L Q S A P T K K P A L P F G D L P M G Y Q H L H T Q L Q Y E C I S P F Y R 420
361 P M Q V Q S R E T P L H Q L Y S A A F S K Q L Q S A P T K K P A L P F G D L P M G Y Q H L H T Q L Q Y E C I S P F Y R 420
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421 R L G S S R R T C L R T G K W S G R A P S C I P I C G K I E N I T A P K T O G L R W P W Q A A I Y R R T S G V H D G S L 480
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661 C T A E T G G I A A V S P P G R A S P E P R W H L M G L V S W S Y D K T C S H R L S T A F T K V L P F K D W I E R N M K 720
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RESULT 3
US-09-989-279-231
; Sequence 231, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C56
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; CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

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 Db 121 YGDCMRCGQVLRAPKQILLESPLNAHCETHHAKPGFVIQLRFWLSLEFDYMCQYD 180

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 Db 181 YVEVRDGDNRDQIILKVCNGNERPAPIQSGSSLHVLPHSDGSKNPGFHAIEEITACS 240

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 Qy 541 LQISAILHPNYDPIILDADIAILKLDKARISTRVOPICLAASRDISTSFQSHIITVAG 600
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 Qy 601 WNVLADVRSFGKNDTLRSGVSVVSDLLCEEQHEHDGIPVSVTDNMFCASWEPTAPSDI 660
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Sequence 231, Application US/09989727
 Patent No. US20020072497A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730PIC65
 CURRENT APPLICATION NUMBER: US/09/989,727
 PRIOR FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
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Query Match 100.0%; Score 3945; DB 9; Length 720;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 720; Conservative 0;

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Db 181 YVEVRDGNDRGQIIRKVCNERPAPIQSIGSSLSHLVLFHSDGSKNFDGFHAIYVEBITACS 240  
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Db 241 SSPCFHDGTCLVLDKAGSYKACLAGYTGQRCENLLBERNCSDPGGVNGYQKITGPGGLI 300  
Qy 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOONGEWSGKQIPICIKACREPKISDLVRRVL 360  
Db 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOONGEWSGKQIPICIKACREPKISDLVRRVL 360  
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Qy 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYVRTSGVHDGSL 480  
Db 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYVRTSGVHDGSL 480  
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Db 661 CTAETGGIAVSPFGRASPPRHLMLGLVSWSDYDKTCSHRLSTAFKVLFPKDWIERNMK 720

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; Sequences 231, Application US/09989731  
; Patent No. US20020103125A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
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; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C70  
; CURRENT APPLICATION NUMBER: US/09/989, 731  
; PRIOR FILING DATE: 2001-11-20  
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DB 181 YVEVRDGNRDGOIIRKVCNRPAPISIGSSHLVLFHSDGSKNDFGHAIYEITACS 240  
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US-09-989-732-231  
Sequence 231, Application US/09989732  
Patent No. US20020123463A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertschen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730FIC57  
CURRENT APPLICATION NUMBER: US/09/989,732  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
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Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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QY	61	VVGVTIPCCNEECNDCSLIHGCTIFENCKSCRNSWGGTLDLDFVYKGFYCAECRAGW	120						
DB	61	VVGVTIPCCNEECNDCSLIHGCTIFENCKSCRNSWGGTLDLDFVYKGFYCAECRAGW	120						
QY	121	YGGDCMRCGVLRAKPGQIILLESYPLNAHCEWTHAKPGFVIQLRFVMLSLEPDYMCQYD	180						
DB	121	YGGDCMRCGVLRAKPGQIILLESYPLNAHCEWTHAKPGFVIQLRFVMLSLEPDYMCQYD	180						
QY	181	YVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSLIHLVLFHSDGSKNFDGFHAIYEEITACS	240						

DB	181	YVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSLIHLVLFHSDGSKNFDGFHAIYEEITACS	240						
QY	241	SSPCFHDGTCVLDKAGSYKCACLAGYTGORCENLEERNCSDPGPVNGYQKITGGPGLI	300						
DB	241	SSPCFHDGTCVLDKAGSYKCACLAGYTGORCENLEERNCSDPGPVNGYQKITGGPGLI	300						
QY	301	NGRHAKITVVSFFCNNSYVLSGNEKRTCOQNGEWSGKQPICIKACREPKISDLVRRVRL	360						
DB	301	NGRHAKITVVSFFCNNSYVLSGNEKRTCOQNGEWSGKQPICIKACREPKISDLVRRVRL	360						
QY	361	PMQVOSRETPHLQLYSAAFSKQLQSAPTKKPALPFGDLPMGYOHLHTQLOVECTISPFYR	420						
DB	361	PMQVOSRETPHLQLYSAAFSKQLQSAPTKKPALPFGDLPMGYOHLHTQLOVECTISPFYR	420						
QY	421	RLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL	480						
DB	421	RLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL	480						
QY	481	HKGAWFLVCSGALVNERTVVVAACHCVDLKGKVTMIKTADLKVLGKFYRDDREKTIQS	540						
DB	481	HKGAWFLVCSGALVNERTVVVAACHCVDLKGKVTMIKTADLKVLGKFYRDDREKTIQS	540						
QY	541	LQISAILHPNYDPTLLDADTALILKLDKARISTRVQPICLAAASRDLSFSQESHITVAG	600						
DB	541	LQISAILHPNYDPTLLDADTALILKLDKARISTRVQPICLAAASRDLSFSQESHITVAG	600						
QY	601	WNVLADVRSPGKNDTLRSVGVVSDSLCEQEHEDHGIPVSVTDNMFCASWEPTAPSDI	660						
DB	601	WNVLADVRSPGKNDTLRSVGVVSDSLCEQEHEDHGIPVSVTDNMFCASWEPTAPSDI	660						
QY	661	CTAETGGIAAVSFFGRASPEPRWHLMLGVSWSYDKTCSHRLSTAFKVLFPKDWIERNMK	720						
DB	661	CTAETGGIAAVSFFGRASPEPRWHLMLGVSWSYDKTCSHRLSTAFKVLFPKDWIERNMK	720						

RESULT 7

US-09-991-073-231

Sequence 231, Application US/09991073

Patent No. US2002012756A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Klijavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tamas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730P1C15

CURRENT APPLICATION NUMBER: US/09/991,073

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

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17 PRIOR FILING DATE: 1998-07-07  
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19 PRIOR FILING DATE: 1998-07-09

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QY 61 VVGTYTPCCRNENECDCLHPGCTIFENCKSCRNCGGTLDDFYVKGFFCAECRAGW 120  
DB 61 VVGTYTPCCRNENECDCLHPGCTIFENCKSCRNCGGTLDDFYVKGFFCAECRAGW 120

QY 121 YGGDCMRCQVLRAPKQGLLESYPLNARCEWTIHAKPGFVQLRPFVMLSLEFDYMCQYD 180  
DB 121 YGGDCMRCQVLRAPKQGLLESYPLNARCEWTIHAKPGFVQLRPFVMLSLEFDYMCQYD 180

QY 181 YVEVRDGNRDGQIKRVCNERNPAPIQSIGSLHLVLFHSDSKNFGDGHAYEITACS 240  
DB 181 YVEVRDGNRDGQIKRVCNERNPAPIQSIGSLHLVLFHSDSKNFGDGHAYEITACS 240

QY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGORCENLLEERNCSPPGGVNGYQKITGGPGLI 300  
DB 241 SSPCFHDGTCVLDKAGSYKACLAGYTGORCENLLEERNCSPPGGVNGYQKITGGPGLI 300

QY 301 NGRHAKIGTVWFFCNNSYVLSGNEKRTCCQNGEWSGKQPICIKACREPKISDLVRRVRL 360  
DB 301 NGRHAKIGTVWFFCNNSYVLSGNEKRTCCQNGEWSGKQPICIKACREPKISDLVRRVRL 360

QY 361 PMQVQSRRETPHLQLYSAAFSKQLQSAPTKPKPALPEGDLPMGVQHLHTLOVECI SPFYR 420  
DB 361 PMQVQSRRETPHLQLYSAAFSKQLQSAPTKPKPALPEGDLPMGVQHLHTLOVECI SPFYR 420

QY 421 RLGSSRRTCLRTGKSGRAPSCIPICGKENITAPKTQGLRWPQAAIYVRTSGVHDGSL 480  
DB 421 RLGSSRRTCLRTGKSGRAPSCIPICGKENITAPKTQGLRWPQAAIYVRTSGVHDGSL 480

QY 481 HKGAWFLVCSGALVNERTVVAACHVCTDLGKVTMTKADLVKLVGKPYRDDRDREKTIQS 540  
DB 481 HKGAWFLVCSGALVNERTVVAACHVCTDLGKVTMTKADLVKLVGKPYRDDRDREKTIQS 540

QY 541 LQISAILHPNYDPILLDADIALKLLDKARISTRVQPICLASRDLSFQESHITVAG 600  
DB 541 LQISAILHPNYDPILLDADIALKLLDKARISTRVQPICLASRDLSFQESHITVAG 600

QY 601 WNVLDVRSFGFNDTLRSQVSVVDSLLCEEQHDHGIPVSVTONMFCASWEPTAPSDI 660  
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RESULT 8  
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; Patent No. US20020132252A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deonoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Gerber, Hanspeter  
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; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC8  
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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 9; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 VVGTYTPCCNEENECDSCLIHGCGTIFENCKSCRNGSGGTLDDFVVGKGYCAECRAGW 120  
Db 61 VVGTYTPCCNEENECDSCLIHGCGTIFENCKSCRNGSGGTLDDFVVGKGYCAECRAGW 120  
Qy 121 YGGDCMRCGQVLRAPKQIILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYD 180  
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QY 181 YVEVRDGNDRDQIIKRVCGNERPAPIQSIGSSHLVLFHSDGSKNFDGFHAIYEITACS 240  
DB 181 YVEVRDGNDRDQIIKRVCGNERPAPIQSIGSSHLVLFHSDGSKNFDGFHAIYEITACS 240  
QY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGORCENILBERNCSDPGFVNGYQKITGGPGLI 300  
DB 241 SSPCFHDGTCVLDKAGSYKACLAGYTGORCENILBERNCSDPGFVNGYQKITGGPGLI 300  
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DB 301 NGRHAKIGTWVFFCNNSVYLSGNEKRTCCQNGWSGKQPICIKACREPKISDLVRRVVL 360  
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DB 361 PMQVOSRETPHLHOLYSAAFSKQKLSAFTKPPALPFGDLPNGYQHLTLQVCECISPPYR 420  
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DB 421 RLGSSRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRPWQAAIYVRTSGVHDGSL 480  
QY 481 HGWFLVCSGALVNERVTVVAAHCVTDLGKVTMIKTADLVKLGKPYRDDDRDEKTIQS 540  
DB 481 HGWFLVCSGALVNERVTVVAAHCVTDLGKVTMIKTADLVKLGKPYRDDDRDEKTIQS 540  
QY 541 LOISAILHPNDPILLDADIAILKLLDKARISTRVQPICLAASRDLSFQESHITVAG 600  
DB 541 LOISAILHPNDPILLDADIAILKLLDKARISTRVQPICLAASRDLSFQESHITVAG 600  
QY 601 WNVLDVRSFGPNDFLRSGVSVVDSLLCEQHDHGIPVSVTDMFCASWEPTAPSDI 660  
DB 601 WNVLDVRSFGPNDFLRSGVSVVDSLLCEQHDHGIPVSVTDMFCASWEPTAPSDI 660  
QY 661 CTAETGGIAAVFPGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLPPKDWIERNNK 720  
DB 661 CTAETGGIAAVFPGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLPPKDWIERNNK 720

RESULT 9  
US-09-991-163-231  
; Sequence 231, Application US/09991163  
; Patent No. US20020132253A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: F2730PIC17  
; CURRENT APPLICATION NUMBER: US/09/991,163  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
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; PRIOR APPLICATION NUMBER: 60/089440

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US-09-993-604-231  
Sequence 231, Application US/09993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Griffling, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC25  
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 3945; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C22
; CURRENT APPLICATION NUMBER: US/09/990,456
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787

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[illegible]

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39	PRIOR APPLICATION NUMBER: 60/090863
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41	PRIOR APPLICATION NUMBER: 60/091360
42	PRIOR FILING DATE: 1998-07-01
43	PRIOR APPLICATION NUMBER: 60/091478
44	PRIOR FILING DATE: 1998-07-02
45	PRIOR APPLICATION NUMBER: 60/091633
46	PRIOR FILING DATE: 1998-07-02
47	PRIOR APPLICATION NUMBER: 60/091544
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49	PRIOR APPLICATION NUMBER: 60/091519
50	PRIOR FILING DATE: 1998-07-02
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54	PRIOR FILING DATE: 1998-07-02
55	PRIOR APPLICATION NUMBER: 60/091978
56	PRIOR FILING DATE: 1998-07-07
57	PRIOR APPLICATION NUMBER: 60/091982
58	PRIOR FILING DATE: 1998-07-07
59	PRIOR APPLICATION NUMBER: 60/092182
60	PRIOR FILING DATE: 1998-07-09

	Query Match	100.0%;	Score 3945;	DB 9;	Length 720;	
	Best Local Similarity	100.0%;	Pred. No. 0;			
	Matches 720;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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Db	1	MELGCTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRCCBYDQIECVCPGKRE	60			
Qy	61	VVGTYTPCCRNEENECDSLHPGCTIFENCKSCRNGSWGTLDDFVYKGFYCAECRAGW	120			
Db	61	VVGTYTPCCRNEENECDSLHPGCTIFENCKSCRNGSWGTLDDFVYKGFYCAECRAGW	120			
Qy	121	YGGDCWRCCGVILRAPKGQILLESYPLNAHCWTHAKPGFVIQLRFVWLSLEFFPYMCQYD	180			



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 Qy 181 YVEVRDGNDRDQIIRKVCNGNERPAPISQISGSSHLVLFHSDGSKNFGFHAHYEEITACS 240  
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 Db 301 NGRHAKITGVVSPFCNNYSYVLSGNEKKTCCQNGEMSKQPCICACREPKISDLVRRRLV 360  
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 Qy 541 LOISAIILHPNDPILLDADIALKJLDKARISTRVQPICLAASRDISTSFQESHITVAG 600  
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 Qy 601 WNVLDVRSFGKNDTLRSVGVSVDLSLCEEHEDHGIPVSVTDNNMFCASWEPTAPSDI 660  
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RESULT 13

US-09-992-598-231  
 ; Sequence 231, Application US/09992598  
 ; Patent No. US20020160384A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Deenoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gertsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kijavin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2730P1C30  
 ; CURRENT APPLICATION NUMBER: US/09/992,598  
 ; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787  
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 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/065186  
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## RESULT 14

US-09-989-293A-231

Sequence 231, Application US/09989293A

Patent No. US20020177164A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Deenoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gertschen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tuma, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P2730PLC66

CURRENT FILING DATE: 2001-11-20

US/09/989,293A

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PRIOR FILING DATE: 1997-06-16

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PRIOR FILING DATE: 1997-11-24

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PRIOR FILING DATE: 1998-05-07

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1 PRIOR APPLICATION NUMBER: 60/090445  
1 PRIOR FILING DATE: 1998-06-24  
1 PRIOR APPLICATION NUMBER: 60/090472  
1 PRIOR FILING DATE: 1998-06-24  
1 PRIOR APPLICATION NUMBER: 60/090535  
1 PRIOR FILING DATE: 1998-06-24  
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1 PRIOR APPLICATION NUMBER: 60/090695  
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1 PRIOR APPLICATION NUMBER: 60/090696  
1 PRIOR FILING DATE: 1998-06-25  
1 PRIOR APPLICATION NUMBER: 60/090862  
1 PRIOR FILING DATE: 1998-06-26  
1 PRIOR APPLICATION NUMBER: 60/090863  
1 PRIOR FILING DATE: 1998-06-26  
1 PRIOR APPLICATION NUMBER: 60/091360  
1 PRIOR FILING DATE: 1998-07-01  
1 PRIOR APPLICATION NUMBER: 60/091478  
1 PRIOR FILING DATE: 1998-07-02  
1 PRIOR APPLICATION NUMBER: 60/091544  
1 PRIOR FILING DATE: 1998-07-01  
1 PRIOR APPLICATION NUMBER: 60/091519  
1 PRIOR FILING DATE: 1998-07-02  
1 PRIOR APPLICATION NUMBER: 60/091626  
1 PRIOR FILING DATE: 1998-07-02  
1 PRIOR APPLICATION NUMBER: 60/091633  
1 PRIOR FILING DATE: 1998-07-02  
1 PRIOR APPLICATION NUMBER: 60/091978  
1 PRIOR FILING DATE: 1998-07-07  
1 PRIOR APPLICATION NUMBER: 60/091982  
1 PRIOR FILING DATE: 1998-07-07  
1 PRIOR APPLICATION NUMBER: 60/092182  
1 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 9; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MELGCTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECEYDQIECVCPGKEE 60  
QY 61 VVGTYTPCCNEENECDSCLHPCGCTIFPENCASCRNCSGGTLLDDPYVKGFYCAECRAGW 120  
DB 61 VVGTYTPCCNEENECDSCLHPCGCTIFPENCASCRNCSGGTLLDDPYVKGFYCAECRAGW 120  
QY 121 YGGDCMRCQVLRAPKGOILLESYPLNAHCWTIHAKPGFVIQLRFVMLSLFEFDYMCQYD 180

DB 121 YGGDCMRCQVLRAPKGOILLESYPLNAHCWTIHAKPGFVIQLRFVMLSLFEFDYMCQYD 180  
QY 181 YVEVRDGNRDGOIILKRVCGNERPAPISIGSSLHLVLFHSDGSKNFDGFHAIYEITACS 240  
DB 181 YVEVRDGNRDGOIILKRVCGNERPAPISIGSSLHLVLFHSDGSKNFDGFHAIYEITACS 240  
QY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLLEERNCSDDPGPVNGYQKITGGPGLI 300  
DB 241 SSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLLEERNCSDDPGPVNGYQKITGGPGLI 300  
QY 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGWSEKQPICIKACREPKISDLVRRVL 360  
DB 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGWSEKQPICIKACREPKISDLVRRVL 360  
QY 361 PMQVOSRETPLHOLYSAAFSKQLQSAFTKAPALPFGDLPMGYOHLHTQLOVEICISPFYR 420  
DB 361 PMQVOSRETPLHOLYSAAFSKQLQSAFTKAPALPFGDLPMGYOHLHTQLOVEICISPFYR 420  
QY 421 RLGSRRCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQOAAIYRRTSGVHDGSL 480  
DB 421 RLGSRRCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQOAAIYRRTSGVHDGSL 480  
QY 481 HKGAWFLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVILGKFYRDDDRDEKTIQS 540  
DB 481 HKGAWFLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVILGKFYRDDDRDEKTIQS 540  
QY 541 LQISAILHPNYDPIILLDADIAILKLDKARISVQPICLAASRDLSSTQESHITVAG 600  
DB 541 LQISAILHPNYDPIILLDADIAILKLDKARISVQPICLAASRDLSSTQESHITVAG 600  
QY 601 WNVLADVRSPGKNDTLRSVVSVVDSLLCBEQHEHDGIPVSVTDNMFCASWEPTAPSDI 660  
DB 601 WNVLADVRSPGKNDTLRSVVSVVDSLLCBEQHEHDGIPVSVTDNMFCASWEPTAPSDI 660  
QY 661 CTAETGGIAAVSPGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFKVLPFKOWIERNNK 720  
DB 661 CTAETGGIAAVSPGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFKVLPFKOWIERNNK 720

RESULT 15  
US-09-989-735-231  
; Sequence 231, Application US/09989735  
; Publication No. US20020193299A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC61  
; CURRENT APPLICATION NUMBER: US/09/989,735

1	CURRENT FILING DATE: 2001-11-19	2	PRIOR APPLICATION NUMBER: 60/049787	3	PRIOR FILING DATE: 1998-06-12	4	PRIOR APPLICATION NUMBER: 60/089101
5	PRIOR FILING DATE: 1997-06-16	6	PRIOR APPLICATION NUMBER: 60/089440	7	PRIOR FILING DATE: 1998-06-16	8	PRIOR APPLICATION NUMBER: 60/089512
9	PRIOR FILING DATE: 1997-10-17	10	PRIOR APPLICATION NUMBER: 60/062250	11	PRIOR FILING DATE: 1998-06-16	12	PRIOR APPLICATION NUMBER: 60/089512
13	PRIOR FILING DATE: 1997-11-12	14	PRIOR APPLICATION NUMBER: 60/065186	15	PRIOR FILING DATE: 1998-06-16	16	PRIOR APPLICATION NUMBER: 60/089514
17	PRIOR FILING DATE: 1997-11-12	18	PRIOR APPLICATION NUMBER: 60/065311	19	PRIOR FILING DATE: 1998-06-16	20	PRIOR APPLICATION NUMBER: 60/089532
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29	PRIOR FILING DATE: 1998-02-25	30	PRIOR APPLICATION NUMBER: 60/078910	31	PRIOR FILING DATE: 1998-06-17	32	PRIOR APPLICATION NUMBER: 60/089599
33	PRIOR FILING DATE: 1998-03-20	34	PRIOR APPLICATION NUMBER: 60/083322	35	PRIOR FILING DATE: 1998-06-17	36	PRIOR APPLICATION NUMBER: 60/089600
37	PRIOR FILING DATE: 1998-04-28	38	PRIOR APPLICATION NUMBER: 60/084600	39	PRIOR FILING DATE: 1998-06-17	40	PRIOR APPLICATION NUMBER: 60/089653
41	PRIOR FILING DATE: 1998-05-07	42	PRIOR APPLICATION NUMBER: 60/087106	43	PRIOR FILING DATE: 1998-06-17	44	PRIOR APPLICATION NUMBER: 60/089801
45	PRIOR FILING DATE: 1998-05-28	46	PRIOR APPLICATION NUMBER: 60/087607	47	PRIOR FILING DATE: 1998-06-18	48	PRIOR APPLICATION NUMBER: 60/089907
49	PRIOR FILING DATE: 1998-06-02	50	PRIOR APPLICATION NUMBER: 60/087609	51	PRIOR FILING DATE: 1998-06-18	52	PRIOR APPLICATION NUMBER: 60/089908
53	PRIOR FILING DATE: 1998-06-02	54	PRIOR APPLICATION NUMBER: 60/087759	55	PRIOR FILING DATE: 1998-06-18	56	PRIOR APPLICATION NUMBER: 60/089947
57	PRIOR FILING DATE: 1998-06-02	58	PRIOR APPLICATION NUMBER: 60/087827	59	PRIOR FILING DATE: 1998-06-19	60	PRIOR APPLICATION NUMBER: 60/089948
61	PRIOR FILING DATE: 1998-06-03	62	PRIOR APPLICATION NUMBER: 60/088021	63	PRIOR FILING DATE: 1998-06-19	64	PRIOR APPLICATION NUMBER: 60/089952
65	PRIOR FILING DATE: 1998-06-04	66	PRIOR APPLICATION NUMBER: 60/088025	67	PRIOR FILING DATE: 1998-06-22	68	PRIOR APPLICATION NUMBER: 60/090246
69	PRIOR FILING DATE: 1998-06-04	70	PRIOR APPLICATION NUMBER: 60/088026	71	PRIOR FILING DATE: 1998-06-22	72	PRIOR APPLICATION NUMBER: 60/090252
73	PRIOR FILING DATE: 1998-06-04	74	PRIOR APPLICATION NUMBER: 60/088028	75	PRIOR FILING DATE: 1998-06-22	76	PRIOR APPLICATION NUMBER: 60/090254
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81	PRIOR FILING DATE: 1998-06-04	82	PRIOR APPLICATION NUMBER: 60/088030	83	PRIOR FILING DATE: 1998-06-23	84	PRIOR APPLICATION NUMBER: 60/090355
85	PRIOR FILING DATE: 1998-06-04	86	PRIOR APPLICATION NUMBER: 60/088033	87	PRIOR FILING DATE: 1998-06-23	88	PRIOR APPLICATION NUMBER: 60/090429
89	PRIOR FILING DATE: 1998-06-04	90	PRIOR APPLICATION NUMBER: 60/088326	91	PRIOR FILING DATE: 1998-06-24	92	PRIOR APPLICATION NUMBER: 60/090431
93	PRIOR FILING DATE: 1998-06-04	94	PRIOR APPLICATION NUMBER: 60/088167	95	PRIOR FILING DATE: 1998-06-24	96	PRIOR APPLICATION NUMBER: 60/090435
97	PRIOR FILING DATE: 1998-06-05	98	PRIOR APPLICATION NUMBER: 60/088202	99	PRIOR FILING DATE: 1998-06-24	100	PRIOR APPLICATION NUMBER: 60/090444
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105	PRIOR FILING DATE: 1998-06-05	106	PRIOR APPLICATION NUMBER: 60/088217	107	PRIOR FILING DATE: 1998-06-24	108	PRIOR APPLICATION NUMBER: 60/090472
109	PRIOR FILING DATE: 1998-06-05	110	PRIOR APPLICATION NUMBER: 60/088655	111	PRIOR FILING DATE: 1998-06-24	112	PRIOR APPLICATION NUMBER: 60/090535
113	PRIOR FILING DATE: 1998-06-09	114	PRIOR APPLICATION NUMBER: 60/088734	115	PRIOR FILING DATE: 1998-06-24	116	PRIOR APPLICATION NUMBER: 60/090540
117	PRIOR FILING DATE: 1998-06-10	118	PRIOR APPLICATION NUMBER: 60/088738	119	PRIOR FILING DATE: 1998-06-24	120	PRIOR APPLICATION NUMBER: 60/090542
121	PRIOR FILING DATE: 1998-06-10	122	PRIOR APPLICATION NUMBER: 60/088742	123	PRIOR FILING DATE: 1998-06-24	124	PRIOR APPLICATION NUMBER: 60/090557
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/ PRIOR FILING DATE: 1998-06-25  
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/ PRIOR FILING DATE: 1998-07-02  
/ PRIOR APPLICATION NUMBER: 60/091978  
/ PRIOR FILING DATE: 1998-07-07  
/ PRIOR APPLICATION NUMBER: 60/091982  
/ PRIOR FILING DATE: 1998-07-07  
/ PRIOR APPLICATION NUMBER: 60/092182  
/ PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 9; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MELCGCTQLGLTFLQLLLSL	PREYTVINEACPGAENIMCRECEYDQIECVCPGKRE	60
Db	1	MELCGCTQLGLTFLQLLLSL	PREYTVINEACPGAENIMCRECEYDQIECVCPGKRE	60
Qy	61	VVGTYTPCCRNEECDSCLIHPGCTIFENCKSCRN	SGWGTLLDDFVYKGFYCAECRAGW	120
Db	61	VVGTYTPCCRNEECDSCLIHPGCTIFENCKSCRN	SGWGTLLDDFVYKGFYCAECRAGW	120
Qy	121	YGGDCRRCQVLRAPKQIILLESYPLNHCETHAKP	GEVIOIRFVMLSLEEDYMCQYD	180
Db	121	YGGDCRRCQVLRAPKQIILLESYPLNHCETHAKP	GEVIOIRFVMLSLEEDYMCQYD	180
Qy	181	YVEVRDGNRDGOIIRKVCNERNPAPIQSIGSLHL	FLFHSDSGNKFDGFHAIYEEITACS	240
Db	181	YVEVRDGNRDGOIIRKVCNERNPAPIQSIGSLHL	FLFHSDSGNKFDGFHAIYEEITACS	240
Qy	241	SSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLL	ERNCSDFGPGVNGYQKITGGPGLI	300
Db	241	SSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLL	ERNCSDFGPGVNGYQKITGGPGLI	300
Qy	301	NGRHAKIGTVVSPFCNNSYVLSGNEKKTCCOENG	ESGKQPICIKACREPKISDLVRRRL	360
Db	301	NGRHAKIGTVVSPFCNNSYVLSGNEKKTCCOENG	ESGKQPICIKACREPKISDLVRRRL	360
Qy	361	PMOVQSRTEPLHOLYSAAFQKQLQSAPTKKPAL	PFQDLPMGYQHLHTQLQYECISPFYR	420
Db	361	PMOVQSRTEPLHOLYSAAFQKQLQSAPTKKPAL	PFQDLPMGYQHLHTQLQYECISPFYR	420
Qy	421	RLGSSRRTECLRTGKWSRAPSCIPICGKIENITAP	KTQGLRWPWQAAIYRRTSGVHDGSL	480
Db	421	RLGSSRRTECLRTGKWSRAPSCIPICGKIENITAP	KTQGLRWPWQAAIYRRTSGVHDGSL	480
Qy	481	HKGAWFLVCSGALNERTVVAACHVTDLGKVTMI	KTADLKVLRKPYRDDDRDEKTIQS	540
Db	481	HKGAWFLVCSGALNERTVVAACHVTDLGKVTMI	KTADLKVLRKPYRDDDRDEKTIQS	540
Qy	541	LQISAILHPNYDPIILLADIAILKLDKARISTRVQ	PICLAASRDLSFQESHITVAG	600
Db	541	LQISAILHPNYDPIILLADIAILKLDKARISTRVQ	PICLAASRDLSFQESHITVAG	600
Qy	601	WNVLADVRSPGFQNDTLRSVGVSVDLLCEEQHE	DHGIPVSVTDNMFCASWEPTAPSDI	660
Db	601	WNVLADVRSPGFQNDTLRSVGVSVDLLCEEQHE	DHGIPVSVTDNMFCASWEPTAPSDI	660
Qy	661	CTAETGGIAAVSPGRASPEPRWHLMLGVLVSN	SYDKTCSHRLSTAFTKVLPPKDWIERNMK	720

Db 661 CTAETGGIAAVSPGRASPEPRWHLMLGVLVSN  
SYDKTCSHRLSTAFTKVLPPKDWIERNMK 720  
Search completed: August 18, 2004, 16:22:31  
Job time : 54 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2004, 16:17:43 ; Search time 13 Seconds  
(without alignments)  
2883.886 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945

Sequence: 1 MELGCWTQLGLTFLQLLLIS.....LSTAFTKVLFPKDWIERNMK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 700 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	672	17.0	1019	1	LFC TACTR
2	665	16.9	1019	1	LFC CARRO
3	478	12.1	699	1	CRAR HUMAN
4	475	12.0	704	1	CRAR MOUSE
5	403.5	10.2	705	1	CIR HUMAN
6	400.5	10.2	686	1	MAS2 HUMAN
7	378.5	9.6	695	1	CASP MEGAU
8	334	8.5	688	1	CIS HUMAN
9	331.5	8.4	1019	1	ENTK HUMAN
10	330.5	8.4	1034	1	ENTK PIG
11	329.5	8.4	3565	1	CSM1 HUMAN
12	329	8.3	3564	1	CSM1 MOUSE
13	328	8.3	855	1	ST14 HUMAN
14	320	8.1	461	1	PRTC MOUSE
15	318	8.1	3487	1	CSM2 HUMAN
16	317.5	8.0	1035	1	ENTK BOVIN
17	315	8.0	444	1	FA7 RABIT
18	314.5	8.0	475	1	FA10 CHICK
19	314	8.0	855	1	ST14 MOUSE
20	310.5	7.9	461	1	PRTC HUMAN
21	309.5	7.8	811	1	TMS6 MOUSE
22	304	7.7	1069	1	ENTK MOUSE
23	302.5	7.7	446	1	FA7 MOUSE
24	297	7.5	459	1	PRTC PIG
25	296	7.5	458	1	PRTC RABIT
26	293.5	7.4	407	1	FA7 BOVIN
27	292	7.4	461	1	PRTC RAT
28	291	7.4	376	1	FA10 TROCA
29	287.5	7.3	811	1	TMS6 HUMAN
30	285.5	7.2	452	1	FA9 CANFA
31	283	7.2	376	1	FA10 HOPST
32	282	7.1	456	1	PRTC BOVIN
33	281	7.1	492	1	FA10 BOVIN

34	280.5	7.1	264	1	CTRL_HUMAN
35	280	7.1	562	1	TPA_HUMAN
36	278.5	7.1	466	1	FA7_HUMAN
37	278	7.0	488	1	FA10_HUMAN
38	278	7.0	1113	1	COR1_MOUSE
39	277	7.0	559	1	TPA_RAT
40	276.5	7.0	655	1	HGFA_HUMAN
41	274.5	7.0	625	1	THRB_BOVIN
42	274.5	7.0	3670	1	CSM3_HUMAN
43	273.5	6.9	566	1	TPA_BOVIN
44	273	6.9	2796	1	CSM3_MOUSE
45	271.5	6.9	244	1	KLK6_HUMAN
46	271	6.9	559	1	TPA_MOUSE
47	270	6.8	477	1	URT1_DESRO
48	270	6.8	490	1	FA10_RABIT
49	264.5	6.7	431	1	URTB_DESRO
50	264.5	6.7	618	1	THRB_MOUSE
51	264	6.7	553	1	HGFA_MOUSE
52	262.5	6.7	461	1	FA9_HUMAN
53	262.5	6.7	461	1	FA9_PANTR
54	262.5	6.7	1042	1	COR1_HUMAN
55	262	6.6	477	1	URT2_DESRO
56	261.5	6.6	442	1	UROK_PIG
57	261	6.6	431	1	UROK_HUMAN
58	261	6.6	433	1	UROK_BOVIN
59	259	6.6	245	1	CTRB_GADMO
60	259	6.6	416	1	FA9_BOVIN
61	258.5	6.6	786	1	STUB_DROME
62	258	6.5	433	1	UROK_PAPCY
63	254	6.4	617	1	THRB_RAT
64	250.5	6.3	347	1	HPT_RABIT
65	250	6.3	306	1	BSS4_MOUSE
66	249.5	6.3	875	1	NETR_HUMAN
67	248.5	6.3	459	1	FA9_MOUSE
68	248	6.3	263	1	CTRB_HUMAN
69	248	6.3	638	1	KAL_HUMAN
70	248	6.3	764	1	CFAB_PANTR
71	247.5	6.3	991	1	BMP1_MOUSE
72	247	6.3	275	1	TRYT_CANFA
73	247	6.3	764	1	CFAB_HUMAN
74	247	6.3	986	1	BMP1_HUMAN
75	246.5	6.2	347	1	HPT_ATSGE
76	246.5	6.2	622	1	THRB_HUMAN
77	246	6.2	812	1	PLMN_BOVIN
78	245	6.2	639	1	BMPH_STRPU
79	244	6.2	638	1	KAL_MOUSE
80	243	6.2	273	1	TRYT_SHEEP
81	241	6.1	346	1	HPT_MESAU
82	239.5	6.1	406	1	HPT_HUMAN
83	239	6.1	245	1	CTRA_BOVIN
84	239	6.1	436	1	HEPS_MOUSE
85	238	6.0	237	1	TRYP_ASTFL
86	238	6.0	263	1	CTR2_CANFA
87	238	6.0	275	1	TRYT_PIG
88	238	6.0	375	1	PCE_TACTR
89	237.5	6.0	810	1	PLMN_ERIEU
90	237	6.0	263	1	CTRB_RAT
91	236.5	6.0	274	1	MCT6_RAT
92	236.5	6.0	707	1	BMP1_XENLA
93	236	6.0	812	1	PLMN_MOUSE
94	235	6.0	270	1	TRYT_MERIN
95	235	6.0	1420	1	APOA_MACMU
96	234.5	5.9	453	1	TMS3_MOUSE
97	233.5	5.9	263	1	CTRA_GADMO
98	232	5.9	416	1	HEPS_RAT
99	232	5.9	638	1	KAL_RAT
100	231.5	5.9	269	1	EL2_BOVIN
101	229.5	5.8	329	1	HPT_CANFA
102	228.5	5.8	2531	1	NTY1_MOUSE
103	227.5	5.8	242	1	TRY1_SALSA
104	227.5	5.8	251	1	KLK6_HUMAN
105	227	5.8	324	1	TEST_MOUSE
106	226.5	5.7	238	1	TRY3_SALSA

P40313	homo sapien
P00750	homo sapien
P08709	homo sapien
P00742	homo sapien
Q92319	mus musculus
P19637	rattus norv
Q04756	homo sapien
P00735	bos taurus
Q28198	bos taurus
Q28198	bos taurus
Q80479	mus musculus
Q92876	homo sapien
P11214	mus musculus
P98119	desmodus ro
O19045	oryctolagus
P98121	desmodus ro
P19221	mus musculus
Q9098	mus musculus
P00740	homo sapien
Q95nd7	pan troglod
Q9y5q5	homo sapien
P15638	desmodus ro
P04185	sus scrofa
P00749	homo sapien
Q05589	bos taurus
P80646	gadus morhu
P00741	bos taurus
Q05319	drosofila
P16237	papio cynoc
P18292	rattus norv
P19007	oryctolagus
Q9er10	mus musculus
P56730	homo sapien
P16294	mus musculus
P17538	homo sapien
P03952	homo sapien
Q864w0	pan troglod
P98083	mus musculus
P15944	canis fami
P00751	homo sapien
P50417	ateles geof
P00734	homo sapien
P06868	bos taurus
P98069	strongyloce
P26262	mus musculus
Q9xm2	ovis aries
O35086	mesocricetu
P00738	homo sapien
P00766	bos taurus
O35453	mus musculus
P00765	astacus flu
P04813	canis fami
Q9n2d1	sus scrofa
P21902	tachyples
Q29485	erinaeus e
P07338	rattus norv
P50343	rattus norv
P98070	xenopus lae
P20918	mus musculus
P50342	meriones un
P14417	macaca mula
Q8k10	mus musculus
P47796	gadus morhu
Q05511	rattus norv
P14272	rattus norv
Q29461	bos taurus
P19006	canis fami
Q01705	mus musculus
P35031	salmo salar
Q9p0g3	homo sapien
Q9jh17	mus musculus
P35033	salmo salar



107	226.5	5.7	761	1	NETR_MOUSE	O08762 mus musculus	180	205.5	5.2	347	1	HPT_RAT	P06866 rattus norv
108	226.5	5.7	1429	1	ATRN_MOUSE	O75882 mus sapien	181	205.5	5.2	492	1	TMS2_HUMAN	O15393 homo sapien
109	226	5.7	394	1	URTG_DESRO	P49150 desmodus ro	182	205	5.2	256	1	HYBP_HYPLI	P35588 hypodermis 1
110	226	5.7	437	1	TMS4_HUMAN	Q0984 homo sapien	183	204.5	5.2	246	1	TRY2_RAT	P30763 rattus norv
111	226	5.7	625	1	FALL_HUMAN	Q0351 homo sapien	184	204.5	5.2	256	1	TRYC_MANSE	P35047 manduca sex
112	225.5	5.7	347	1	HPT_PIG	Q08987 sus scrofa	185	204.5	5.2	2470	1	NTC2_MOUSE	Q35516 mus musculus
113	225.5	5.7	457	1	TMS5_HUMAN	Q09383 homo sapien	186	204	5.2	260	1	KLK8_HUMAN	O60259 homo sapien
114	225	5.7	615	1	FALL2_HUMAN	P00748 homo sapien	187	203.5	5.2	247	1	TRY2_HUMAN	P07478 homo sapien
115	224.5	5.7	271	1	EL2_RAT	P00774 rattus norv	188	203.5	5.2	263	1	CFAD_RAT	P32038 rattus norv
116	224.5	5.7	274	1	TRY1_ANOGA	P35035 anopheles g	189	203.5	5.2	285	1	FA9_CAVPO	P16295 cavia porce
117	224.5	5.7	347	1	HPT_MOUSE	O61646 mus musculus	190	202	5.1	241	1	TRY1_GADMO	P16049 gadus morhu
118	224.5	5.7	1022	1	TLD_BRARE	O57460 brachydanio	191	202	5.1	246	1	KLK_PIG	P00752 sus scrofa
119	224	5.7	245	1	CTRE_BOVIN	P00767 bos taurus	192	202	5.1	2321	1	NTC3_HUMAN	Q0847 homo sapien
120	224	5.7	490	1	TMS2_MOUSE	Q931q8 mus musculus	193	201.5	5.1	246	1	TRY2_MOUSE	P07146 mus musculus
121	223.5	5.7	348	1	HPT_HUMAN	P00739 homo sapien	194	201.5	5.1	256	1	KLK_HUMAN	Q92825 homo sapien
122	223.5	5.7	1242	1	JAG1_BRARE	Q09057 brachydanio	195	200.5	5.1	231	1	TRYP_PIG	P00761 sus scrofa
123	223	5.7	454	1	TMS3_HUMAN	P57727 homo sapien	196	200.5	5.1	752	1	CO2_HUMAN	P06681 homo sapien
124	222.5	5.6	417	1	HEPS_HUMAN	P05981 homo sapien	197	200.5	5.1	810	1	PLMN_MACMU	P12545 macaca mula
125	222.5	5.6	434	1	UROK_CHICK	P15120 gallus gall	198	200	5.1	385	1	TSS0_HUMAN	Q9138 homo sapien
126	222.5	5.6	455	1	TMS5_MOUSE	Q98r04 mus musculus	199	199.5	5.1	247	1	TRY3_RAT	P08426 rattus norv
127	222.5	5.6	790	1	EL2_PIG	P06867 sus scrofa	200	199.5	5.1	257	1	KLK1_MACFA	Q07276 macaca fasc
128	222	5.6	269	1	EL2_PIG	P08419 sus scrofa	201	199.5	5.1	275	1	TRY3_ANOGA	P35037 anopheles g
129	222	5.6	275	1	TRY2_HUMAN	P20231 homo sapien	202	199.5	5.1	2556	1	NTC1_HUMAN	P46531 homo sapien
130	222	5.6	275	1	TRYA_HUMAN	P15157 homo sapien	203	198.5	5.0	243	1	TRY1_BOVIN	P00760 bos taurus
131	222	5.6	422	1	DE51_HUMAN	Q9152 homo sapien	204	198.5	5.0	311	1	TRYG_MOUSE	Q9217 mus musculus
132	221.5	5.6	2531	1	NTC1_RAT	Q07008 rattus norv	205	198	5.0	235	1	TRYD_HUMAN	Q9b2j3 homo sapien
133	221	5.6	231	1	TRY2_SALSA	P35032 salmo salar	206	198	5.0	259	1	DEP3_DERPA	P49275 dermatophag
134	221	5.6	268	1	CLCR_RAT	P55091 rattus norv	207	198	5.0	760	1	CO2_MOUSE	P21180 mus musculus
135	221	5.6	273	1	MCT7_RAT	P27435 rattus norv	208	198	5.0	1024	1	SZ6L_HUMAN	Q9b1h1 homo sapien
136	220.5	5.6	1057	1	TLD_DROME	P25723 drosophila	209	197.5	5.0	226	1	COGS_UCAPU	P00771 uca pugilat
137	220	5.6	275	1	TRB1_HUMAN	Q15661 homo sapien	210	197.5	5.0	248	1	KLKC_HUMAN	Q9ukr0 homo sapien
138	219.5	5.6	244	1	TRY2_XENLA	P70059 xenopus lae	211	197	5.0	338	1	PLMN_HORSE	P80010 equus cabal
139	219.5	5.6	271	1	EL2_MOUSE	P05208 mus musculus	212	196.5	5.0	269	1	ELB2_HUMAN	P80218 homo sapien
140	219.5	5.6	347	1	HPT_MOUSE	Q60574 mus caroli	213	196.5	5.0	570	1	FEB3_STRPU	P49013 strongyloce
141	219.5	5.6	761	1	CFAB_MOUSE	P04186 mus musculus	214	196.5	5.0	2524	1	NOTC_XENLA	P21783 xenopus lae
142	219	5.6	343	1	PS88_HUMAN	Q16651 homo sapien	215	196	5.0	270	1	EL3B_HUMAN	P08861 homo sapien
143	218.5	5.5	435	1	TMS4_MOUSE	Q8vca5 mus musculus	216	195.5	5.0	257	1	GRAM_HUMAN	P51124 homo sapien
144	217	5.5	239	1	KLX2_CAVPO	P12323 cavia porce	217	195.5	5.0	271	1	FA9_PIG	P16293 sus scrofa
145	217	5.5	268	1	CLCR_HUMAN	Q99895 homo sapien	218	195.5	5.0	752	1	CO2_PANTR	Q86q74 pan troglod
146	217	5.5	273	1	MCT7_MOUSE	Q02844 mus musculus	219	195.5	5.0	2471	1	NTC2_HUMAN	Q04721 mus sapien
147	217	5.5	603	1	FALL2_CAVPO	Q04962 cavia porce	220	195	4.9	261	1	KLK6_MOUSE	P15947 mus musculus
148	217	5.5	2703	1	NOTC_DROME	P07207 drosophila	221	195	4.9	432	1	UROK_RAT	P29598 rattus norv
149	216.5	5.5	2616	1	NDL_DROME	P98159 drosophila	222	194.5	4.9	246	1	TRY1_RAT	P00762 rattus norv
150	216	5.5	1218	1	JAG1_MOUSE	Q98xx0 mus musculus	223	194.5	4.9	343	1	PLMN_SHEEP	P81286 ovis aries
151	215.5	5.5	248	1	TRY2_CANFA	P06872 canis famli	224	194	4.9	259	1	CFAD_PIG	P51779 sus scrofa
152	215.5	5.5	247	1	TRY3_CHICK	Q90629 gallus gall	225	194	4.9	267	1	TRY7_ANOGA	P35041 anopheles g
153	215.5	5.5	317	1	BS84_HUMAN	Q99zn4 homo sapien	226	193.5	4.9	2471	1	NTC2_RAT	Q9gw30 rattus norv
154	215	5.4	241	1	PLMN_GADMO	Q91041 gadus morhu	227	193	4.9	253	1	CAC3_BOVIN	P05805 bos taurus
155	215	5.4	810	1	TRYX_HUMAN	P00747 homo sapien	228	192.5	4.9	256	1	TRYP_CHOFU	P35042 choristoneu
156	214.5	5.4	247	1	TRY2_BOVIN	Q29463 bos taurus	229	191.5	4.9	247	1	TRY1_HUMAN	P07477 homo sapien
157	214.5	5.4	593	1	FALL2_BOVIN	P98140 bos taurus	230	191.5	4.9	830	1	LEM3_HUMAN	P16109 homo sapien
158	214.5	5.4	1428	1	ATRN_MOUSE	Q9wa60 mus musculus	231	191	4.8	254	1	KLK4_HUMAN	Q9y5k2 homo sapien
159	214	5.4	342	1	PS88_RAT	Q98e87 rattus norv	232	190.5	4.8	768	1	LEM3_MOUSE	Q01102 mus musculus
160	212.5	5.4	250	1	KLK8_HUMAN	Q9ubx7 homo sapien	233	190.5	4.8	1064	1	FEB1_STRPU	P10079 strongyloce
161	212	5.4	260	1	NRPN_MOUSE	Q61955 mus musculus	234	189	4.8	246	1	TRYB_RAT	P32822 rattus norv
162	211.5	5.4	418	1	HATT_HUMAN	Q60235 homo sapien	235	189	4.8	247	1	TRY4_RAT	P12788 rattus norv
163	211	5.3	276	1	MCT6_MOUSE	P21845 mus musculus	236	189	4.8	253	1	KLK7_HUMAN	P49862 homo sapien
164	211	5.3	1218	1	JAG1_HUMAN	P78504 homo sapien	237	189	4.8	646	1	LEM3_BOVIN	P42201 bos taurus
165	210.5	5.3	342	1	TRYP_STMVI	Q95048 simulum vi	238	188.5	4.8	282	1	FA9_RAT	P26296 rattus norv
166	210.5	5.3	247	1	PS88_MOUSE	Q95ed1 mus musculus	239	188.5	4.8	290	1	PR27_HUMAN	Q9bqr3 homo sapien
167	210.5	5.3	1219	1	JAG1_RAT	Q63722 rattus norv	240	188.5	4.8	714	1	DLL1_RAT	P97677 rattus norv
168	210	5.3	2437	1	NTC1_BRARE	P46530 brachydanio	241	188	4.8	253	1	CFAD_HUMAN	P00746 homo sapien
169	209.5	5.3	347	1	HPT_MUSSA	Q62558 mus saxicol	242	188	4.8	263	1	KLK8_PRANA	P32824 praomys nat
170	209	5.3	433	1	UROK_MOUSE	P06869 mus musculus	243	188	4.8	333	1	PLMN_CANFA	P80009 canis famli
171	207.5	5.3	256	1	TRYB_MANSE	P35046 manduca sex	244	187.5	4.8	304	1	TRY3_HUMAN	P35030 homo sapien
172	207.5	5.3	268	1	EL2A_HUMAN	P08217 homo sapien	245	187	4.7	246	1	TRYA_RAT	P32821 rattus norv
173	207	5.2	238	1	TRY5_ABDAA	P29787 aedes aegypt	246	187	4.7	271	1	CTR1_PENYA	Q00871 penaeus van
174	207	5.2	260	1	NRPN_RAT	Q88780 rattus norv	247	185.5	4.7	261	1	DER3_DERPT	P39675 dermatophag
175	206.5	5.2	256	1	TRYA_MANSE	P35045 manduca sex	248	185.5	4.7	711	1	HGFL_HUMAN	P26927 homo sapien
176	206.5	5.2	321	1	TRYG_HUMAN	Q9nr12 homo sapien	249	185.5	4.7	928	1	NRP1_XENLA	P28824 xenopus lae
177	206	5.2	430	1	SNAP_DROME	P05049 drosophila	250	185	4.7	256	1	KLK4_MOUSE	P00757 mus musculus
178	206	5.2	4548	1	APOA_HUMAN	P08519 homo sapien	251	185	4.7	258	1	KLK1_PAPHA	Q28773 papio hamad
179	205.5	5.2	269	1	TRYM_CANFA	P19236 canis famli	252	184.5	4.7	1213	1	JAG3_BRARE	Q90y54 brachydanio

253	184	4.7	314	1	TEST HUMAN	Q9y6m0 homo sapien	326	172	4.4	242	1	FIBC_LIMRU	P83298 lumbricus r
254	183	4.6	161	1	PRTC_MACMU	Q28506 macaca mula	327	172	4.4	254	1	TRYP_SARBU	P51588 sarcophaga
255	183	4.6	261	1	KLK1_RAT	P00758 rattus norv	328	172	4.4	260	1	ESTA_CANFA	P09582 canis fami
256	183	4.6	392	1	EAST_DROME	P13582 drosophila	329	172	4.4	261	1	KLK8_MOUSE	P07628 mus musculu
257	182.5	4.6	248	1	TRV1_CHICK	Q90627 gallus gall	330	172	4.4	262	1	TRV1_DROME	P42278 drosophila
258	182.5	4.6	468	1	PCO1_RAT	Q08628 rattus norv	331	172	4.4	415	1	ACRO_PIG	P08001 sus scrofa
259	182.5	4.6	484	1	LLM1_MOUSE	P98110 sus scrofa	332	172	4.4	1427	1	JAG2_MOUSE	Q9qve5 mus musculu
260	182.5	4.6	722	1	DLK1_MOUSE	Q61483 mus musculu	333	171.5	4.3	262	1	KLK1_HUMAN	P06870 homo sapien
261	182	4.6	484	1	KLK5_MOUSE	P15945 mus musculu	334	171	4.3	260	1	GRAA_MOUSE	P11032 mus musculu
262	182	4.6	261	1	TRV1_DROER	P54628 drosophila	335	171	4.3	266	1	EL1_RAT	P00773 rattus norv
263	182	4.6	1238	1	JAG2_HUMAN	Q9y219 homo sapien	336	171	4.3	273	1	TRV6_ANOGA	P35040 anopheles g
264	181.5	4.6	247	1	GRAB_MOUSE	Q04187 mus musculu	337	171	4.3	277	1	KLK3_HUMAN	Q9ukr3 homo sapien
265	181.5	4.6	258	1	GRAM_RAT	Q03238 rattus norv	338	171	4.3	611	1	LEM2_CANFA	P33730 canis fami
266	181.5	4.6	437	1	ACRO_RAT	P00756 mus musculu	339	170	4.3	2339	1	CRB_DROME	P10040 drosophila
267	181	4.6	261	1	KLK3_MOUSE	P00756 mus musculu	340	170	4.3	245	1	MCT1_SHEEP	P80931 ovis aries
268	181	4.6	1271	1	YC81_CASEL	Q19981 caenorhabdi	341	170	4.3	248	1	GRL2_RAT	P06606 rattus norv
269	180.5	4.6	248	1	TRV2_CHICK	Q06628 gallus gall	342	170	4.3	256	1	TRVE_DROME	P35005 drosophila
270	180.5	4.6	261	1	EUM3_EURMA	O97370 euroglyphus	343	169.5	4.3	251	1	MCT3_SHEEP	Q46683 ovis aries
271	180.5	4.6	275	1	FA9_RABIT	P16292 oryctolagus	344	169.5	4.3	261	1	KLK3_MACMU	P33619 macaca mula
272	180.5	4.6	436	1	ACRO_MOUSE	P23578 mus musculu	345	169	4.3	214	1	ACH2_LONAC	P23605 lonomia ach
273	180	4.6	157	1	PRTC_HORSE	Q28380 equus cabal	346	169	4.3	246	1	MCT1_MERUN	P50340 meriones un
274	180	4.6	261	1	KLKB_MOUSE	P15946 mus musculu	347	169	4.3	259	1	KLKC_RAT	P36376 rattus norv
275	180	4.6	275	1	TRV4_ANOGA	P35038 anopheles g	348	168.5	4.3	248	1	GRL1_RAT	Q06605 rattus norv
276	179.5	4.6	243	1	TRV1_XENLA	P39798 xenopus lae	349	168	4.3	262	1	TRVU_DROME	P42279 drosophila
277	179.5	4.6	250	1	KLK9_HUMAN	Q9ukq9 homo sapien	350	168	4.3	923	1	NRP1_HUMAN	O14786 homo sapien
278	179.5	4.6	258	1	TRVU_DROER	P54629 drosophila	351	167.5	4.2	261	1	KLK3_HUMAN	P07288 homo sapien
279	179.5	4.6	259	1	CFAD_MOUSE	P03953 mus musculu	352	167.5	4.2	383	1	DLK_HUMAN	P80370 homo sapien
280	179.5	4.6	274	1	FA9_SHEEP	P16291 ovis aries	353	167	4.2	247	1	MCT8_MOUSE	P43430 mus musculu
281	179	4.5	253	1	TRV6_DROER	P54625 drosophila	354	166.5	4.2	723	1	DLK1_HUMAN	O00548 homo sapien
282	179	4.5	266	1	EL1_PIG	P00772 sus scrofa	355	166.5	4.2	769	1	LEM3_SHEEP	P98109 ovis aries
283	179	4.5	280	1	TRV2_DROME	P42280 drosophila	356	166	4.2	157	1	PRTC_FELCA	Q28412 felis silve
284	179	4.5	549	1	LEM2_RAT	P98105 rattus norv	357	166	4.2	597	1	BP10_PARLI	P42674 paracentrot
285	179	4.5	612	1	LEM2_MOUSE	Q06690 mus musculu	358	165.5	4.2	616	1	DEP6_STRPU	P98068 strongyloce
286	178.5	4.5	255	1	TRV4_LUCUC	P35044 lucilia cup	359	164.5	4.2	279	1	SEAF_DRFPA	P49278 dermatophag
287	178.5	4.5	468	1	PCO1_MOUSE	Q61398 mus musculu	360	164.5	4.2	1231	1	CFAH_HUMAN	P08603 homo sapien
288	178.5	4.5	922	1	NRP1_RAT	Q9qvi9 rattus norv	361	164	4.2	2871	1	FBN1_MOUSE	O61554 mus musculu
289	178.5	4.5	923	1	NRP1_MOUSE	P97333 mus musculu	362	163.5	4.1	252	1	TRV1_DROME	P52905 drosophila
290	178	4.5	157	1	PRTC_CANFA	Q28278 canis fami	363	163.5	4.1	859	1	ST7_HUMAN	Q9y561 homo sapien
291	178	4.5	253	1	TRVU_DROER	P54626 drosophila	364	162.5	4.1	253	1	TRYB_DROME	P98065 oryctolagus
292	178	4.5	528	1	GD_DROME	O62589 drosophila	365	162	4.1	253	1	TRYB_DROME	P35004 drosophila
293	177.5	4.5	248	1	NKPL1_RAT	P18291 rattus norv	366	162	4.1	261	1	KLK2_MOUSE	P36369 mus musculu
294	177.5	4.5	1964	1	NTC4_MOUSE	P31695 mus musculu	367	161.5	4.1	226	1	DDN1_BOVIN	P80219 bos taurus
295	177	4.5	271	1	CRT2_PENVA	P36178 penaeus van	368	161.5	4.1	248	1	GRAE_MOUSE	P08884 mus musculu
296	177	4.5	473	1	FP2_MYTGA	Q25464 mytilus gal	369	161.5	4.1	250	1	TRYP_PLEPL	P35034 pleuronecte
297	176.5	4.5	925	1	NRP2_RAT	Q35276 rattus norv	370	161.5	4.1	261	1	CATG_MOUSE	P28293 mus musculu
298	176.5	4.5	931	1	NRP2_MOUSE	Q35375 mus musculu	371	161.5	4.1	1025	1	CR2_MOUSE	P19070 mus musculu
299	176.5	4.5	2003	1	NTC4_HUMAN	Q99466 homo sapien	372	161	4.1	293	1	KLK5_HUMAN	Q9y337 homo sapien
300	176	4.5	261	1	KLK7_RAT	P36373 rattus norv	373	160.5	4.1	661	1	P13B_HUMAN	P05160 homo sapien
301	176	4.5	261	1	KLK9_MOUSE	P15949 mus musculu	374	160	4.1	262	1	GRAA_HUMAN	P12544 homo sapien
302	176	4.5	264	1	VDP_BOMMO	Q07943 bombyx mori	375	160	4.1	610	1	LEM2_HORSE	Q95191 equus cabal
303	176	4.5	270	1	EL3A_HUMAN	P09093 homo sapien	376	160	4.1	2871	1	FBN1_HUMAN	P35555 homo sapien
304	176	4.5	2318	1	NTC3_MOUSE	Q61982 mus musculu	377	159.5	4.0	248	1	GRAD_MOUSE	P11033 mus musculu
305	176	4.5	2319	1	NTC3_RAT	Q9r172 rattus norv	378	159	4.0	244	1	KLKA_RAT	P36375 rattus norv
306	175.5	4.4	274	1	TRV5_ANOGA	P35039 anopheles g	379	159	4.0	261	1	KLKG_MOUSE	P04071 mus musculu
307	175	4.4	421	1	ACRO_HUMAN	P10323 homo sapien	380	159	4.0	2907	1	PNB2_MOUSE	O61555 mus musculu
308	175	4.4	931	1	NRP2_HUMAN	Q06462 homo sapien	381	159	4.0	2911	1	PNB2_HUMAN	P35556 homo sapien
309	174.5	4.4	246	1	TRV1_CANFA	P06871 canis fami	382	158.5	4.0	247	1	MCT3_RAT	P50339 rattus norv
310	174	4.4	258	1	EL1_HUMAN	Q9unil homo sapien	383	158.5	4.0	256	1	HYPA_HYPLI	P35587 hypoderma l
311	174	4.4	259	1	KLK1_MOUSE	P15948 mus musculu	384	158.5	4.0	385	1	DLK_MOUSE	Q09163 mus musculu
312	174	4.4	261	1	KLK1_MOUSE	P00755 mus musculu	385	158.5	4.0	833	1	DLK_MOUSE	P10041 drosophila
313	174	4.4	266	1	EL1_BOVIN	Q28153 bos taurus	386	158	4.0	256	1	TRVE_DROER	P54627 drosophila
314	174	4.4	1295	1	GLP1_CASEL	P13508 caenorhabdi	387	158	4.0	522	1	TOH2_CASEL	P98067 caenorhabdi
315	173.5	4.4	260	1	COGS_HYPLI	P08897 hypoderma l	388	157.5	4.0	259	1	VSPI_VIPLE	Q9pt41 vipera lebe
316	173.5	4.4	914	1	TRP1_CHICK	P79795 gallus gall	389	157	4.0	281	1	TRYZ_DROER	P54630 drosophila
317	173	4.4	229	1	TRYP_SQUAC	P00764 squallus aca	390	157	4.0	610	1	LEM2_HUMAN	P16581 homo sapien
318	173	4.4	248	1	MCT8_RAT	P97594 rattus norv	391	157	4.0	686	1	DLK4_MOUSE	Q9ji71 mus musculu
319	173	4.4	768	1	LEM3_RAT	P98106 rattus norv	392	156.5	4.0	275	1	TSG6_MOUSE	O08859 mus musculu
320	172.5	4.4	248	1	GRAC_MOUSE	P08882 mus musculu	393	156.5	4.0	1429	1	LI12_CASEL	P14585 caenorhabdi
321	172.5	4.4	277	1	TRV2_ANOGA	P08882 mus musculu	394	156.5	4.0	3718	1	LMAS_MOUSE	Q61001 mus musculu
322	172.5	4.4	431	1	ACRO_RABIT	P48038 oryctolagus g	395	156	4.0	253	1	TRYD_DROME	P42276 drosophila
323	172.5	4.4	449	1	PCO1_HUMAN	Q15113 homo sapien	396	156	4.0	259	1	KLK2_RAT	P00759 rattus norv
324	172.5	4.4	1202	1	JAG2_HUMAN	P97607 rattus norv	397	156	4.0	261	1	KLK2_HUMAN	P20151 homo sapien
325	172	4.4	157	1	PRTC_CAPHI	Q28315 capra hircu	398	155.5	3.9	213	1	ACHI_LONAC	P23604 lonomia ach

399	155.5	3.9	485	1	LEM2_BOVIN	P98107 bos taurus	472	140	3.5	260	1	VSP4_AGRAC	Q918w9 agkistrodon
400	155	3.9	253	1	TRYG_DROME	P43277 drosophila	473	140	3.5	396	1	PRTZ_BOVIN	P00744 bos taurus
401	155	3.9	1033	1	CR2_HUMAN	P20023 homo sapien	474	140	3.5	4590	1	FATH_HUMAN	Q14517 homo sapien
402	155	3.9	1376	1	CRBH_HUMAN	P82279 homo sapien	475	139.5	3.5	256	1	TRP3_PSEAM	Q93267 pseudopleur
403	154.5	3.9	252	1	C4BB_HUMAN	P20851 homo sapien	476	139.5	3.5	258	1	CTR2_ANOGA	Q17025 anopheles g
404	154	3.9	248	1	TRYP_FUSOX	P35049 fusarium ox	477	139.5	3.5	407	1	DAF2_MOUSE	Q61476 mus musculus
405	154	3.9	685	1	CFAH_BOVIN	Q28085 bos taurus	478	139.5	3.5	514	1	UVS2_XENLA	P42664 xenopus lae
406	154	3.9	2039	1	CR1_HUMAN	P17927 homo sapien	479	139	3.5	464	1	SRPX_HUMAN	P23946 homo sapien
407	154	3.9	2871	1	FBNI_PIG	Q9tv36 sus scrofa	480	138.5	3.5	247	1	MCT1_MOUSE	Q08879 mus musculus
408	153.5	3.9	260	1	MCT1_RAT	P09650 rattus norv	481	138.5	3.5	705	1	FBL1_MOUSE	Q09101 drosophila
409	153.5	3.9	551	1	LEM2_RABIT	P27113 oryctolagus	482	138	3.5	958	1	HIG_DROME	Q24664 saccharopol
410	153.5	3.9	1866	1	LMB1_MOUSE	P03469 mus musculus	483	137	3.5	227	1	TRYB_SACER	Q63515 rattus norv
411	153	3.9	151	1	CFAB_PIG	P03710 sus scrofa	484	137	3.5	258	1	C4BB_RAT	P20836 rattus norv
412	153	3.9	254	1	TRY3_AEDAE	P29786 aedes aegypt	485	137	3.5	372	1	LEM1_RAT	P52195 papio hamad
413	153	3.9	2871	1	FBNI_BOVIN	P98133 bos taurus	486	136.5	3.5	247	1	MCT1_PAPHA	P00770 rattus norv
414	152.5	3.9	248	1	GRAF_MOUSE	P08883 mus musculus	487	136.5	3.5	247	1	MCT2_RAT	Q9nyj7 homo sapien
415	152.5	3.9	264	1	GRAB_HUMAN	P49863 homo sapien	488	136.5	3.5	618	1	DLL3_HUMAN	P02749 homo sapien
416	152.5	3.9	400	1	PRTZ_HUMAN	P22891 homo sapien	489	136	3.4	345	1	APCH_HUMAN	Q01016 herpesvirus
417	152	3.9	247	1	GRAB_HUMAN	P10144 h granzyme	490	136	3.4	360	1	CCPH_HSVSA	P02468 mus musculus
418	151.5	3.8	261	1	KLK8_RAT	P36374 rattus norv	491	136	3.4	1607	1	LMG1_MOUSE	P08607 mus musculus
419	151.5	3.8	716	1	HGFL_MOUSE	P26928 mus musculus	492	135.5	3.4	469	1	C4BP_MOUSE	O42182 brachydanio
420	151	3.8	249	1	MCT1_CANFA	P21842 canis famli	493	135	3.4	681	1	FBL1_BRARE	P34576 caenorhabdi
421	151	3.8	261	1	KLK6_MOUSE	P36368 mus musculus	494	135	3.4	3767	1	MUA3_CABEL	Q94813 homo sapien
422	150.5	3.8	277	1	TS66_HUMAN	P98066 homo sapien	495	134.5	3.4	1529	1	SLT2_HUMAN	P81661 bothrops ja
423	150.5	3.8	685	1	DLA4_HUMAN	Q9nr61 homo sapien	496	134	3.4	232	1	VSPA_BOTJA	Q35161 mus musculus
424	150	3.8	263	1	VCP_VACCV	P10998 vaccinia vi	497	134	3.4	3034	1	CUR1_MOUSE	P08174 homo sapien
425	150	3.8	267	1	ELNE_HUMAN	P08246 homo sapien	498	133.5	3.4	381	1	DAF_HUMAN	O13062 trimeresuru
426	150	3.8	276	1	KLKA_HUMAN	O43240 homo sapien	499	133	3.4	257	1	VSPC_TRIGA	Q62919 rattus norv
427	150	3.8	703	1	FBL1_HUMAN	P23142 homo sapien	500	133	3.4	810	1	NEL1_RAT	Q95180 pan troglod
428	150	3.8	3712	1	LMA_DROME	Q00174 drosophila	501	132.5	3.4	247	1	MCT1_WACFA	Q95198 macaca mula
429	149.5	3.8	236	1	VSPA_DABRU	P18964 daboia ruse	502	132.5	3.4	260	1	VSP1_AGRAC	Q28768 papio hamad
430	149.5	3.8	259	1	TRYP_STRGR	P00775 streptomyce	503	132	3.3	246	1	MCTX_MOUSE	Q00356 mus musculus
431	149.5	3.8	260	1	VSPB_TRIGA	O13061 trimeresuru	504	132	3.3	345	1	AFOP_PANTR	Q95180 pan troglod
432	149	3.8	216	1	CTR2_VESOR	P00768 vespa orien	505	132	3.3	372	1	LEM1_MACNU	Q28768 papio hamad
433	149	3.8	1408	1	SERR_DROME	P18168 drosophila	506	132	3.3	372	1	LEM1_PAPHA	Q60401 cavia porce
434	148.5	3.8	271	1	S24D_ANOGA	Q17004 anopheles g	507	132	3.3	558	1	C4BP_RAT	P55067 rattus norv
435	148	3.8	218	1	CTR2_VESCR	P00769 vespa crabr	508	132	3.3	830	1	SREC_HUMAN	Q14162 homo sapien
436	148	3.8	464	1	SRFX_RAT	Q63769 rattus norv	509	132	3.3	2109	1	PGCA_CHICK	P07898 gallus gall
437	148	3.8	668	1	F13B_MOUSE	Q07968 mus musculus	510	131.5	3.3	263	1	GRAB_MOUSE	Q35205 mus musculus
438	148	3.8	1504	1	SLIT_DROME	P24014 drosophila	511	131.5	3.3	810	1	NEL1_HUMAN	Q92832 homo sapien
439	147.5	3.7	244	1	MCT2_MOUSE	P15119 mus musculus	512	131.5	3.3	1268	1	PCGN_MOUSE	P55066 mus musculus
440	147.5	3.7	1786	1	LMB1_HUMAN	P07942 homo sapien	513	130.5	3.3	507	1	DAF_CAVPO	Q60401 cavia porce
441	147.5	3.7	3695	1	LMA5_HUMAN	O15230 homo sapien	514	130.5	3.3	1257	1	PCGN_RAT	P55067 rattus norv
442	147.5	3.7	4391	1	PGBM_HUMAN	P98160 homo sapien	515	130.5	3.3	3672	1	LM2_CABEL	Q21313 caenorhabdi
443	147	3.7	259	1	KLK9_RAT	P07647 rattus norv	516	130	3.3	258	1	VSP3_TRIGA	Q13063 trimeresuru
444	147	3.7	262	1	VSP1_AGRCA	Q91053 agkistrodon	517	130	3.3	390	1	DAF1_MOUSE	Q61475 mus musculus
445	147	3.7	1535	1	LM11_CABEL	O18823 caenorhabdi	518	130	3.3	592	1	DLL3_MOUSE	O88516 mus musculus
446	147	3.7	3084	1	LM1_MOUSE	P19137 mus musculus	519	129.5	3.3	246	1	MCT9_MOUSE	O35164 mus musculus
447	146.5	3.7	236	1	VSPC_DABRU	P18965 daboia ruse	520	129.5	3.3	652	1	CD93_HUMAN	Q9npv3 homo sapien
448	146.5	3.7	3707	1	PGBM_MOUSE	Q05793 mus musculus	521	129	3.3	235	1	VSP2_AGRBI	Q9psn3 agkistrodon
449	146	3.7	238	1	VSP1_AGRKA	P81176 agkistrodon	522	129	3.3	246	1	MCT4_RAT	P97592 rattus norv
450	146	3.7	256	1	TRYA_DROER	P54624 drosophila	523	128.5	3.3	232	1	VSP1_BOTJA	P81824 bothrops ja
451	145.5	3.7	598	1	FBL1_CERAE	Q8mj9 cercopithe	524	128.5	3.3	255	1	CATG_HUMAN	P08311 homo sapien
452	145	3.7	256	1	TRVA_DROME	P04814 drosophila	525	128.5	3.3	833	1	SRC2_MOUSE	P59222 mus musculus
453	145	3.7	260	1	VSP1_AGRKH	Q9vgj2 agkistrodon	526	128.5	3.3	2923	1	CLR2_HUMAN	Q9hcu4 homo sapien
454	145	3.7	372	1	LEM1_MOUSE	P18337 mus musculus	527	128	3.2	219	1	CA7_PIG	P80015 sus scrofa
455	144.5	3.7	246	1	MCT4_MOUSE	P21812 mus musculus	528	127.5	3.2	1389	1	LTBS_MOUSE	Q8cg18 mus musculus
456	144	3.7	260	1	VSP2_AGRKH	Q9vg16 agkistrodon	529	127.5	3.2	1713	1	LTBL_MOUSE	Q8cg19 mus musculus
457	143	3.6	234	1	VSP2_AGRKO	P92981 agkistrodon	530	127	3.2	258	1	GRAB_RAT	P49864 rattus norv
458	143	3.6	246	1	MCT2_SHEEP	P79204 ovie aries	531	127	3.2	1609	1	LMG1_HUMAN	P11047 homo sapien
459	143	3.6	258	1	VSP2_AGRKA	O42207 agkistrodon	532	127	3.2	3106	1	LM2_MOUSE	Q60675 mus musculus
460	143	3.6	3075	1	LM11_HUMAN	P25391 homo sapien	533	127	3.2	3110	1	LM2_MOUSE	P24043 homo sapien
461	142.5	3.6	247	1	MCT5_MOUSE	P21844 mus musculus	534	126.5	3.2	448	1	FBL5_RAT	Q9vvh8 rattus norv
462	142.5	3.6	258	1	VSP2_TRIJE	Q9df67 trimeresuru	535	126	3.2	257	1	VSP5_TRIMU	Q91511 trimeresuru
463	142	3.6	257	1	VSP2_BOTJA	O13069 bothrops ja	536	126	3.2	265	1	SER1_DROME	P17205 drosophila
464	141.5	3.6	310	1	ASTL_COTJA	P42662 coturnix co	537	126	3.2	272	1	SER3_DROME	P17207 drosophila
465	141.5	3.6	372	1	LEM1_HUMAN	P14151 homo sapien	538	126	3.2	330	1	FHR1_HUMAN	Q03591 homo sapien
466	141.5	3.6	372	1	LEM1_PANTR	Q95237 pan troglod	539	126	3.2	5147	1	FAT_DROME	P33450 drosophila
467	141.5	3.6	1881	1	LMG3_MOUSE	Q9r0b6 mus musculus	540	125.5	3.2	254	1	CTR1_HALRU	P35003 haliohis ru
468	141	3.6	246	1	GRAB_HUMAN	P20718 homo sapien	541	125.5	3.2	597	1	C4BP_HUMAN	P04003 homo sapien
469	140.5	3.6	246	1	MCT1_MOUSE	P11034 mus musculus	542	125	3.2	257	1	VSP3_TRIMU	Q91509 trimeresuru
470	140.5	3.6	372	1	LEM1_PONPY	Q95235 pongo pygma	543	125	3.2	443	1	FBL4_MOUSE	Q9vvg9 mus musculus
471	140.5	3.6	1234	1	CFAH_MOUSE	P06909 mus musculus	544	125	3.2	589	1	DLL3_RAT	O88671 rattus norv

545	125	3.2	1790	1	LMB1 DROME	P11046 drosophila	618	115.5	2.9	1679	1	FUR2 DROME	P30432 drosophila
546	124.5	3.2	248	1	GRAG MOUSE	P13366 mus musculus	619	115	2.9	133	1	AWN HORSE	P80720 equus caball
547	124.5	3.2	260	1	VSP1 TRIFL	P05620 trimeresuru	620	115	2.9	956	1	MTN2 HUMAN	O00339 homo sapien
548	124.5	3.2	268	1	TRYP STRGA	O54179 streptonyce	621	115	2.9	1207	1	EGP HUMAN	P01133 homo sapien
549	124	3.1	883	1	PGCB RAT	P55068 rattus norv	622	114.5	2.9	270	1	PHR2 HUMAN	P36980 homo sapien
550	124	3.1	1221	1	FBL2 MOUSE	P37889 mus musculus	623	114.5	2.9	443	1	FBL4 HUMAN	O95967 homo sapien
551	124	3.1	2333	1	PGCA CANFA	O28343 canis famil	624	114.5	2.9	816	1	NEL2 MOUSE	O61220 mus musculus
552	124	3.1	3333	1	LMG3 MOUSE	O61789 mus musculus	625	114.5	2.9	1798	1	LMB2 HUMAN	P55268 homo sapien
553	123.5	3.1	259	1	CTRI ANOGA	O27289 anopheles g	626	114	2.9	255	1	VSPA BOTAT	P04971 bothriops at
554	123.5	3.1	370	1	LEMI BOVIN	P98131 bos taurus	627	114	2.9	846	1	ITBX DROME	P11584 drosophila
555	123.5	3.1	1184	1	FBL2 HUMAN	P98095 homo sapien	628	113.5	2.9	879	1	LDLR RAT	P35952 rattus norv
556	123.5	3.1	2144	1	CLR2 RAT	O90722 rattus norv	629	113.5	2.9	1712	1	LTBL RAT	O00818 rattus norv
557	123.5	3.1	2213	1	SORL RABIT	O95209 o sortilin-	630	113	2.9	250	1	CFBL CHICK	P81475 gallus gall
558	123	3.1	340	1	DAF PONPY	P49457 pongo pygma	631	113	2.9	462	1	KRM2 HUMAN	O8ncw0 homo sapien
559	123	3.1	798	1	FBL1 CAEEL	O77469 caenorhabdi	632	113	2.9	3301	1	CLR3 MOUSE	O91210 mus musculus
560	123	3.1	816	1	NEL CHICK	O90827 gallus gall	633	113	2.9	3312	1	CLR3 HUMAN	O9nyq7 homo sapien
561	122.5	3.1	603	1	CFAB MOUSE	O61129 mus musculus	634	113	2.9	4349	1	PAT2 HUMAN	O9nyq8 homo sapien
562	122	3.1	198	1	CABE BOVIN	O28066 bos taurus	635	112.5	2.9	264	1	CERC SCMA	P12546 schistosoma
563	122	3.1	257	1	VSP3 AGKAC	O918x0 agkistrodon	636	112.5	2.9	379	1	MCP CAVPO	P70105 cavia porce
564	122	3.1	257	1	VSP7 TRIMU	O9dg84 trimeresuru	637	112.5	2.9	643	1	CD93 RAT	O9et61 rattus norv
565	122	3.1	258	1	VSP2 AGKAC	O918x1 agkistrodon	638	112.5	2.9	1228	1	EMI4 HUMAN	O13201 homo sapien
566	122	3.1	676	1	PRTS HUMAN	P07225 homo sapien	639	112.5	2.9	1247	1	NID0 HUMAN	P14543 homo sapien
567	122	3.1	1808	1	TENA CHICK	P10039 gallus gall	640	112.5	2.9	1403	1	NID2 MOUSE	O88322 mus musculus
568	122	3.1	1955	1	AGRI CHICK	P31696 gallus gall	641	112	2.8	228	1	VSPA LACMU	P33589 lachesis mu
569	122	3.1	3313	1	CLR3 RAT	O88278 rattus norv	642	112	2.8	493	1	FBL3 HUMAN	O12805 homo sapien
570	121.5	3.1	245	1	GILX HELHO	P43685 heloderma h	643	112	2.8	1125	1	TIE2 BOVIN	O06807 bos taurus
571	121.5	3.1	610	1	C4BP BOVIN	O28065 bos taurus	644	112	2.8	3562	1	PGCV CHICK	O90953 gallus gall
572	121.5	3.1	5376	1	ZAN MOUSE	O88799 mus musculus	645	111.5	2.8	816	1	NEL2 RAT	O62918 rattus norv
573	121	3.1	257	1	VSP2 TRIMU	O91508 trimeresuru	646	111.5	2.8	1328	1	AGRI DISOM	O90404 discopys o
574	121	3.1	1627	1	PAPA HUMAN	O13219 homo sapien	647	111.5	2.8	1587	1	LMG3 HUMAN	O9v6n6 homo sapien
575	121	3.1	3396	1	PGCV HUMAN	P13611 homo sapien	648	111.5	2.8	4351	1	FAT2 RAT	O88277 rattus norv
576	120.5	3.1	247	1	MCT2 MERUN	P50341 meriones un	649	111	2.8	231	1	VSP1 AGKCO	P09872 agkistrodon
577	120.5	3.1	345	1	APOF CANFA	P33703 canis famil	650	111	2.8	254	1	PRN3 MOUSE	O61096 mus musculus
578	120.5	3.1	646	1	PRTS RABIT	P98118 oryctolagus	651	110.5	2.8	234	1	VSP1 AGKRH	P26324 agkistrodon
579	120.5	3.1	728	1	HGF MOUSE	O80048 mus musculus	652	110.5	2.8	297	1	APOF RAT	P26644 rattus norv
580	120.5	3.1	1394	1	LTBS HUMAN	P22064 homo sapien	653	110.5	2.8	583	1	CFAL HUMAN	P05156 homo sapien
581	120.5	3.1	1595	1	LTBL HUMAN	O14766 homo sapien	654	110.5	2.8	755	1	COMP MOUSE	O9r096 mus musculus
582	120.5	3.1	1801	1	LBM2 RAT	P15800 rattus norv	655	110.5	2.8	961	1	TSPA HUMAN	P35443 homo sapien
583	120	3.0	257	1	VSP1 TRIMU	O91507 trimeresuru	656	110.5	2.8	1217	1	EGF MOUSE	P01132 mus musculus
584	120	3.0	493	1	FBL3 RAT	O35568 rattus norv	657	110	2.8	258	1	VSP1 TRIGA	O13059 trimeresuru
585	120	3.0	644	1	CD93 MOUSE	O89103 mus musculus	658	110	2.8	569	1	FHR5 HUMAN	O9bxr6 homo sapien
586	120	3.0	912	1	PGCB BOVIN	O28062 bos taurus	659	110	2.8	1124	1	TIE2 HUMAN	O02763 homo sapien
587	120	3.0	1877	1	PKCS MOUSE	O45592 mus musculus	660	109.5	2.8	2364	1	PGC2 BOVIN	P13608 bos taurus
588	120	3.0	3358	1	PGCV MOUSE	O62059 mus musculus	661	109.5	2.8	2920	1	CLR2 MOUSE	O9r0md mus musculus
589	120	3.0	3381	1	PGCV BOVIN	P81282 bos taurus	662	109.5	2.8	4705	1	FAT2 DROME	O9vw71 drosophila
590	119.5	3.0	675	1	PRTS BOVIN	P07224 bos taurus	663	109	2.8	379	1	WIFI MOUSE	O9wual mus musculus
591	119.5	3.0	3579	1	STAN DROME	O9v5n8 drosophila	664	109	2.8	1172	1	LMB3 HUMAN	O13751 homo sapien
592	119	3.0	258	1	VSP1 TRIST	O91516 trimeresuru	665	108.5	2.8	773	1	AD11 MOUSE	O9rlv4 mus musculus
593	119	3.0	870	1	SRC2 HUMAN	O26996 homo sapien	666	108	2.7	251	1	CAP7 HUMAN	P20160 homo sapien
594	119	3.0	2738	1	PGCV RAT	O9erB4 rattus norv	667	108	2.7	448	1	FBL5 HUMAN	O9ubx5 homo sapien
595	118.5	3.0	515	1	APX1 CAEEL	P41990 caenorhabdi	668	108	2.7	1321	1	PGCN HUMAN	O14594 homo sapien
596	118.5	3.0	728	1	HGF HUMAN	P14210 homo sapien	669	108	2.7	1450	1	SREJ STRPU	O26637 strongyloce
597	118.5	3.0	728	1	HGF RAT	P17945 rattus norv	670	108	2.7	1700	1	BAR3 CHITE	O03376 chironomus
598	118	3.0	133	1	AWN PIG	P26776 sus scrofa	671	108	2.7	2215	1	SORL MOUSE	O88307 m sortilin-
599	118	3.0	257	1	VSP4 TRIMU	O91510 trimeresuru	672	108	2.7	2476	1	ZAN PIG	O28983 sus scrofa
600	118	3.0	374	1	WIFI XENILA	O9w6f8 xenopus lae	673	107.5	2.7	331	1	FHR4 HUMAN	O24456 homo sapien
601	118	3.0	883	1	PGCB MOUSE	O61361 mus musculus	674	107.5	2.7	539	1	NTG1 MOUSE	O8r490 mus musculus
602	118	3.0	931	1	ENR1 MOUSE	O61549 mus musculus	675	107.5	2.7	769	1	AD11 HUMAN	O75078 homo sapien
603	117.5	3.0	188	1	KLK3 RAT	P15950 rattus norv	676	107.5	2.7	3014	1	CLR1 HUMAN	O9nyq6 homo sapien
604	117.5	3.0	649	1	PRTS MACMU	O28520 macaca mula	677	107.5	2.7	4289	1	TENX HUMAN	P22105 homo sapien
605	117.5	3.0	2214	1	SORL HUMAN	O92673 h sortilin-	678	107	2.7	4544	1	LRP1 HUMAN	O07954 homo sapien
606	117.5	3.0	3375	1	UN52 CAEEL	O6561 caenorhabdi	679	107	2.7	260	1	VSP1 TRIJE	O9df68 trimeresuru
607	117	3.0	704	1	FBL1 CHICK	O73775 gallus gall	680	107	2.7	379	1	WIFI HUMAN	O9y5w5 homo sapien
608	117	3.0	1639	1	LMG1 DROME	P15215 drosophila	681	106.5	2.7	165	1	TRY3 LUCCU	P35043 lucilia cup
609	116.5	3.0	377	1	MCP HUMAN	P15529 homo sapien	682	106.5	2.7	192	1	YD24 AQUAE	O67344 aquifex aeo
610	116.5	3.0	378	1	WIFI BRARE	O9w6f9 brachydanio	683	106.5	2.7	604	1	CFAL RAT	O9wuw3 rattus norv
611	116.5	3.0	443	1	FBL4 CRIGR	O50508 cricetus	684	106.5	2.7	755	1	COMP RAT	P35444 rattus norv
612	116.5	3.0	587	1	C08B ONCNY	O90x85 oncorhynch	685	106.5	2.7	2813	1	VWF CANFA	O28295 canis famil
613	116.5	3.0	1799	1	LBM2 MOUSE	O61292 mus musculus	686	106	2.7	280	1	SLI1 HUMAN	O23642 homo sapien
614	116	2.9	258	1	VSP3 TRIJE	O9df66 trimeresuru	687	106	2.7	1133	1	EGF RAT	P07522 rattus norv
615	116	2.9	1375	1	NID2 HUMAN	O41112 homo sapien	688	105.5	2.7	816	1	NEL2 HUMAN	O99435 homo sapien
616	115.5	2.9	256	1	PRN3 HUMAN	P24158 homo sapien	689	105	2.7	260	1	VSP2 VIPLE	O9pt40 vipera lebe
617	115.5	2.9	448	1	FBL5 MOUSE	O9wvh9 mus musculus	690	105	2.7	260	1	VSP6 TRIMU	O9d963 trimeresuru

691 105 2.7 860 1 LDLR HUMAN P01130 homo sapien  
 692 105 2.7 1107 1 YLX2-CAEEL P41950 caenorhabdi  
 693 105 2.7 1746 1 TENA\_PIG Q29116 sus scrofa  
 694 105 2.7 2201 1 TENA\_HUMAN P24821 homo sapien  
 695 105 2.7 2812 1 ZAN\_HUMAN Q9Y493 homo sapien  
 696 104.5 2.6 322 1 FSA\_BRAVE Q9Y494 brachydanio  
 697 104.5 2.6 345 1 APOH\_MOUSE P01339 mus musculu  
 698 104.5 2.6 4655 1 LRP2\_MOUSE P98164 homo sapien  
 699 104 2.6 280 1 SLI1\_MOUSE P97447 mus musculu  
 700 104 2.6 345 1 APOH\_BOVIN P17690 bos taurus

## ALIGNMENTS

RESULT 1  
 LFC\_TACTR  
 ID\_LFC\_TACTR STANDARD; PRT; 1019 AA.  
 AC P28175;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Limulus clotting factor C precursor (PC 3.4.21.84) (FC).  
 OS Tachyploous tridentatus (Japanese horseshoe crab).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;  
 OC Limulidae; Tachypieus.  
 OC NCBI\_TaxID=6853;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND PARTIAL SEQUENCE.  
 RX MEDLINE=91177916; PubMed=2007602;  
 RA Ikohara Y., Iwanaga S.;  
 RA Miyata T., Miyata T., Sasaki Y., Tokunaga F., Nakamura T., Toh Y.,  
 RT "Limulus factor C. An endotoxin-sensitive serine protease zymogen  
 RT with a mosaic structure of complement-like, epidermal growth  
 RT factor-like, and lectin-like domains";  
 RL J. Biol. Chem. 266:6554-6561(1991).  
 CC -!- FUNCTION: This enzyme is closely associated with an endotoxin-  
 CC sensitive hemolymph coagulation system which may play important  
 CC roles in both hemostasis and host defense mechanisms. Its active  
 CC form catalyzes the activation of factor B.  
 CC -!- CATALYTIC ACTIVITY: Selective cleavage of 103-Arg-Ser-104 and  
 CC 124-Ile-Ile-125 bonds in Limulus clotting factor B to form  
 CC activated factor B. Cleavage of Pro-Arg-Xaa bonds in synthetic  
 CC substrates.  
 CC -!- ENZYME REGULATION: Activated by Gram-negative bacterial  
 CC lipopolysaccharides and chymotrypsin.  
 CC -!- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by  
 CC a disulfide bond.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Long;  
 CC IsoId=P28175-1; Sequence=Displayed;  
 CC Name=Short;  
 CC IsoId=P28175-2; Sequence=VSP\_005413, VSP\_005414;  
 CC -!- SIMILARITY: Belongs to peptidase family S1.  
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.  
 CC -!- SIMILARITY: Contains 1 EGF-like domain.  
 CC -!- SIMILARITY: Contains 1 LCCL domain.  
 CC -!- SIMILARITY: Contains 5 Sushi (SCR) domains.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 CC EMBL; D90271; BAA14315.1; -;  
 CC EMBL; D90272; BAA14316.1; -;  
 CC FIR; A38738; A38738.  
 CC HSSP; P00763; LDPO.  
 CC MEROPS; S01.219; -.

DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR004043; LCCL\_dom.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
 DR Pfam; PF03815; LCCL; 1.  
 DR Pfam; PF00059; lectin\_C; 1.  
 DR Pfam; PF00084; sushi\_5.  
 DR Pfam; PF00089; trypsin\_1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00032; CCP; 5.  
 DR SMART; SM00034; CLECT; 1.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00603; LCCL; 1.  
 DR SMART; SM00020; Tryp\_SPC; 1.  
 DR PROSITE; PS00615; C\_TYPE\_LECTIN\_1; FALSE\_NEG.  
 DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
 DR PROSITE; PS50026; EGF\_3; 1.  
 DR PROSITE; PS50820; LCCL; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR KW Hemolysase; Serine protease; Signal; Alternative splicing; Lectin;  
 KW Hemolymph clotting; Glycoprotein; Cell adhesion; EGF-like domain;  
 KW Sushi; Repeat.  
 FT SIGNAL 1 25  
 FT CHAIN 26 1019 LIMULUS CLOTTING FACTOR C.  
 FT CHAIN 26 690 LIMULUS CLOTTING FACTOR C, HEAVY CHAIN.  
 FT CHAIN 691 1019 LIMULUS CLOTTING FACTOR C, LIGHT CHAIN.  
 FT CHAIN 691 762 LIMULUS CLOTTING FACTOR C, A CHAIN.  
 FT CHAIN 763 1019 LIMULUS CLOTTING FACTOR C, B CHAIN.  
 FT CHAIN 102 137 EGF-LIKE.  
 FT DOMAIN 142 195 SUSHI 1.  
 FT DOMAIN 200 254 SUSHI 2.  
 FT DOMAIN 260 321 SUSHI 3.  
 FT DOMAIN 325 421 LCCL.  
 FT DOMAIN 436 568 C-TYPE LECTIN.  
 FT DOMAIN 576 634 SUSHI 4.  
 FT DOMAIN 685 748 SUSHI 5.  
 FT DOMAIN 763 1019 SERINE PROTEASE.  
 FT ACT\_SITE 809 809 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 865 865 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 966 966 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT BINDING 960 960 SUBSTRATE (BY SIMILARITY).  
 FT DOMAIN 643 689 PRO-RICH.  
 FT DISULFID 106 118 BY SIMILARITY.  
 FT DISULFID 112 125 BY SIMILARITY.  
 FT DISULFID 127 136 BY SIMILARITY.  
 FT DISULFID 436 447 BY SIMILARITY.  
 FT DISULFID 464 564 BY SIMILARITY.  
 FT DISULFID 538 556 BY SIMILARITY.  
 FT DISULFID 794 810 BY SIMILARITY.  
 FT DISULFID 932 951 BY SIMILARITY.  
 FT DISULFID 962 996 BY SIMILARITY.  
 FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 534 534 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 740 740 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 767 767 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 912 912 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 492 498 LTTTWIG -> TDNVVAT (in isoform Short).  
 FT VARSPLIC 499 1019 /FTID=VSP\_005413.  
 FT VARSPLIC 499 1019 Missing (in isoform Short).  
 FT SEQUENCE 1019 AA; 112346 MW; 5BC2864C6715289B CRC64;  
 SQ

Query Match 17.0%; Score 672; DB 1; Length 1019;  
 Best Local Similarity 25.6%; Pred. No. 7.4e-43;

Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;

QY 34 PGAEWIM-...-CRECEYDQIE-...-CVCPRKREVVGYTIPCCRNENEEDCSLIHPGCT 86

Db 184 PNCQWSFPKPCIKCAKVSPEHGKNAPSGNMIEGATL-...-RFGCDS-...-PYL 233

QY 87 IPENCSCR-NGSWGGLT-...-PCKKLVFCPLDPVNHAEHQVIGVEQKYGFPOGTEVYT 103

Db 234 IGQETLTCQNGQWSGQIPCKKLVFCPLDPVNHAEHQVIGVEQKYGFPOGTEVYT 293

QY 104 --DDFYKGYCAECR--AGWYGG--DCMR-...-CGQVLR--APKG 137

Db 294 CSGNYFLMGFTLKNCPDGSWSQSCVKAVDREVDSCAKVDFLDDVGEPRVRIHCPAG 353

QY 138 QILLES-...-YPLNAHCEWTIA-...-KGFVI-...-Q 163

Db 354 CSLTAGTWTGTAIYHELSSVCRAIHAGKLPNSGGAVHVNNVNGPYDFGLDNLGKISEE 413

QY 164 LRFVMLSLEPDYM-...-COYDVEVRD-...-GDRGQIYKRCGN--ERPAP 206

Db 414 LKSLARSFRDYVSSSTAGSGCPDQWFEVEENCYVTSKQRAWERAQGYCTNMAARLAV 473

QY 207 IQS--IGSSHLVLFHSDG-SKNPDGPH-...-AIYEITACSSSPCF 245

Db 474 LKXDLIPSSLTETLRGKGLTTTIGLHRLDAEKPFWELMDRNVNLDNLTFWASGEPG 533

QY 246 HDGTCV-LDRAGS-...-YKCACLAGVTGQRCENLLBERN-...-CSDPGPVNGYOKITGGP 297

Db 534 NETNCVYLDLRDQLOPWKTKSCFPSSFAQMDLSDRNKAKCDDPCPLENGHATLHGQS 593

QY 298 GLNGRHAKITGVVSPFCNNYSVLSNEKKTCCOENGWSKQICIK--ACREPKISDLV 355

Db 594 --IDGFA--GSSIRYSCVLEHLSTETVTCTTNGTWSAPKPCIKVITCQNPVPFSG 649

QY 356 RRVLPNQVOSRETPHLQLYSAFQKQ-...-SAPTKKALPFGD-...-LP 400

Db 650 SVEIKP-...-PSRTNISIRVSGPFLRLPLPLPLARAAPPPKPRSSOPSTVDLASKVKLP 706

QY 401 MGYQHLHTQYQECISPFYRRLGSSRTCLRTGKWSGRAPSCIPICGKIENITAP-...-455

Db 707 EGHYRVGSRATYCESRYELLGSGRCDNSGNWSGRPASCIPVCGRSDSPRPFITWG 766

QY 456 -KTGRLWPHQAAIYRTSGVHDSLHKGAWFLVCSGALVNTVVVAACHVTLGKVTM 514

Db 767 NSTEIGQWPQAGISRLA-...-DHNWMLFCGGLLNEKWIYVTAACHVTSYATAEI 819

QY 515 IKTADLVKVLGKFRDDEKTIQSLQISAILHPNYDPILLDADIAIKLKDARIST 574

Db 820 IDFSQFIYLGKTYRDSRDDYVQVREALEIHVNPYDFGNLNFDAIQLKTPVTLTT 879

QY 575 RVQPICLAASRDLSTSFQESH-...-TVAGMNVLDVRSFGKNDLRSVGVVVDL 628

Db 880 RVQPICLPT--DITT--REHLKEGLVAVTGMG-...-LNENNTYSEMIQOAVLPVVAAS 930

QY 629 LCEQEDHGPVSVTNNMCASWEPTAPSDICTAETGGAANVSFFGRASPERHLMGL 688

Db 931 TCEGEYKEADLPVTNMFPCAGYK-KGRYDACSQSGG--PLVFAADDSRTERRVWLEGI 987

QY 689 VMSYDKTCSH-RLSTAFKTVLPFKDWIER 717

Db 988 VMSGSPGCGKANQYGGFTKVVFLSWIRQ 1017

RESULT 2

LFC\_CARRO STANDARD; PRT; 1019 AA.

AC Q26422;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Limulus clotting factor C precursor (EC 3.4.21.84) (FC).

OS Carinocarpus rotundicauda (Southeast Asian horseshoe crab).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;

OC Limulidae; Carinocarpus.

RN NCBI\_TaxID=6848;

CC [1]

CC SEQUENCE FROM N.A.

CC TISSUE=Blood;

CC MEDLINE=95268506; PubMed=7538401;

CC Ding J.L., Navas M.A. III, Ho B.;

CC "Molecular cloning and sequence analysis of factor C cDNA from the

CC Singapore horseshoe crab, Carinocarpus rotundicauda.";

CC Mol. Mar. Biol. Biotechnol. 4:90-103(1995).

CC -!- FUNCTION: This enzyme is closely associated with an endotoxin-

CC sensitive hemolymph coagulation system which may play important

CC roles in both hemostasis and host defense mechanisms. Its active

CC form catalyzes the activation of factor B.

CC -!- CATALYTIC ACTIVITY: Selective cleavage of 103-Arg-|-Ser-104 and

CC 124-Ile-|-Ile-125 bonds in Limulus clotting factor B to form

CC activated factor B. Cleavage of Pro-Arg-|-Xaa bonds in synthetic

CC substrates.

CC -!- ENZYME REGULATION: Activated by Gram-negative bacterial

CC lipopolysaccharides and chymotrypsin (By similarity).

CC -!- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by

CC a disulfide bond (By similarity).

CC -!- SIMILARITY: Belongs to peptidase family S1.

CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

CC -!- SIMILARITY: Contains 1 EGF-like domain.

CC -!- SIMILARITY: Contains 1 LCCL domain.

CC -!- SIMILARITY: Contains 5 Sushi (SCR) domains.

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CC -----

CC EMBL; S77063; AAB34361.1; --

CC HSSP; P00763; LDPO.

CC MEROPS; S01.219; --

CC InterPro; IPR009003; Cys\_Ser\_trypsin.

CC InterPro; IPR006209; EGF\_like.

CC InterPro; IPR006210; IEGF.

CC InterPro; IPR004043; LCCL\_dom.

CC InterPro; IPR001304; Lectin\_C.

CC InterPro; IPR001254; Peptidase\_S1.

CC InterPro; IPR001314; Peptidase\_S1A.

CC InterPro; IPR000436; Sushi\_SCR\_CCP.

CC Pfam; PF03815; LCCL; 1.

CC Pfam; PF00059; lectin\_c; 1.

CC Pfam; PF00084; sushi; 5.

CC Pfam; PF00089; trypsin; 1.

CC PRINTS; PR00722; CHYMOTRYPSIN.

CC SMART; SM00032; CCP; 5.

CC SMART; SM00034; CLECT; 1.

CC SMART; SM00181; EGF; 1.

CC SMART; SM00603; LCCL; 1.

CC SMART; SM00020; tryp\_spc; 1.

CC PROSITE; PS00615; C\_TYPE\_LLECTIN\_1; FALSE\_NEG.

CC PROSITE; PS50041; C\_TYPE\_LLECTIN\_2; 1.

CC PROSITE; PS00022; EGF\_1; 1.

CC PROSITE; PS01186; EGF\_2; FALSE\_NEG.

CC PROSITE; PS50026; EGF\_3; 1.

CC PROSITE; PS50820; LCCL; 1.

CC PROSITE; PS50240; TRYPSIN\_DOM; 1.

CC PROSITE; PS00134; TRYPSIN\_HIS; 1.

CC PROSITE; PS00135; TRYPSIN\_SER; 1.

CC Hydrolase; Serine protease; Signal; Lectin; Hemolymph clotting;

CC Glycoprotein; Cell adhesion; EGF-like domain; Sushi; Repeat.

CC SIGNAL 1 25

CC CHAIN 26 1019 LIMULUS CLOTTING FACTOR C.

CC CHAIN 26 690 LIMULUS CLOTTING FACTOR C.

CC CHAIN 691 1019 LIMULUS CLOTTING FACTOR C.

CC CHAIN 691 762 LIMULUS CLOTTING FACTOR C, A CHAIN.



FT CHAIN 763 1019 LIMULUS CLOTTING FACTOR C, B CHAIN.  
 FT DOMAIN 102 137 EGF-LIKE.  
 FT 142 195 SUSHI 1.  
 FT DOMAIN 200 254 SUSHI 2.  
 FT 260 321 SUSHI 3.  
 FT DOMAIN 325 421 LCCL.  
 FT 436 568 C-TYPE LECTIN.  
 FT DOMAIN 576 634 SUSHI 4.  
 FT DOMAIN 685 748 SUSHI 5.  
 FT 763 1019 SERINE PROTEASE.  
 FT ACT SITE 809 809 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 865 865 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT 966 966 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT BINDING 960 960 SUBSTRATE (BY SIMILARITY).  
 FT DOMAIN 643 689 PRO-RICH.  
 FT DISULFID 106 118 BY SIMILARITY.  
 FT DISULFID 112 125 BY SIMILARITY.  
 FT DISULFID 127 136 BY SIMILARITY.  
 FT DISULFID 436 447 BY SIMILARITY.  
 FT DISULFID 464 564 BY SIMILARITY.  
 FT DISULFID 538 556 BY SIMILARITY.  
 FT DISULFID 794 810 BY SIMILARITY.  
 FT DISULFID 932 951 BY SIMILARITY.  
 FT DISULFID 962 956 BY SIMILARITY.  
 FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 534 534 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 740 740 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 767 767 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 912 912 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 1019 AA; 112429 MW; 918ALED8817B6C3 CRC64;  
 Query Match 16.9%; Score 665; DB 1; Length 1019;  
 Best Local Similarity 25.4%; Pred. No. 2.5e-42;  
 Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;  
 QY 34 PGAEVNMRECEVDQIECVCPKRE-----VVGTYIPCCRNENECDSCLIH 82  
 DB 184 PNGQSNFPFKICR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RPSGDS----- 229  
 QY 83 PGCTIPENCCKSR-NGSWGGLT-----YPLNAHCETIHA-----KPGFVI----- 103  
 DB 230 PYLLIGQETLTQCGQWNGQIPQCKNLVFCPLDPVNAEHKVIQVGEQKYGQFPQGT 289  
 QY 104 -----DDPYVGYGCAECR--AGWYGG--DCNR-----CGQVLR-- 133  
 DB 290 VTYTCGNYFLMGFTLCKNPGDSGSGQSCVKVADREVDCDSKAVDFLDVGPVRIH 349  
 QY 134 APKGQILLES-----YPLNAHCETIHA-----KPGFVI----- 162  
 DB 350 CPAGCSLTAGTWGTAIYHELSSVCRAAIAHAKLPNSGGAVHVNNGPYSDPLGSDLNGI 409  
 QY 163 ---QLRFVNLSEFDYM-----CQDYVEVRD-----GDNRDGQIIIRKVCN--E 202  
 DB 410 KSEELKSLARSFRFDYVRSSTAGKSCPDGWFVEVDENVYVTSKQRAWERAGVCTNMAA 469  
 QY 203 RPAPTQS---IGSLHLVLFHSDG-SKNFDGFH-----AYEETACSS 241  
 DB 470 RLAVLDKDVIPNSLTETLRGKLTWTWIGLHRLDAEKPFIFELMDRSNVVLDNLTFWAS 529  
 QY 242 SPCFDHGTCLV---DKAGS--YKACLAGYTGRCENILEERN---CSDPGGPNVGYOKI 293  
 DB 530 GPGFGNETNCVYMDIQLOQSVWKTSCFOPSFACWMLDSLRNKAACDDPGSLENGHATL 589  
 QY 294 TGGPGLINGRHAKIGITVWVFFCNNSVYLSNGEKRTCCQNGEWSGKQPICIK--ACREPKI 351  
 DB 590 HGQS--IDGFWA--GSSIRYSEVLHLYLSTGTCTTGTWTSAPKPRCIVITQNPV 645  
 QY 352 SLVRRRVLPQVQSRHTPLHLYSNAFQKQKLO---SAPTKPALPFGD----- 398  
 DB 646 PSYGSVEIKP---PSRTNISIRVSPFLRLPLPLAARAAKPPKPRSSQPSSTVDLASK 702  
 QY 399 --LPMGYQHLHTQLOVEICISPFVRLIGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAP- 455

DB 703 VKLPEGYRVGSRATYTCESRYEYELLSQGRCDNSNGWGRPASCIPVCGRSDSPSPF 762  
 QY 456 -----KTQGLRWPMQAAIYRTSTGVHDGSLHKGAWFLVCSGALVNERTVVVAARHCVTDLG 510  
 DB 763 IWNGNSTEIGQWPHQAGISRWLA-----DHNWFLQCGGSLNKKWIVTAACHVTYSA 815  
 QY 511 KVTWIKTADLKVILGKPYRDDREKTIQSLQISAILHNPYDPIILDADIAILKLDKA 570  
 DB 816 TAETIDPNQFMYLGYKYYRDRDDYVQVREALEIHVNPYDNGNLNFDIALIQLKTPV 875  
 QY 571 RISTRVOPICLAASRDLSTSFQESHI-----TVAGNVLADVRSFGKNDTLRSGVVSV 624  
 DB 876 TLTRVOPICLPT--DITT---REHLKEGTUAVVTGMG-----LNENYTSITIOQAVLPV 926  
 QY 625 VDSLLCEEQHEHDGIPVSTDNMFCASWEPTAPSDICTAETGGIAAVSFGRASPEPRWH 684  
 DB 927 VAASTCEEGYKEADPLTVIENMEFCAGYK-KGYDACSDDSGG--PLVFADDSDRTERRVW 983  
 QY 685 LMGVLVSWSYDKTCSH-RLSTAFATKVLFPFKOWIER 717  
 DB 984 LEGIVSWGSPSGCGKANQYGGFTKVNVELSWIRQ 1017  
 RESULT 3  
 CHAR HUMAN  
 ID CRAR HUMAN STANDARD; PRT; 699 AA.  
 AC P48740; O95570; Q9UF09;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Complement-activating component of Ra-reactive factor precursor  
 DE (EC 3.4.21.-) (Ra-reactive factor serine protease p100) (RaRF)  
 DE (Mannan-binding lectin serine protease 1) (Mannose-binding protein  
 DE associated serine protease) (MASP-1).  
 GN MASP1 OR CRARF OR CRARF1 OR PRSS5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RX NCBI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=94055062; PubMed=8240317;  
 RA Takada F., Takayama Y., Hattuse H., Kawakami M.;  
 RT "A new member of the C1s family of complement proteins found in a  
 RT bactericidal factor, Ra-reactive factor, in human serum.";  
 RL Biochem. Biophys. Res. Commun. 196:1003-1009(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Fetal liver;  
 RX MEDLINE=94289349; PubMed=8018603;  
 RA Sato T., Endo Y., Matsushita M., Fujita T.;  
 RT "Molecular characterization of a novel serine protease involved in  
 RT activation of the complement system by mannose-binding protein.";  
 RL Int. Immunol. 6:665-669(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=97079701; PubMed=8921412;  
 RA Endo Y., Sato T., Matsushita M., Fujita T.;  
 RT "Exon structure of the gene encoding the human mannose-binding  
 RT protein-associated serine protease light chain: comparison with  
 RT complement C1r and C1s genes.";  
 RL Int. Immunol. 8:1355-1358(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99402590; PubMed=10475605;  
 RA Takayama Y., Takada F., Nowatari M., Kawakami M., Matsura N.;  
 RT "Gene structure of the P100 serine-protease component of the human Ra-  
 RT reactive factor.";  
 RL Mol. Immunol. 36:505-514(1999).  
 CC -!- FUNCTION: Component of the bactericidal ra-reactive factor raarf



which specifically binds to RA and R2 polysaccharides expressed by certain enterobacteria. It triggers the activation of complement cascade by activating the C4 and C2 components. It activates the C4 component by cleaving the alpha-chain of C4.

-1- SUBUNIT: RAHF consists of a complement-activating component (CRAPF) and a polysaccharide-binding (mannose-binding) component. CRAPF is an heterodimer of a heavy (p70) and a light chain (p29) linked by a disulfide bond.

-1- DOMAIN: CRAPF has a module organization similar to C1r and C1s.

-1- SIMILARITY: Belongs to peptidase family S1.

-1- SIMILARITY: Contains 2 CUB domains.

-1- SIMILARITY: Contains 1 EGF-like domain.

-1- SIMILARITY: Contains 2 Sushi (SCR) domains.

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EMBL; D17525; BAA04477.1; --  
EMBL; D28593; BAA0528.1; --  
EMBL; D61695; BAA34864.1; --  
EMBL; AB010822; BAA34864.1; JOINED.  
EMBL; AB010813; BAA34864.1; JOINED.  
EMBL; AB010814; BAA34864.1; JOINED.  
EMBL; AB010815; BAA34864.1; JOINED.  
EMBL; AB010816; BAA34864.1; JOINED.  
EMBL; AB010817; BAA34864.1; JOINED.  
EMBL; AB010818; BAA34864.1; JOINED.  
EMBL; AB010819; BAA34864.1; JOINED.  
EMBL; AB010820; BAA34864.1; JOINED.  
EMBL; AB010821; BAA34864.1; JOINED.  
EMBL; D61690; BAA34864.1; JOINED.  
EMBL; D61691; BAA34864.1; JOINED.  
EMBL; D61692; BAA34864.1; JOINED.  
EMBL; D61693; BAA34864.1; JOINED.  
EMBL; D61694; BAA34864.1; JOINED.  
EMBL; AB007617; BAA89206.1; --  
EMBL; AB007602; BAA89206.1; JOINED.  
EMBL; AB007603; BAA89206.1; JOINED.  
EMBL; AB007604; BAA89206.1; JOINED.  
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EMBL; AB007606; BAA89206.1; JOINED.  
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EMBL; AB007609; BAA89206.1; JOINED.  
EMBL; AB007610; BAA89206.1; JOINED.  
EMBL; AB007611; BAA89206.1; JOINED.  
EMBL; AB007612; BAA89206.1; JOINED.  
EMBL; AB007613; BAA89206.1; JOINED.  
EMBL; AB007614; BAA89206.1; JOINED.  
EMBL; AB007615; BAA89206.1; JOINED.  
EMBL; AB007616; BAA89206.1; JOINED.  
EMBL; PIR; I54763; I54763.  
HSSP; P00736; LAPO.  
MEROPS; S01.198; --  
Genow; HGNC:6901; MASPL.  
MIM; 600521; --  
GO; GO:0004252; F:serine-type endopeptidase activity; TAS.  
GO; GO:0006956; P:complement activation; TAS.  
InterPro; IPR000152; Asx\_hydroxyl\_S.  
InterPro; IPR000859; CUB.  
InterPro; IPR009003; Cys\_Ser\_trypsin.  
InterPro; IPR001881; EGF\_Ca.  
InterPro; IPR006209; EGF-like.  
InterPro; IPR001254; Peptidase S1.  
InterPro; IPR001314; Peptidase S1A.  
InterPro; IPR000436; Sushi\_SCR\_CCP.  
Pfam; PF00431; CUB; 2.  
Pfam; PF00084; sushi; 2.

Pfam; PF00089; trypsin; 1.  
PRINTS; PR00722; CHYMOTRYPSIN.  
SMART; SM00032; CCP; 2.  
SMART; SM00042; CUB; 2.  
SMART; SM00179; EGF\_CA; 1.  
SMART; SM00020; TRY\_SPC; 1.  
PROSITE; PS00010; ASX\_HYDROXYL; 1.  
PROSITE; PS01180; CUB; 2.  
PROSITE; PS01186; EGF\_2; 1.  
PROSITE; PS01187; EGF\_CA; 1.  
PROSITE; PS0240; TRYPSIN\_DOM; 1.  
PROSITE; PS0240; TRYPSIN\_HIS; 1.  
PROSITE; PS00134; TRYPSIN\_SER; 1.  
PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydroxylase; Complement pathway; Serine protease; Protease; Glycoprotein; Sushi; Repeat; Signal; EGF-like domain; Hydroxylation.  
FT SIGNAL 1 19  
FT CHAIN 20 699  
FT CHAIN 20 448  
FT CHAIN 449 699  
FT DOMAIN 20 138  
FT DOMAIN 139 182  
FT DOMAIN 185 297  
FT DOMAIN 300 363  
FT DOMAIN 366 433  
FT DOMAIN 449 699  
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FT ACT\_SITE 552 552  
FT ACT\_SITE 646 646  
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FT DISULFID 73 91  
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FT DISULFID 436 572  
FT DISULFID 614 631  
FT DISULFID 642 672  
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FT CARBOHYD 385 385  
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FT CONFLICT 543 543  
FT CONFLICT 552 552  
FT CONFLICT 643 643  
SQ SEQUENCE 699 AA; 79258 MW; ADD9697AE6AB01B5 CRC64;  
Query Match 12.1%; Score 478; DB 1; Length 699;  
Best Local Similarity 24.6%; Pred. No. 2.1e-28;  
Matches 176; Conservative 93; Mismatches 217; Indels 228; Gaps 38;  
QY 69 CRNEECDSCLHPGCTIFENCKSRNGSWGTLDDFFYKGYCAECRAGWY----GGD 124  
DB 143 CKEREDEELSCDHY-----CHN-----YIGGYCS-CRFGYILHTDNR 180  
QY 125 C-MRCQVLRAPKGOILL-----ESYPLNAHCWTTHAKPGFVIOLRFLVMSLEFDY 176  
DB 181 CRVECSNLTQTQTGTVITSPDFPNPKSECDYITIELEGFMVNLQFEDI----FDIQDH 237  
QY 177 ----CYDYVEVRDGNRDGQIIKRVCGNERPAPIQISIGSSLHVLPHSDGSKNDFGHAI 232  
DB 238 PEVPCPYDIKIKVGP-----KVLGPGCGEKAPEPISTQSHSVLLFHSNDAENRGWRL- 292



FT DISULFID 372 419 POTENTIAL.  
FT DISULFID 402 437 INTERCHAIN (POTENTIAL).  
FT DISULFID 441 577 INTERCHAIN (POTENTIAL).  
FT DISULFID 619 636 POTENTIAL.  
FT DISULFID 647 677 POTENTIAL.  
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 704 AA, 71444F3012D2C67F CRC64;  
Query Match 12.0%; Score 475; DB 1; Length 704;  
Best Local Similarity 23.3%; Pred. No. 3.5e-28;  
Matches 196; Conservative 109; Mismatches 256; Indels 280; Gaps 46;  
QY 11 LTELQLLLSL-----PREYTV-INE-----ACPG-----AEWIMCRE----- 44  
DB 4 LSFWRLLLYHALCLAUPEVSAHVELNEMFGQIQSPGPDSPDSYSDSEVTWNIIVPGFRI 63  
QY 45 -----CCEYDQIE-----CVC-----PGREV----- 61  
DB 64 KLYFMHFNLSYLCEDYDYKVEDQVLATFCGRETDTTQTPGQEVLSPTGFMSTVF 123  
QY 62 -----VGTIPCCNEEENECCLHPGCTIFENCKSCNCGSWGGLTD 104  
DB 124 RSDFSNEERTGPDHYMAVDVDEKERDEELSCDHY-----CHN----- 164  
QY 105 DFYVKGPGYACACRAGWY-----GGDC-MRC-GQVLRAPKGOILL-----ESYPLNAHCEWTI 154  
DB 165 --YIGGYCS-CHFGYLLHNDNTRCEVCSGNLFTQRTGTITSPDPNPNPKSECSYTI 221  
QY 155 HAKPGFVIQRLFVMSLEFD-----YMCQDYVEVRDGNDRGQIIRKVCNERNPAPIQ 208  
DB 222 DLEEGFMVSLQFEDI---FDIEDHPVPCPDYDIKIKAGSKWGPFF-----CGEKSPEPIS 274  
QY 209 SIGSLHLVPHSDGSKNFDGFHAIYEITACSSPCFHDCTCVLDKAGSKYKACLAGTYG 268  
DB 275 TQTHSVQILFRSDNSNGENRWRL-----SYRAA-----G 303  
QY 269 QRCENLEERNCDPDPGVNGYQKITGGPGLNGRHAIGITVVSFFCNNSY-VLSGNE-- 325  
DB 304 NECPKL-----QP--PV--YKIEPSSQAVYS--FKQQLVYS--CDTGYKVLKONGVM 347  
QY 326 ---KRTCCQNGEWGKQIPIC- IKACREPKISDLVRRRLVLMQVQSRETPHLQHSYAAPSK 381  
DB 348 DTFQIECLKDGAWSNKIPTCKIVDCGAP-----AGLK 379  
QY 382 OKLOSAPTKKPALPFGLPMGYQHLHTQLOVEICISPYRELGSRR--RTCLRTGKWSGRA 439  
DB 380 HGLVTFSTRNLTTY-----KSEIRYSQQPYKMLHNTTGYVTSAGHTWNTKV 429  
QY 440 -----PSCIPICG-----KIENI--TAPKTQGLRWPMQAAIYRRTSGVHDGSLHKGAW 485  
DB 430 LKESLPTCLVCGVPKFSRQISRIENGRPAQKG-TMPWTAML-----SHLNGQP 478  
QY 486 FLVCSGALVNERVTWVAACHV-----TDLGKVTMIKTADLKVLVGLKPY-RDDRDEK 536  
DB 479 F--CGGSLGSMVWLTAAHLQSLDPEEPTLHSSYLLSPSDFPKIIMGKHWRRSDEDE- 535  
QY 537 TIQSLOISAILHPNDYDPIILLDADIALKLKDKARISTRVQPCILAAASRLDLSFQESHI 596  
DB 536 --QHLHVKRTTLPLYNPSTFENDGLVSELSFRLNDFWNPCLPE-----QPSSTETGMV 599  
QY 597 TVAGWNVLDVRSFGPKNDLRSQVSVSDLSLCEQHEHDGHPVSVYTDNNFCASWEPTA 656  
DB 590 IVSGWKGQFLQRP-----ENLMEIEIPIVNSDTCQEAATP--LKKKVTKDMICAG-EKEG 642  
QY 657 PSDICTABTGGIAAVSPGRASPEPRHMLGLVSWSYDKTCSHRLSTAFKVLVFPKDWIE 716  
DB 643 GKDACAGDSGGPMVT-----KDAERDQWYLVGVWSWGEDCGKDRYG-VYSYIYFNKDWIQ 697  
QY 717 R 717

DB 698 R 698  
RESULT 5  
ID CLR\_HUMAN STANDARD; PRT; 705 AA.  
AC P00736;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Complement C1r component precursor (EC 3.4.21.41).  
GN C1r.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=87026566; PubMed=3021205;  
RA Leytus S.P., Kurachi K., Sakariassen K.S., Davie E.W.;  
RT "Nucleotide sequence of the cDNA coding for human complement C1r.";  
RL Biochemistry 25:4855-4863(1986).  
RN [2]  
RP SEQUENCE FROM N.A. AND VARIANT LEU-152.  
RX MEDLINE=87156625; PubMed=3030286;  
RA Journet A., Tosi M.;  
RT "Cloning and sequencing of full-length cDNA encoding the precursor of  
human complement component C1r.";  
RL Biochem. J. 240:783-787(1986).  
RN [3]  
RP SEQUENCE OF 18-463.  
RX MEDLINE=87241248; PubMed=3036070;  
RA Arlaud G.J., Willis A.C., Gagnon J.;  
RT "Complete amino acid sequence of the A chain of human complement-  
classical-pathway enzyme C1r.";  
RL Biochem. J. 241:711-720(1987).  
RN [4]  
RP SEQUENCE OF 464-705.  
RX MEDLINE=83204782; PubMed=6303394;  
RA Arlaud G.J., Gagnon J.;  
RT "Complete amino acid sequence of the catalytic chain of human  
complement subcomponent C1-r.";  
RL Biochemistry 22:1758-1764(1983).  
RN [5]  
RP SEQUENCE OF 152-186, AND HYDROXYLATION.  
RX MEDLINE=88005128; PubMed=2820791;  
RA Arlaud G.J., van Dorsselaer A., Bell A., Mancini M., Aude C.,  
RT "Identification of erythro-beta-hydroxyasparagine in the EGF-like  
domain of human C1r.";  
RL FEBS Lett. 222:129-134(1987).  
RN [6]  
RP SEQUENCE OF 133-137; 187-211 AND 609-613, AND PHOSPHORYLATION.  
RX MEDLINE=96221263; PubMed=8635594;  
RA Felloux S., Thielens N.M., Hudry-Clergeon G., Petitot Y., Filhol O.,  
RA Arlaud G.J.;  
RT "Identification of a cryptic protein kinase CK2 phosphorylation site  
in human complement protease C1r, and its use to probe intramolecular  
interaction.";  
RL FEBS Lett. 386:15-20(1996).  
RN [7]  
RP STRUCTURE BY NMR OF 140-192.  
RX MEDLINE=98138432; PubMed=9477945;  
RA Bersch B., Hernandez J.-P., Marion D., Arlaud G.J.;  
RT "Solution structure of the epidermal growth factor (EGF)-like module  
of human complement protease C1r, an atypical member of the EGF  
family";  
RL Biochemistry 37:1204-1214(1998).  
CC -!- FUNCTION: C1r B chain is a serine protease that combines with C1q  
and C1s to form C1, the first component of the classical pathway  
of the complement system.  
CC -!- CATALYTIC ACTIVITY: Selective cleavage of Lys(or Arg)-|-Ile bond  
in complement subcomponent C1s to form the active form of C1s

(EC 3.4.21.42).  
 - SUBUNIT: C1 is a calcium-dependent trimolecular complex of C1q, C1r and C1s in the molar ratio of 1:2:2. C1r is a dimer of identical chains, each of which is activated by cleavage into two chains, A and B, connected by disulfide bonds.  
 - SIMILARITY: Belongs to peptidase family S1.  
 - SIMILARITY: Contains 2 CUB domains.  
 - SIMILARITY: Contains 1 EGF-like domain.  
 - SIMILARITY: Contains 2 Sushi (SCR) domains.  
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 EMBL; X04701; CAA28407.1; -  
 DR EMBL; M14058; AAS1851.1; -  
 DR PIR; A24170; C1HURB.  
 DR PDB; 1APQ; 17-SEP-97.  
 DR PDB; 1GPZ; 31-JUL-02.  
 DR MEROPS; S01.192; -  
 DR Genew; HGNC:1246; C1r.  
 DR MIM; 216950; -  
 DR GO; GO:0003815; F:complement component C1r activity; TAS.  
 DR GO; GO:0008236; F:serine-type peptidase activity; TAS.  
 DR GO; GO:0006955; P:immune response; TAS.  
 DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
 DR InterPro; IPR000859; CUB.  
 DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
 DR Pfam; PF00431; CUB; 2.  
 DR Pfam; PF00084; sushi; 2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00032; CCP; 2.  
 DR SMART; SM00042; CUB; 2.  
 DR SMART; SM00179; EGF\_Ca; 1.  
 DR SMART; SM00020; TRYP\_SPC; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS01180; CUB; 2.  
 DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS01187; EGF\_Ca; 1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; FALSE\_NEG.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Complement pathway; plasma; Glycoprotein; Serine protease; Hydrolase;  
 KW Hydroxylation; Phosphorylation; Sushi; Repeat; Signal;  
 KW EGF-like domain; 3D-structure; Polymorphism.  
 FT SIGNAL 1 17  
 FT CHAIN 18 463 COMPLEMENT C1R HEAVY CHAIN.  
 FT CHAIN 464 705 COMPLEMENT C1R LIGHT CHAIN.  
 FT DOMAIN 18 141 CUB 1.  
 FT DOMAIN 142 190 EGF-LIKE, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 193 305 CUB 2.  
 FT DOMAIN 308 372 SUSHI 1.  
 FT DOMAIN 375 448 SUSHI 2.  
 FT DOMAIN 464 705 SERINE PROTEASE.  
 FT ACT\_SITE 502 502 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 557 557 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 654 654 CHARGE RELAY SYSTEM.  
 FT MOD\_RES 167 167 HYDROXYLATION.  
 FT MOD\_RES 206 206 PHOSPHORYLATION (BY CK2).  
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 514 514 N-LINKED (GLCNAC. . .).

FT CARBOHYD 581 581 N-LINKED (GLCNAC. . .).  
 FT DISULFID 71 89 PROBABLE.  
 FT DISULFID 146 165  
 FT DISULFID 161 174  
 FT DISULFID 176 189  
 FT DISULFID 193 220 PROBABLE.  
 FT DISULFID 250 268 PROBABLE.  
 FT DISULFID 309 358 PROBABLE.  
 FT DISULFID 338 371 PROBABLE.  
 FT DISULFID 376 429 PROBABLE.  
 FT DISULFID 406 447 PROBABLE.  
 FT DISULFID 451 577 INTERCHAIN (PROBABLE).  
 FT DISULFID 620 639 POTENTIAL.  
 FT DISULFID 650 680 POTENTIAL.  
 FT VARIANT 152 152 S -> L (in dbSNP:1801046).  
 FT TURN 145 147 /FTid=VAR\_016103.  
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 FT TURN 160 161  
 FT STRAND 164 168  
 FT TURN 169 170  
 FT STRAND 171 175  
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 FT STRAND 189 190  
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 Query Match 10.2%; Score 403.5; DB 1; Length 705;  
 Best Local Similarity 22.9%; Pred. No. 8.9e-23;  
 Matches 178; Conservative 96; Mismatches 259; Indels 245; Gaps 41;  
 QY 44 ECEYDQIEC-----VC-----PGKEVVGYTIPCC-----RNEECED 77  
 DB EGCFYDVYKISADKSLGRFCGLGSLGNPPGKFKFMSQGNKMLLTFHTDFSNEEN--G 126  
 QY 78 SCLHPGCTIF---ENCKSCENGSGGTLD-----DFYVKGFGYCAECRAG----- 120  
 DB TIMFKGFLAYYQAVLDDECASSRSGEEDPQOCQHLCHNYGVGYPCS-CRPGTELOED 185  
 QY 121 ---YGGDCMRGQVLRAPKQI-LLE---SYPLNAHCEWTTHAKPGFVIQLRFVMSLSEF 173  
 DB RHSCQAECSSELYTEASGYISSLEYPRSYPLDLRCNYSIRVERGLTLHLKLE---PF 240  
 QY 174 D-----YMCQYDVYVVRDGNRDGQIIKRVCGNERPAPIOSIGSSSLHLVLFHSDGSKNFD 227  
 DB DIDDHQVHCYDQIQI---YANGKNIGFCGKQRPDLDTSSNAVDLLFTFDESQDSR 296  
 QY 228 GFHAIY-EEITACSSSPCFHDGTCLVDKAGSYKACLAGYTGQRCENLEERNCSDPGP 286  
 DB GWKURYTTEIIKCPQPKTLDFTIIQNLPQYQ---FRDYFIATCK----- 339  
 QY 287 VNGYQKITGGPGLINGRHAKIGTVVSPFCNNYSYVLGSGNEKRTCCQNGSWSGKQPTIC- 345  
 DB -GGYKISDLVRRVLPQVQSRPTPLHQLYSAAPSKQLQSAPTYKPPALPGDL-----PM 401  
 QY 346 CREPKISDLVRRVLPQVQSRPTPLHQLYSAAPSKQLQSAPTYKPPALPGDL-----PM 401  
 DB CGQPR-----CGQPR-----NLPNGDFRYTTM 393  
 QY 402 GVOHLHTLOQECISPFYR---RLGSSRR---TCLRTGKWSG-----RAPSCIPICGK 448  
 DB GUNYKARIQYTCHEPYKQYKQTRAGSRESEGVYTCAGGIWKQEKQKQKPRCLPVGCK 453  
 QY 449 TEN-----ITAPKTQGLRWPMQAAIYRRRTSGVHDGSLHKGAWFLVCSGALVNRVTV 500  
 DB PWNVPEQRRIIGGQKAKMGFPWQV---FTNIHG---RG-----GGALLDRWIL 498  
 QY 501 VAAHCVTLGKVTMIKTADLKVILKGFYRDDDRDEKTIQSLQ-----ISAILLPNY-- 552  
 DB TAAHTLYPKHEAQ-SNASLDVFLG-----HTNVEELMKLGNHPIRRVSHPDYRQ 548  
 QY 553 -DPILLDADIAILKLDKARISTRVQPICLAASRDLSSTFQESHI-TVAGWNVLAD----- 606

Db 549 DESVNEFDIALLELENSVTLGPNLLPICLP---DNDTFYDLGLMGVSGFGVMEKIAH 605  
 Qy 607 ---VSPGKNDTLRSGVVVDLLCERQEDHGIPVSVTDNMFCSWEPAPSDICT 662  
 Db 606 DLRFVRLP-----VANPQCEWLKGRKMDVFSQNMPCAG-HPSLKQDACQ 651  
 Qy 663 AETGGIAAFAVFPGRASPEPRHMLGLVSWSYDKTCSHRLSTAFKVLPPKDWIERNMK 720  
 Db 652 GDSGGVFAVRDPN----TDRWATGIVSWGIG--CS-RGVGFTVKLVNYVDWIKEME 702

RESULT 6  
 MAS2 HUMAN  
 ID MAS2 HUMAN STANDARD; PRT; 696 AA.  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Mannan-binding lectin serine protease 2 precursor (EC 3.4.21.-)  
 DE (Mannose-binding protein associated serine protease 2) (MASP-2)  
 DE (MBL-associated serine protease 2).  
 GN MASP2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Liver;  
 RX MEDLINE=97242412; PubMed=9087411;  
 RA Thiel S., Jensen T.V., Stover C.M., Schwaebler W.J., Laursen S.B.,  
 RA Poulsen K., Willis A.C., Eggleton P., Hansen S., Holmskov U.,  
 RA Reid K.B.M., Jensenius J.C.,  
 RA "A second serine protease associated with mannan-binding lectin that  
 RT activates complement.";  
 RL Nature 386:506-510 (1997).  
 [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Thiel S., Vorup-Jensen T., Stover C.M., Schwaebler W., Laursen S.B.,  
 RA Poulsen K., Willis A.C., Eggleton P., Hansen S., Holmskov U.,  
 RA Reid K.B.M., Jensenius J.C.,  
 RA "Identification and characterization of a novel protein of the human  
 RT complement system, mannan-binding lectin-associated serine protease-2  
 (MASP-2).";  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE=Liver;  
 RX MEDLINE=99192764; PubMed=10092804;  
 RA Stover C.M., Thiel S., Thelen M., Lynch N.J., Vorup-Jensen T.,  
 RA Jensenius J.C., Schwaebler W.J.,  
 RA "Two constituents of the initiation complex of the mannan-binding  
 RT lectin activation pathway of complement are encoded by a single  
 structural gene.";  
 RL J. Immunol. 162:3481-3490 (1999).  
 [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RX MEDLINE=99262289; PubMed=10330290;  
 RA Takahashi M., Endo Y., Fujita T., Matsushita M.,  
 RA "A truncated form of mannose-binding lectin-associated serine  
 RT protease (MASP)-2 expressed by alternative polyadenylation is a  
 component of the lectin complement pathway.";  
 RL Int. Immunol. 11:859-863 (1999).  
 [5]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RA Park D., Kim B., Baek K., Yoon J.,  
 RA "Structure of human MASP-2 gene.";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Trypsin protease that presumably plays an important role  
 CC in the initiation of the mannose-binding lectin (MBL) complement  
 CC activation pathway. After activation it cleaves C4 generating C4a  
 CC and C4b.

CC -1- SUBUNIT: Isoform 2 binds to MASP-1.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=O00187-1; Sequence=Displayed;  
 CC Name=2; Synonyms=MAP19, Small MBL-associated protein, sMAP;  
 CC IsoId=O00187-2; Sequence=VSP\_005383, VSP\_005384;  
 CC -1- SIMILARITY: Belongs to peptidase family S1.  
 CC -1- SIMILARITY: Contains 2 CUB domains.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.  
 CC -1- SIMILARITY: Contains 2 Sushi (SCR) domains.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; Y09926; CAA71059.1; -;  
 CC EMBL; X98400; CAA67050.1; -;  
 CC EMBL; Y18281; CAB50728.1; -;  
 CC EMBL; Y18283; CAB50730.1; -;  
 CC EMBL; Y18284; CAB50731.1; -;  
 CC EMBL; Y18286; CAB50732.1; -;  
 CC EMBL; Y18286; CAB50733.1; -;  
 CC EMBL; Y18287; CAB50734.1; -;  
 CC EMBL; Y18287; CAB50735.1; -;  
 CC EMBL; A3008047; BAA78616.1; -;  
 CC EMBL; A3033742; BAA85658.1; -;  
 CC EMBL; AF321562; AAG50274.1; -;  
 CC EMBL; AF321558; AAG50274.1; JOINED.  
 CC EMBL; AF321559; AAG50274.1; JOINED.  
 CC EMBL; AF321560; AAG50274.1; JOINED.  
 CC EMBL; AF321561; AAG50274.1; JOINED.  
 CC EMBL; AF321558; AAG50275.1; -;  
 CC PIR; A59271; A59271.  
 CC HSP; P00763; IDPO.  
 CC MEROPS; S01.229; -;  
 CC Genew; HGNC:6902; MASP2.  
 CC MIM; 605102; -;  
 CC GO; GO:0004252; F-serine-type endopeptidase activity; TAS.  
 CC GO; GO:0006960; P-antimicrobial humoral response (sensu Inver. . . ; TAS.  
 CC GO; GO:0006956; P-complement activation; TAS.  
 CC InterPro; IPR000152; Asx hydroxyl\_S.  
 CC InterPro; IPR000859; CUB.  
 CC InterPro; IPR009003; Cys\_Ser\_trypsin.  
 CC InterPro; IPR01881; EGF\_Ca.  
 CC InterPro; IPR006209; EGF\_Like.  
 CC InterPro; IPR01254; Peptidase\_S1.  
 CC InterPro; IPR01314; Peptidase\_S1A.  
 CC InterPro; IPR000436; Sushi\_SCR\_CCP.  
 CC Pfam; PF00431; CUB; 2.  
 CC Pfam; PF00084; sushi; 2.  
 CC PRINTS; P00089; trypsin; 1.  
 CC SMART; SM00032; CCP; 2.  
 CC SMART; SM00042; CUB; 2.  
 CC SMART; SM00179; EGF\_Ca; 1.  
 CC SMART; SM00020; Tryp\_Spc; 1.  
 CC PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 CC PROSITE; PS01180; CUB; 2.  
 CC PROSITE; PS01186; EGF\_2; 1.  
 CC PROSITE; PS01187; EGF\_Ca; 1.  
 CC PROSITE; PS02040; TRYPSIN\_DOM; 1.  
 CC PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 CC PROSITE; PS00135; TRYPSIN\_SER; 1.  
 CC Hydrolase; Complement pathway; Serine protease; Protease;  
 CC Glycoprotein; Sushi; Repeat; Signal; EGF-like domain; Hydroxylation;  
 CC Alternative splicing.  
 CC SIGNAL 1 15 POTENTIAL.  
 CC CHAIN 15 686 MANNAN-BINDING LECTIN SERINE PROTEASE 2.  
 FT





DR InterPro; IPR000152; Abx\_hydroxyl\_S.  
 DR InterPro; IPR000859; CUB.  
 DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
 DR Pfam; PF00431; CUB; 2.  
 DR Pfam; PF00008; EGF; 1.  
 DR Pfam; PF00084; sushi; 2.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00032; CCP; 2.  
 DR SMART; SM00042; CUB; 2.  
 DR SMART; SM00179; EGF\_Ca; 1.  
 DR SMART; SM00200; Tryp\_Ser; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS01180; CUB; 2.  
 DR PROSITE; PS00022; EGF\_1; FALSE NEG.  
 DR PROSITE; PS01186; EGF\_2; FALSE NEG.  
 DR PROSITE; PS01187; EGF\_Ca; 1.  
 DR PROSITE; PS02040; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; FALSE NEG.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolase; Serine protease; Extracellular matrix; Calcium-binding;  
 KW Vitamin K; Repeat; Signal; EGF-like domain; Sushi; Glycoprotein;  
 KW Gamma-carboxyglutamic acid; Hydroxylation.  
 FT SIGNAL 1 21  
 FT CHAIN 22 695  
 FT CHAIN 22 444  
 FT CHAIN 445 695  
 FT DOMAIN 22 124  
 FT DOMAIN 22 136  
 FT DOMAIN 181 296  
 FT DOMAIN 297 349  
 FT DOMAIN 352 415  
 FT DOMAIN 137 178  
 FT DOMAIN 155 155  
 FT MOD\_RES 482 482  
 FT ACT\_SITE 536 536  
 FT ACT\_SITE 638 638  
 FT DISULFID 141 153  
 FT DISULFID 149 162  
 FT DISULFID 164 177  
 FT CARBOHYD 180 180  
 FT CARBOHYD 413 413  
 FT SEQUENCE 695 AA; E924F7E6340700D0 CRC64;  
 Query Match 9.6%; Score 378.5; DB 1; Length 695;  
 Best Local Similarity 21.8%; Pred. No. 6.7e-21;  
 Matches 168; Conservative 81; Mismatches 227; Indels 293; Gaps 35;  
 QY 137 GQILL-----ESYPLNAHCEWTIHKAPGVIGLRFVWLSLEPDYMCQDYVEVRGDNRDG 192  
 DB 27 GEILSPNYQAYPNEMETKTDIEVPEGFGVRLYETHLDMSELSECEYDSVQIISGVVEEG 86  
 QY 193 QIIKRVCGNERP-----API-----QSIGSLHLVLFHSDGS---KNFDGHHAYI-----BEIT 237  
 DB 87 -----RLCGQRTSKVANSPIVEEFQIPYKQVIFRSDFSNEERTGTGAAYAAIDVNECT 142  
 QY 238 ACSSSPCFHDGTCVLKAGSKYKCACLAGY-----  
 DB 143 DFTDVPCHSFNCNFI---GGYFCPCPEYFLHDDMRNGVNCGNVFTALIGEISSNYP 199  
 QY 267 -----TGQRCEN---LIEE-----RNCSDP----- 283  
 DB 200 NPYPENSRCYQILLEEGFVVVTTIQREDFDVEPADSQGNQDSLLFAAKVRQGFPGCN 259  
 QY 284 -----GGPVNGYQKITGCP----- 297

Db 260 GFPPEPTIETHSNTLDIVFQDTLQTECKGKWLRYHGDPIPCPKBITANSVMAPEKAKYVF 319  
 QY 298 -----GLNGRHAKIGTIVVSPFCNNSYVLSGNEKRTCCQNGEWSGK---QPICIKACR 347  
 Db 320 KDVVKISCVDGFEAVEGNGSTFFYS-----TCQNGQWNSRLRCQFV---DCG 366  
 QY 348 EPKISDLVRRRLVPMQVQSRRETPLHQLYSNAPSQKQLQSAPTKKPALPFGDLPMGYQHLH 407  
 Db 367 IPE-----PIQNGKVDPTLFGSV----- 387  
 QY 408 TQLQYECISPFY-----RRLGSSRRRTCLRTCKWSG-----RAPSCIPICGKIENITAPKTQ 458  
 Db 388 --IHYCEEPTTYMEHAHGEYR-CAANGSWNDDELTELPCKVPVCG-----VPTE 437  
 QY 459 GLRWPQAAIYRRTSGVHDGSLHKGAW-----FLVCSGALVNERTVVVAHCVTDLGKVT 513  
 Db 438 PFR-----IQQRIFGGFPKIQSFQWFFEPFRAGGALIGEHWLTAHVVEGSDPS 491  
 QY 514 M-IKTADLKVLGKFYRDDDRDEKTIQSLOISAILHPNYDP-----ILLDADIALK 565  
 Db 492 MYVGSTSVRM-----ENLANYQKLTDRVIIHPGKPGDDLSTRTNFNDIALVR 541  
 QY 566 LLDKARISTRVQPICLAASRDLSLTSFQESH---ITVAGW-----NVLADVRSPGPKNDT 616  
 Db 542 LKDPVMGPTVSFICLPGI---SSEYEPSEGDLGLISGWRTERNVIVQLR----- 590  
 QY 617 LRSQVSVVVDL-----LCEEQHEHGIPVSVTDNMFCASWEPTAPSDICTAETGGTAAV 671  
 Db 591 --GAKLPVTSLEKCRQVKEENPKARADDYVFTSNMICAGEKGV---DSQCGSDGGAFAL 644  
 QY 672 SFGRASPAPRWHLMLGWSYDKTCSHRLSTAFTKVLFPKDWIERNMK 720  
 Db 645 PVEN--VRDPKFFYVAGLVNMG--KKCG--TYGIYTKVQYKDWILQTMQ 687  
 RESULT 8  
 CLS\_HUMAN  
 ID CLS\_HUMAN STANDARD; PRT; 688 AA.  
 AC P09871; Q9UCU7; Q9UCU8; Q9UCU9; Q9UCV0; Q9UCV1; Q9UCV2; Q9UCV3;  
 AC Q9UCV4; Q9UCV5; Q9UM14;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Complement C1s component precursor (EC 3.4.21.42) (C1 esterase).  
 GN C1S.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89017187; PubMed=2459702;  
 RA Kusumoto H., Hiroseawa S., Salier J.-P., Hagen F.S., Kurachi K.;  
 RT "Human genes for complement components C1r and C1s in a close  
 RT tail-to-tail arrangement";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:7307-7311(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=88082788; PubMed=3500856;  
 RA McKinnon C.M., Carter P.E., Smyth S.J., Dunbar B., Fothergill J.E.;  
 RT "Molecular cloning of cDNA for human complement component C1s. The  
 RT complete amino acid sequence.";  
 RL Eur. J. Biochem. 169:547-553(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88163522; PubMed=2831944;  
 RA Tesi M., Duponchel C., Mao T., Jülicher C.;  
 RT "Complete cDNA sequence of human complement C1s and close physical  
 RT linkage of the homologous genes C1s and C1r";  
 RL Biochemistry 26:8516-8524(1987).  
 RN [4]



RP SEQUENCE FROM N.A.  
RC TISSUE=PNS;  
RX MEDLINE=2338257; PubMed=12477932;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wegner L., Shemen C.N., Schuler G.D.,  
RA Altschul S.F., Ziegler B., Bueckel K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Lomellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RA "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP SEQUENCE OF 1-329 FROM N.A.  
RC TISSUE=Peripheral blood leukocytes;  
RX MEDLINE=99008558; PubMed=9794427;  
RA Endo Y., Takahashi M., Nakao M., Saiga H., Sekine H., Matsushita M.,  
RA Nonaka M., Fujita T.,  
RT "Two lineages of mannose-binding lectin-associated serine protease  
RT (MASP) in vertebrates";  
RL J. Immunol. 161:4924-4930(1998).  
RN [6]  
RP SEQUENCE OF 291-688 FROM N.A.  
RX MEDLINE=90040704; PubMed=2553984;  
RA Tosi M., Duponchel C., Meo T., Couture-Tosi E.,  
RT "Complement genes C1r and C1s feature an intronless serine protease  
RT domain closely related to haptoglobin";  
RL J. Mol. Biol. 208:709-714(1989).  
RN [7]  
RP SEQUENCE OF 16-61; 168-219; 287-334 AND 384-445.  
RX MEDLINE=86164350; PubMed=3007145;  
RA Spycher S.E., Nick H., Rickli E.E.,  
RT "Human complement component C1s. Partial sequence determination of  
RT the heavy chain and identification of the peptide bond cleaved during  
RT activation";  
RL Eur. J. Biochem. 156:49-57(1986).  
RN [8]  
RP SEQUENCE OF 438-500; 503-534; 542-601; 617-623 AND 626-656.  
RX MEDLINE=84104122; PubMed=6362661;  
RA Carter P.E., Dunbar B., Fothergill J.E.,  
RT "The serine proteinase chain of human complement component C1s.  
RT Cyanogen bromide cleavage and N-terminal sequences of the  
RT fragments";  
RL Biochem. J. 215:565-571(1983).  
RN [9]  
RP PARTIAL SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=91308095; PubMed=1854725;  
RA Illy C., Thielens N.M., Gagnon J., Arlaud G.J.,  
RT "Effect of lactoperoxidase-catalyzed iodination on the Ca(2+)-  
RT dependent interactions of human C1s. Location of the iodination  
RT sites";  
RL Biochemistry 30:7135-7141(1991).  
RN [10]  
RP DISULFIDE BONDS.  
RX MEDLINE=91175725; PubMed=2007122;  
RA Hess D., Schaller J., Rickli E.E.,  
RT "Identification of the disulfide bonds of human complement C1s";  
RL Biochemistry 30:2827-2833(1991).  
RN [11]  
RP PARTIAL SEQUENCE, AND 3D-STRUCTURE MODELING OF CATALYTIC DOMAIN.  
RX MEDLINE=95298736; PubMed=7779774;

RA Rossi V., Gaboriaud C., Lacroix M., Ulrich J., Pontecilla-Camps J.C.,  
RA Gagnon J., Arlaud G.J.,  
RT "Structure of the catalytic region of human complement protease C1s:  
RT study by chemical cross-linking and three-dimensional homology  
RT modeling";  
RL Biochemistry 34:7311-7321(1995).  
RN [12]  
RA MEDLINE=21286517; PubMed=11390518;  
RX Dragon-Durey M.-A., Quartier P., Fremeaux-Bacchi V., Blouin J.,  
RA de Barace C., Prieur A.-M., Weiss L., Fridman W.-H.,  
RT "Molecular basis of a selective C1s deficiency associated with early  
RT onset multiple autoimmune diseases";  
RL J. Immunol. 166:7612-7616(2001).  
CC -|- FUNCTION: C1s B chain is a serine protease that combines with C1q  
CC and C1r to form C1, the first component of the classical pathway  
CC of the complement system. C1r activates C1s so that it can, in  
CC turn, activate C2 and C4.  
CC -|- CATALYTIC ACTIVITY: Cleaves component C4 to C4a and C4b (Arg-|-Ala  
CC bond), and component C2 to C2a and C2b (Lys(or Arg)-|-Lys bond).  
CC -|- SUBUNIT: C1 is a calcium-dependent trimolecular complex of C1q,  
CC C1r and C1s in the molar ratio of 1:2:2. Activated C1s is an  
CC disulfide-linked heterodimer of a heavy chain and a light chain.  
CC -|- DISEASE: Defects in C1S are the cause of selective C1s deficiency  
CC [MIM:120580]; that is associated with early onset multiple  
CC autoimmune diseases.  
CC -|- SIMILARITY: Belongs to peptidase family S1.  
CC -|- SIMILARITY: Contains 2 CUB domains.  
CC -|- SIMILARITY: Contains 1 EGF-like domain.  
CC -|- SIMILARITY: Contains 2 Sushi (SCR) domains.  
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CC -----  
DR EMBL; X06596; CAA29817.1; -;  
DR EMBL; J04080; AAA51852.1; -;  
DR EMBL; M18767; AAA51853.1; -;  
DR EMBL; BC056903; AAU56903.1; -;  
DR EMBL; AB009076; BA86864.1; -;  
DR PDB; 1ELV; 14-MAR-01.  
DR MEROPS; S01.193; -;  
DR SWISS-2DPAGE; P09871; HUMAN.  
DR Genew; HGNC:1247; C1S.  
DR MIM; 120580; -;  
DR GO; GO:0003816; P:complement component C1s activity; TAS.  
DR GO; GO:0008236; F:serine-type peptidase activity; TAS.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR009003; Cys\_Ser\_trypsin.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
DR Pfam; PF00431; CUB; 2.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00084; eushi; 2.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS01180; CUB; 2.  
DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; FALSE\_NEG.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Complement pathway; Plasma; Glycoprotein; Serine protease; Hydrolase;

Hydroxylation; Sushu; Repeat; Signal; EGF-like domain;  
Calcium-binding; Polymorphism; 3D-structure.

SIGNAL 1 15  
CHAIN 16 437 COMPLEMENT C1S HEAVY CHAIN.  
CHAIN 438 688 COMPLEMENT C1S LIGHT CHAIN.  
DOMAIN 16 130 CUB 1.  
DOMAIN 131 172 EGF-LIKE, CALCIUM-BINDING (POTENTIAL).  
DOMAIN 175 290 CUB 2.  
DOMAIN 293 355 SUSHU 1.  
DOMAIN 358 422 SUSHU 2.  
DOMAIN 438 688 SERINE PROTEASE.  
ACT\_SITE 475 475 CHARGE RELAY SYSTEM.  
ACT\_SITE 529 529 CHARGE RELAY SYSTEM.  
ACT\_SITE 632 632 CHARGE RELAY SYSTEM.  
MOD\_RES 149 149 HYDROXYLATION (PROBABLE).  
CARBOHYD 174 174 N-LINKED (GLCNAC. . .).  
CARBOHYD 406 406 N-LINKED (GLCNAC. . .).  
DISULFID 65 83  
DISULFID 135 147

Query Match 8.5%; Score 334; DB 1; Length 688;  
Best Local Similarity 21.7%; Pred. No. 1.5e-17;  
Matches 163; Conservative 83; Mismatches 246; Indels 260; Gaps 37;

QY 137 GOILL-----ESYPLNAHCEHTIAXPGFVIQLRPVMSLEFDYMCQDYVEVRDGNRDG 192  
DB 21 GEILSPNPOAYPSEVEKSDIEVPEGYGIHLFTHLDIELSENCAVDSVQIISGDEEG 80  
QY 193 QIIKRVCGNERPAPI-----OSIGSLHLVPHSDGS--KNFDGPHAIY--BEITACS--S 241  
DB 81 RLCGQRSSNPHPIVEEPQVFNKLVIFKSDFSNEERTGTGAANYVATDINECTDFVD 140  
QY 242 SPCFHDGTCLVDKAGSYKCACLAGY----- 266  
DB 141 VPCSHFCNFI---GGYFCSCPPEYFLHDDMKNGVNSGDVFTALIGETASPNPKYP 197  
QY 267 TGORCENLL-----FERNCS-----PGPVNGQKIT 294  
DB 198 ENSRCQIRLEKGFQVVVTLRREDFDVEAADSAGNCLDSLAVAGDQPGFYCGH----- 253  
QY 295 GGPGLIN-----GRHAK--I 307  
DB 254 GFQPLNIETKSNALDIIFQDTDLTGKKGWKLRYHGDPMCPKEDTPNSWVEPAKAYVF 313  
QY 308 GTVVSFFCNYS-VLSG-----NEKRTQQNGWMSGK-----QPTICAKREPISDLVRR 357  
DB 314 RDVVQITCLDGFVEVGRVCGATSFYSTCQNGKWSNKLKCPV---DCGIP----- 362  
QY 358 RVLPMQVQSRTEPLHQLYSAFSKQKQSAPTKP-ALPFGDLPNGVQHLHTQLQYECIS 416  
DB 363 -----ESIENGKVEDPESTLFGSV-----IRYTCEE 388  
QY 417 PFY--RRLGSSRRTLCTRTGKWSGRA-----PSCIPICGKIENITAPKTQGLRWPQAAIY 469  
DB 389 PYYMENGSGGGEVHCAGNSWNEVLGPPLKCPVCG-----VP-----RPFPEEK-- 435  
QY 470 RRTSGVHDSGLHKGANFLV-----CSGALVNERVTVVAAHCVTDLKGVTMIKTADLKVIL 524  
DB 436 QRIIGSDADIKNPPMQVFPDNPWAGGALLINEYVLTAAHVGEGRPTM-----YV 487  
QY 525 GKFRDDEKTKTQSLQISAILHPNYDPILL-----DADIALKLLDKARISTRVQ 577  
DB 488 GSTSVQTSRLAKS-KMLTPHFVTHPGKULLEVPPEGRNTFNDIALVRLKDPVYMGFTVS 546  
QY 578 PICLAASRDLSFQESHITVAGWNLADVRSFGKND-----TLRSGVSVVSDLSLCEEQH 634  
DB 547 PICLPGTSSDYNLMDGLGLISGW-----RTE--KEDRAVRLKARLPVAPLRKCKEVK 599  
QY 635 EDHGIPVS-----VTDNMFCASWEPTAPSDICTAETGTGTAASVFPGRASPERPHLMGL 688  
DB 600 VEK--PTADAAYVFTENMTGAGGE--KGMDSCKGSDGGFAVQDP---NDKTKFVAAGL 652  
QY 689 VMSYDKTCSHRLSTAFTKVLPPFKDIERNMK 720

DB 653 VSWG--PQCG--TYGLYTRVKNYVDWIMTMQ 680

RESULT 9

ENTK\_HUMAN STANDARD; PRT; 1019 AA.

AC P98073;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Enteropeptidase precursor (EC 3.4.21.9) (Enterokinase).  
GN PRSS7 OR ENTK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Duodenum;  
RX MEDLINE=95234679; PubMed=7718557;  
RA Kitamoto Y., Veille R.A., Denis-Keller H., Sadler J.E.;  
RT "cDNA sequence and chromosomal localization of human enterokinase,  
RL Biochemistry 34:4562-4568 (1995)."  
RN [2]  
RP SEQUENCE FROM N.A., AND DISEASE.  
RX MEDLINE=21606074; PubMed=11719902;  
RA Holzinger A., Maier E.M., Buck C., Mayerhofer P.U., Kappler M.,  
RA Haworth J.C., Moroz S.P., Hadorn H.-B., Sadler J.E., Roscher A.A.;  
RT "Mutations in the proenteropeptidase gene are the molecular cause of  
RL congenital enteropeptidase deficiency.";  
Am. J. Hum. Genet. 70:20-25 (2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20289799; PubMed=10830953;  
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,  
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,  
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,  
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,  
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,  
RA Rosenthal A., Sasaki T., Shibuya K., Kawasaki K., Asakawa S.,  
RA Shintani A., Shimizu N., Nordliek G., Mitsuyama S., Antonarakis S.E.,  
RA Minoshima S., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,  
RA Scharfe M., Beck A., Klages S., Hennig S., Rieselmann L., Dagand E.,  
RA Ramser J., Borzym K., Gardiner K., Nizetic D., Francis F.,  
RA Wehrmeyer S., Reinhardt R., Vaspo M.-L.;  
RT "The DNA sequence of human chromosome 21.";  
RL Nature 405:311-319 (2000).  
RN [4]  
RP SEQUENCE OF 749-1019 FROM N.A.  
RC TISSUE=Duodenum;  
RX MEDLINE=94329561; PubMed=8052624;  
RA Kitamoto Y., Yuan X., Wu Q., McCourt D.W., Sadler J.E.;  
RT "Enterokinase, the initiator of intestinal digestion, is a mosaic  
RL protease composed of a distinctive assortment of domains.";  
Proc. Natl. Acad. Sci. U.S.A. 91:7588-7592 (1994).  
CC -I- FUNCTION: Responsible for initiating activation of pancreatic  
CC proteolytic proenzymes (trypsin, chymotrypsin and carboxypeptidase  
CC A). It catalyzes the conversion of trypsinogen to trypsin which in  
CC turn activates other proenzymes including chymotrypsinogen,  
CC procarboxypeptidases, and proelastases.  
CC -I- CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-|-Ile-7 bond in  
CC trypsinogen.  
CC -I- SUBUNIT: Heterodimer of a catalytic (light) chain and a  
CC multidomain (heavy) chain linked by a disulfide bond.  
CC -I- SUBCELLULAR LOCATION: Type II membrane protein (Probable).  
CC -I- TISSUE SPECIFICITY: Intestinal brush border.  
CC -I- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS  
CC CLEAVED BY A TRYPSIN-LIKE PROTEASE.  
CC -I- DISEASE: Defects in PRSS7 are a cause of enterokinase deficiency  
CC [MIM:226200]; a life-threatening intestinal malabsorption disorder

characterized by diarrhea and failure to thrive.

-1- SIMILARITY: Belongs to peptidase family S1.  
 -1- SIMILARITY: Contains 2 CUB domains.  
 -1- SIMILARITY: Contains 2 LDL-receptor class A domains.  
 -1- SIMILARITY: Contains 1 MAM domain.  
 -1- SIMILARITY: Contains 1 SEA domain.  
 -1- SIMILARITY: Contains 1 SRCR domain.  
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EMBL; U09860; AAC50138.1; -  
 EMBL; Y19124; CAB65555.1; -  
 EMBL; Y19125; CAB65555.1; JOINED.  
 EMBL; Y19126; CAB65555.1; JOINED.  
 EMBL; Y19127; CAB65555.1; JOINED.  
 EMBL; Y19128; CAB65555.1; JOINED.  
 EMBL; Y19129; CAB65555.1; JOINED.  
 EMBL; Y19130; CAB65555.1; JOINED.  
 EMBL; Y19131; CAB65555.1; JOINED.  
 EMBL; Y19132; CAB65555.1; JOINED.  
 EMBL; Y19133; CAB65555.1; JOINED.  
 EMBL; Y19134; CAB65555.1; JOINED.  
 EMBL; Y19135; CAB65555.1; JOINED.  
 EMBL; Y19136; CAB65555.1; JOINED.  
 EMBL; Y19137; CAB65555.1; JOINED.  
 EMBL; Y19138; CAB65555.1; JOINED.  
 EMBL; Y19139; CAB65555.1; JOINED.  
 EMBL; Y19140; CAB65555.1; JOINED.  
 EMBL; Y19141; CAB65555.1; JOINED.  
 EMBL; Y19142; CAB65555.1; JOINED.  
 EMBL; Y19143; CAB65555.1; JOINED.  
 EMBL; AL163218; CAB90392.1; -  
 EMBL; AL163217; CAB90389.1; -  
 PIR; A56318; A56318.  
 HSP; P00763; LDPO.  
 MEROPS; S01.156; -  
 Genew; HGNC:9490; PRS57.  
 MIM; 606635; -  
 MIM; 228200; -  
 GO; GO:0005903; C:brush border; TAS.  
 InterPro; IPR000859; CUB.  
 InterPro; IPR009003; Cys Ser trypsin.  
 InterPro; IPR002172; LDL\_receptor\_A.  
 InterPro; IPR000998; MAM\_domain.  
 InterPro; IPR001254; Peptidase\_S1.  
 InterPro; IPR001314; Peptidase\_S1A.  
 InterPro; IPR000082; SEA\_domain.  
 InterPro; IPR001190; Srcf\_receptor.  
 Pfam; PF00431; CUB; 2.  
 Pfam; PF00057; ldl\_recept\_a; 2.  
 Pfam; PF00629; MAM; 1.  
 Pfam; PF01390; SEA; 1.  
 Pfam; PF00530; SRCR; 1.  
 Pfam; PF00089; trypsin; 1.  
 PRINTS; PR00722; CHYMOTRYPSIN.  
 PRINTS; PR00261; LDLRECEPTOR.  
 PRINTS; PR00020; MAMDOMAIN.  
 SMART; SM00042; CUB; 2.  
 SMART; SM00192; LDLa; 2.  
 SMART; SM00137; MAM; 1.  
 SMART; SM00200; SEA; 1.  
 SMART; SM00202; SR; 1.  
 SMART; SM00020; Tryp\_SPC; 1.  
 PROSITE; PS01180; CUB; 2.  
 PROSITE; PS01209; LDLRA\_1; 2.  
 PROSITE; PS00068; LDLRA\_2; 2.  
 PROSITE; PS00740; MAM\_1; 1.

DR PROSITE; PS50060; MAM\_2; 1.  
 DR PROSITE; PS50024; SEA; 1.  
 DR PROSITE; PS00420; SRCR\_1; FALSE\_NEG.  
 DR PROSITE; PS0287; SRCR\_2; 1.  
 DR PROSITE; PS50240; TRYPsin\_DOM; 1.  
 DR PROSITE; PS00134; TRYPsin\_HIS; 1.  
 DR PROSITE; PS00135; TRYPsin\_SER; 1.  
 KW Signal-anchor; Glycoprotein; Myristate; Hydrolase; Serine protease;  
 KW Zymogen; Transmembrane; Repeat; Lipoprotein.  
 FT CHAIN 1 784  
 FT CHAIN 785 1019  
 FT DOMAIN 1 18  
 FT TRANSMEM 19 47  
 FT DOMAIN 48 1019  
 FT DOMAIN 52 169  
 FT DOMAIN 182 223  
 FT DOMAIN 225 334  
 FT DOMAIN 342 504  
 FT DOMAIN 524 634  
 FT DOMAIN 641 679  
 FT DOMAIN 678 771  
 FT DOMAIN 785 1019  
 FT ACT\_SITE 825 825  
 FT ACT\_SITE 876 876  
 FT ACT\_SITE 971 971  
 FT LIPID 2 2  
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 FT DISULFID 650 668  
 FT DISULFID 662 677  
 FT DISULFID 772 772  
 FT DISULFID 810 826  
 FT DISULFID 910 977  
 FT DISULFID 941 956  
 FT DISULFID 967 995  
 FT CARBOHYD 116 116  
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 FT CARBOHYD 179 179  
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 FT CARBOHYD 503 503  
 FT CARBOHYD 534 534  
 FT CARBOHYD 630 630  
 FT CARBOHYD 682 682  
 FT CARBOHYD 706 706  
 FT CARBOHYD 725 725  
 FT CARBOHYD 848 848  
 FT CARBOHYD 887 887  
 FT CARBOHYD 909 909  
 FT CARBOHYD 949 949  
 FT CONFLICT 134 134  
 FT CONFLICT 732 732  
 FT CONFLICT 754 771

Query Match 8.4%; Score 331.5; DB 1; Length 1019;  
 Best Local Similarity 22.9%; Pred. No. 3.8e-17;  
 Matches 136; Conservative 90; Mismatches 22; Indels 143; Gaps 27;  
 QY 143 SYPLNAHCEWTHAKPGFVQLRFLVMSLEFDYMCQDYVEVRDGNDRDQGIKRVCGNE 202  
 Db 545 SYPLNAFCVWILNAQKGNQLHLP---QEFDELINVDWEIRDGEADSLLVAVTG-- 598  
 QY 203 RPAPIQSIGSSLH-----VLFHSDGSKNP-DGFHAYVEEITACSSPCFDGTCV 251  
 Db 599 -PGPVKQVFTNTRMTVLLITNDVLARGGFKANFTTGYHLGIPE-----PC----- 643

252 LKAGSYKC---ACLA-----GYTORCENLLEERNCSDFGPNVNGYKQITGGPGLNG 302  
644 --KADHFOCKNGECVPLVNLCDGHL--HCBGSDGDEAD-----VRFNGTNNNGLVRP 693  
303 RHAKIGTVVSFFCNCNSVLSGNEKRTCOQNGESGKQPCIKACREPKISDLVRRVLPM 362  
694 RIQSIW-----HTACAENWTTQISNDVC-----QLLGL 721  
363 QVQSRETPHLQLYSAAFSKOKLOSAPTKPALPFGDLPMGYOHLHTQLOVEICISPFYRRL 422  
722 GSGNSSKPIFSTDGPP--VKLNTAPD-----GHLILTPSQCLQDSLRL 765  
423 GSRRTCLRTGKSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSLHK 482  
766 QCNHKSC-----GKLLAODITPKI--VGGSNAGEGAPWVVGLY-----YGR-- 807  
483 GANFLVCSGALVNERTVVAACHVTDLGVKMTKTADLKVLGKFRDDEKTKTQSLQ 542  
808 ----LUCGSLVSDWLVSAAHCV--YGR--NLEPSKWTAILGLHMKSNILTSQTVPRL- 858  
543 ISAILHPNYDPILLADIAILKLDKARISTRVQPCILASRDLSFQESHITVAGWN 602  
859 IDEBIVPNYRRKNDKNDIAWHELPKVNVDYIQCILPEENQVPPGR--NCSTIAGWG 916  
603 VLADVSPGPNITLSCGVSVVDSLLCERQEDHGIPVSVDNMPCASHEPTAPSDICT 662  
917 T---VYQGTANTILQEADVLLSNRCQQMPEY---NITENNICAGYE--EGGIDSCQ 968  
663 AETGGIAAVSPGRASPEPWHMLGLVSNYSYDKTCSHRLSTFTKVLPPFKDWE 716  
969 GDSGG-----PLMCQENNRWFLAGVTSFGYKALPNR--PGVYARVSRFTENIQ 1015  
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RESULT 10  
ENTK\_PIG STANDARD; PRT; 1034 AA.  
AC P98074;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DE 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Enteroproteptidase precursor (EC 3.4.21.9) (Enterokinase).  
GN PSS7 OR ENTK.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OC NCBI\_TaxID=9823;  
RN [1]  
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Ductal mucosa;  
RX MEDLINE=94327548; PubMed=8051081;  
RA Matsushima M., Ichinose M., Yahagi N., Kakei N., Tsukada S.,  
RA Miki K., Kurokawa K., Tashiro K., Shiohara K., Shinomiya K.,  
RA Uneyama H., Inoue H., Takahashi T., Takahashi K.;  
RT "Structural characterization of porcine enteroproteptidase";  
RL J. Biol. Chem. 269:19976-19982(1994).  
CC -1- FUNCTION: Responsible for initiating activation of pancreatic  
CC proteolytic proenzymes (trypsin, chymotrypsin and carboxypeptidase  
CC A). It catalyzes the conversion of trypsinogen to trypsin which in  
CC turn activates other proenzymes including chymotrypsinogen,  
CC procarboxypeptidases, and proelastases.  
CC -1- CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-|-Ile-7 bond in  
CC trypsinogen.  
CC -1- SUBUNIT: Heterotrimer of a catalytic (light) chain, a multidomain  
CC (heavy) chain, and a mini chain.  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Probable).  
CC -1- PFM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS  
CC CLEAVED BY A TRYPSIN-LIKE PROTEASE.  
CC -1- PFM: THE MINI CHAIN MAY BE CLEAVED BY ELASTASE.  
CC -1- SIMILARITY: Belongs to peptidase family S1.  
CC -1- SIMILARITY: Contains 2 CUB domains.  
CC -1- SIMILARITY: Contains 1 LDL-receptor class A domains.  
CC -1- SIMILARITY: Contains 1 MAM domain.  
CC -1- SIMILARITY: Contains 1 SEA domain.

CC -1- SIMILARITY: Contains 1 SRCR domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL; D30799; BAA06459.1; -  
CC HSP; P00763; IDPO.  
CC MEROPS; S01.156; -  
CC InterPro; IPR000859; CUB.  
CC InterPro; IPR009003; Cys\_ser\_trypsin.  
CC InterPro; IPR002172; LDL\_receptor\_A.  
CC InterPro; IPR000998; MAM domain.  
CC InterPro; IPR001254; Peptidase\_S1.  
CC InterPro; IPR001314; Peptidase\_S1A.  
CC InterPro; IPR000082; SEA\_domain.  
CC InterPro; IPR001190; Srcr\_receptor.  
CC Pfam; PF00431; CUB; 2.  
CC Pfam; PF00057; ldl\_recept\_a; 2.  
CC Pfam; PF00629; MAM; 1.  
CC Pfam; PF01390; SEA; 1.  
CC Pfam; PF00330; SRCR; 1.  
CC Pfam; PF00089; trypsin; 1.  
CC PRINTS; PR00722; CHYMOTRYPSIN.  
CC PRINTS; PR00261; LDLRECEPTOR.  
CC PRINTS; PR00020; MAMDOMAIN.  
CC SMART; SM00042; CUB; 2.  
CC SMART; SM00192; LDLA; 2.  
CC SMART; SM00137; MAM; 1.  
CC SMART; SM00200; SEA; 1.  
CC SMART; SM00202; SR; 1.  
CC SMART; SM00020; Tryp\_SPC; 1.  
CC PROSITE; PS01180; CUB; 2.  
CC PROSITE; PS01209; LDLRA\_1; 2.  
CC PROSITE; PS00088; LDLRA\_2; 2.  
CC PROSITE; PS00740; MAM\_1; 1.  
CC PROSITE; PS00060; MAM\_2; 1.  
CC PROSITE; PS00024; SEA; 1.  
CC PROSITE; PS00420; SRCR\_1; FALSE\_NEG.  
CC PROSITE; PS0287; SRCR\_2; 1.  
CC PROSITE; PS0240; TRYPsin\_DOM; 1.  
CC PROSITE; PS00134; TRYPsin\_HIS; 1.  
CC PROSITE; PS00135; TRYPsin\_SER; 1.  
CC Signal-anchor; Glycoprotein; Myristate; Hydrolase; Serine protease;  
CC Zymogen; Transmembrane; Repeat; Lipoprotein.  
CC CHAIN 52 117 NON-CATALYTIC M CHAIN (MINI CHAIN).  
CC CHAIN 118 799 NON-CATALYTIC H CHAIN (HEAVY CHAIN).  
CC CHAIN 800 1034 CATALYTIC L CHAIN (LIGHT CHAIN).  
CC DOMAIN 1 18 CYTOPLASMIC (POTENTIAL).  
CC TRANSMEM 19 47 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
CC (POTENTIAL).  
CC DOMAIN 48 1034 EXTRACELLULAR (POTENTIAL).  
CC DOMAIN 52 169 SEA.  
CC DOMAIN 197 238 LDL-RECEPTOR CLASS A 1.  
CC DOMAIN 240 349 CUB 1.  
CC DOMAIN 357 519 MAM.  
CC DOMAIN 539 649 CUB 2.  
CC DOMAIN 656 694 LDL-RECEPTOR CLASS A 2.  
CC DOMAIN 693 786 SRCR.  
CC DOMAIN 800 1034 SERINE PROTEASE.  
CC ACT\_SITE 840 840 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC ACT\_SITE 891 891 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC ACT\_SITE 986 986 CHARGE RELAY SYSTEM (BY SIMILARITY).  
CC LIPID 2 2 N-myristoyl glycine (Potential).  
CC DISULFID 199 212 BY SIMILARITY.  
CC DISULFID 206 225 BY SIMILARITY.  
CC DISULFID 219 236 BY SIMILARITY.  
CC DISULFID 658 670 BY SIMILARITY.  
CC DISULFID 665 683 BY SIMILARITY.

FT DISULFID 677 911 BY SIMILARITY. 692  
 FT DISULFID 787 911 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 825 841 BY SIMILARITY.  
 FT DISULFID 925 992 BY SIMILARITY.  
 FT DISULFID 956 971 BY SIMILARITY.  
 FT DISULFID 982 1010 BY SIMILARITY.  
 FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 485 485 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 518 518 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 549 549 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 645 645 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 697 697 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 701 701 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 721 721 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 740 740 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 761 761 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 804 804 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 863 863 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 902 902 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 964 964 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 1034 AA; 114776 MW; 0388C64CF64CC368 CRC64;

Query Match 8.4%; Score 330.5; DB 1; Length 1034;  
 Best Local Similarity 22.9%; Pred. No. 4.6e-17;  
 Matches 137; Conservative 86; Mismatches 224; Indels 151; Gaps 27;

QY 143 SYPLNAHCETTHAKPGFVIQRLVFLSLFPMQCYDYVEVRDGRDQIIKRVCGNE 202  
 DB 560 NYPNQAFVWNLNAQKRNQIQLHFE----EPDENIADVEIRDEEDSLLAVYTG-- 613  
 QY 203 RPAPTQSTGSS---LHVLFHSDGS-----KNP-DGFHAIYEETACSSSPCFHD---- 247  
 DB 614 -PGPVEDVFSTTRMTVLTITDALTAKGFKANFTTGVHLGIPE-----PKCEDNFQC 665  
 QY 248 --GTCVLDKAGSKYKACLAGYTGQRCENLLBERNCSDPGPGVNGYQKITGGGLINGRHA 305  
 DB 666 ENGECVL-----LVNLCDFSHCKGSDENHCVRFUNGTFANNSGLVQFRIQ 711  
 QY 306 KIGTVVFFCNNSYVLSGNEKTKCOQNGSWGSKQPCIKACREPKISDLVRRRVLPQMVO 365  
 DB 712 SIW-----HTACAEWTTQTSDVDC-----QLLGLGTG 739  
 QY 366 SRETPHLQLYSAFSAKQKQLOSAFTKPKALPFGDLPNGVQHLHTQYECISPFYRLGSS 425  
 DB 740 NSSMPFFSGGGGPF--VKLNTAPNGSLIITASE-----OCFDSLILLOCN 783  
 QY 426 RTCLRTGWSGRAPSCIPICIKENITAPKTQGLR-----WPMOALYRRTSGVHDGS 479  
 DB 784 HKSC---GK-----KQVAQEVSPKIVGGNDSREGAWPVWVALY-----YNGQ 822  
 QY 480 LHKGAFLVCSGALVNERTVVAHVCTDGLKVITWIKTADLVKLVGKFRDDEKTIQ 539  
 DB 823 -----LLCGASLVSRDLVSAACHCV--YGR--NLEPSKAKAILG-LHMTSNLTSPOIV 870  
 QY 540 SLQISAILHPNYPDILLADAILKLLDKARISRTVQIPICLAASRDLSFQESHITV 598  
 DB 871 TRLIDEIVNPHNRRKSDSIAMHLEPKVNTYDIQICILPENQV---PFGRICSI 927  
 QY 599 AGWNVLDVRSFGKNDTLRSGVSVVDSLLCEQHEHDGIPVSVTDNMFCAWSWPTAPS 658  
 DB 928 AGWKVIYOGSPA---DILQADVPVLSNKKCQOQMPY-----NITENWMCAGYE-EGGI 979  
 QY 659 DICTAFTGTGIAVSPFGRASBPFRHMLGLVNSWYDKTCSHRLSTAFTKVLPFKDWIE 716  
 DB 980 DSCQGDGSG-----PLMCLENNRLLAGVTSFGYQCALPNR-PGVYARVPKFTIEWIQ 1030

RESULT 11  
 CSML\_HUMAN STANDARD; PRT; 3565 AA.  
 AC Q96PZ7; Q96QU9; Q96RM4;  
 DT 15-MAR-2004 (Rel. 43, Created)  
 DT 15-MAR-2004 (Rel. 43, last sequence update)  
 DE CUB and esushi multiple domains protein 1 precursor (UNQ5952/PRO19863).  
 GN CSMD1 OR KIAA1890.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RX MEDLINE=21365705; PubMed=11472063;  
 RA Sun P.C., Uppaluri R., Schmidt A.P., Pashia M.E., Quant E.C.,  
 RA Sunwoo J.B., Gollin S.M., Scholnick S.B.;  
 RL "Transcript map of the 8p23 putative tumor suppressor region.";  
 RL Genomics 75:17-25(2001).  
 RN [2]  
 RP SEQUENCE OF 1319-3565 FROM N.A. (ISOFORM 3).  
 RX TISSUE=Brain;  
 RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,  
 RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,  
 RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,  
 RA Yanashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,  
 RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,  
 RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;  
 RL "NEDO human cDNA sequencing project.";  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 825-3565 FROM N.A. (ISOFORM 4).  
 RX MEDLINE=22887296; PubMed=12975309;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P.;  
 RL "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";  
 RL Genome Res. 13:2265-2270(2003).  
 RN [4]  
 RP SEQUENCE OF 966-2013 FROM N.A. (ISOFORM 4), AND TISSUE SPECIFICITY.  
 RX TISSUE=Brain;  
 RA MEDLINE=21456161; PubMed=11572484;  
 RA Nagase T., Kikuno R., Ohara O.;  
 RL "Prediction of the coding sequences of unidentified human genes. XXI. The complete sequences of 60 new cDNA clones from brain which code for large proteins.";  
 RL DNA Res. 8:179-187(2001).  
 RN [5]  
 RP DISEASE.  
 RX MEDLINE=22581359; PubMed=12696061;  
 RA Toomes C., Jackson A., Maguire K., Wood J., Gollin S., Ishwad C.,  
 RA Paterson I., Prime S., Parkinson K., Bell S., Woods G., Markham A.,  
 RA Oliver R., Woodward R., Sloan P., Dixon M., Read A., Thakker N.;  
 RL "The presence of multiple regions of homozygous deletion at the CSMD1 locus in oral squamous cell carcinoma question the role of CSMD1 in head and neck carcinogenesis.";  
 RL Genes Chromosomes Cancer 37:132-140(2003).  
 RN [6]  
 RP DISEASE.  
 RX MEDLINE=22868729; PubMed=14506705;  
 RA Scholnick S.B., Richter T.M.;  
 RL "The role of CSMD1 in head and neck carcinogenesis.";

Genes Chromosomes Cancer 38:281-283(2003).  
 CC -1- FUNCTION: Potential suppressor of squamous cell carcinomas.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=4;  
 CC Name=1;  
 CC IsoId=Q96P27-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Short;  
 CC IsoId=Q96P27-2; Sequence=VSP\_009034, VSP\_009035;  
 CC Name=3;  
 CC IsoId=Q96P27-3; Sequence=VSP\_009030, VSP\_009031;  
 CC Note=No experimental confirmation available;  
 CC Name=4;  
 CC IsoId=Q96P27-4; Sequence=VSP\_009032, VSP\_009033;  
 CC -1- TISSUE SPECIFICITY: Weakly expressed in most tissues, except in brain. Expressed at intermediate level in brain, including cerebellum, substantia nigra, hippocampus and fetal brain.  
 CC -1- DISEASE: Defects in CSMD1 may be a cause of oral and oropharyngeal squamous cell carcinomas (OSCCs). Ref.5 and Ref.6 are however in disagreement: while Ref.6 considers CSMD1 as a strong candidate for OSCCs, Ref.5 thinks it is not.  
 CC -1- SIMILARITY: Belongs to the CSMD family.  
 CC -1- SIMILARITY: Contains 14 CUB domains.  
 CC -1- SIMILARITY: Contains 28 Sushi (SCR) domains.  
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 CC -----  
 CC EMBL; AF333704; AAC73475.2; -;  
 CC EMBL; AY017307; AAC52948.1; -;  
 CC EMBL; AK126936; BAC86754.1; ALT\_INIT.  
 CC EMBL; AY358174; AAC88541.1; ALT\_INIT.  
 CC EMBL; AB067477; BAB67783.1; -;  
 CC Genew; HGNC:14036; CSMD1.  
 CC InterPro; IPR000859; CUB.  
 CC InterPro; IPR000436; Sushi\_SCR\_CCP.  
 CC Pfam; PF00431; CUB; 14.  
 CC Pfam; PF00084; sushi; 27.  
 CC SMART; SM00032; CCP; 24.  
 CC SMART; SM00042; CUB; 14.  
 CC PROSITE; PS01180; CUB; 14.  
 CC Repeat; Signal; Transmembrane; Sushi; Alternative splicing.  
 CC SIGNAL 1 26  
 CC CHAIN 27 3565  
 CC CUB AND SUSHI MULTIPLE DOMAINS PROTEIN 1.  
 CC EXTRACELLULAR (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).  
 CC CUB 1.  
 CC SUSHI 1.  
 CC CUB 2.  
 CC SUSHI 2.  
 CC CUB 3.  
 CC SUSHI 3.  
 CC CUB 4.  
 CC SUSHI 4.  
 CC CUB 5.  
 CC SUSHI 5.  
 CC CUB 6.  
 CC SUSHI 6.  
 CC CUB 7.  
 CC SUSHI 7.  
 CC CUB 8.  
 CC SUSHI 8.  
 CC CUB 9.  
 CC SUSHI 9.  
 CC CUB 10.  
 CC SUSHI 10.  
 CC CUB 11.

FT	DOMAIN	1916	1971	SUSHI 11.
FT	DOMAIN	1975	2083	CUB 12.
FT	DOMAIN	2088	2143	SUSHI 12.
FT	DOMAIN	2147	2258	CUB 13.
FT	DOMAIN	2259	2316	SUSHI 13.
FT	DOMAIN	2320	2431	CUB 14.
FT	DOMAIN	2433	2491	SUSHI 14.
FT	DOMAIN	2496	2553	SUSHI 15.
FT	DOMAIN	2558	2618	SUSHI 16.
FT	DOMAIN	2623	2676	SUSHI 17.
FT	DOMAIN	2681	2734	SUSHI 18.
FT	DOMAIN	2739	2797	SUSHI 19.
FT	DOMAIN	2802	2855	SUSHI 20.
FT	DOMAIN	2863	2916	SUSHI 21.
FT	DOMAIN	2921	2975	SUSHI 22.
FT	DOMAIN	2980	3035	SUSHI 23.
FT	DOMAIN	3040	3093	SUSHI 24.
FT	DOMAIN	3098	3151	SUSHI 25.
FT	DOMAIN	3159	3213	SUSHI 26.
FT	DOMAIN	3218	3273	SUSHI 27.
FT	DOMAIN	3276	3331	SUSHI 28.
FT	CARBOHYD	40	40	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	57	57	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	588	588	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	687	687	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	956	956	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1016	1016	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1035	1035	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1185	1185	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1198	1198	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1400	1400	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1455	1455	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1573	1573	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1645	1645	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1793	1793	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1806	1806	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1883	1883	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2019	2019	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2150	2150	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2155	2155	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2188	2188	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2359	2359	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2395	2395	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2401	2401	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2446	2446	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2471	2471	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2504	2504	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2606	2606	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2751	2751	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2762	2762	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2796	2796	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2895	2895	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2964	2964	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	3023	3023	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	3057	3057	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	3106	3106	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	3229	3229	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	3261	3261	N-LINKED (GLCNAC. .) (POTENTIAL).

Query Match 8.4%; Score 329.5; DB 1; Length 3565;  
 Best Local Similarity 20.8%; Pred. No. 2.6e-16;  
 Matches 163; Conservative 93; Mismatches 239; Indels 287; Gaps 34;  
 QY 48 YDQIECVCP-----GKREVGVYIP-C-----CRNEECDCSLHPGTTIFENCK 92  
 Db 693 FGQNECHDPGIPNGRRFGDFLLGSSVSFHCDDGFVKQTQGSSEITCILQDG----- 744  
 QY 93 SCENGSGGTLDDFFVYKGFYCAECRAGWYGGDCMRGCVLRAPKGOILLESYP-----LNA 148  
 Db 745 ---NVVWSSTV-----PCGHLTASSGVILPFGVYKDSL 783  
 QY 149 HCEWTHAKPGFVIQIRFVWLSLEFDYMCQDYVEVRDGNDRDQGIKRVCGNERPAPIQ 208



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Db 784 HCEWIEIARPGHSIRKWTDFRQTEVN-----YDTEVRDGPASSSPLEIGYHGTOAQOFLI 839
QY 209 STGSSHLVHFDSDGKNFDGPHAYIEITACSSSPCFHDGTCVLVDKAGSYKACLAGVTG 268
Db 840 STGNFWYLLFTDNRSSIGFLIHESVT-----868
QY 269 QRCENLLEERNCDPGPGVNGYQKITGGFLNGHAKIGTVVSPFCNNSVYLSGNEKRT 328
Db 869 -----LESDSCLDPGIPVNGHR-----HGGDFGIRSTVTSPSCDPGYTSLSDPELV 913
QY 329 COONGESWKQPCICIKAC-----346
Db 914 CERNQMHNPALPCDALCGYITQSGSTVLSGFFDFPNSLNCWTWTEVSHGKGVQMPF 973
QY 347 -----REPKISDLVRR---RVLPQMVQ-----SRETPLHQL 374
Db 974 HTFHLESSHVDYLLITEDGFSFSEPVARTGSLVPLHTIKAGLFQNFPAQLRPFISDFSISVEG 1033
QY 375 YSAARSKQLQSAPTKAPALPGDLPNGYQH-LHTQLQYECISPPYRLGSSRRRTCLRTG 433
Db 1034 FNITSEYDLE--PCDDPGVPAPSRRIQGFHFGVDSLTFCFLG-YRLEGATKLTCLGGG 1090
QY 434 K--WGRAPSCIPICGKIENITAPKTQGLRWEPWQAIVRRTSQVHDSGLHKGAWFLVCSG 491
Db 1091 RRVNSAPLPRCVAECG-----ASV-----KG-----1111
QY 492 ALVNERTVVV-----AAHCV---TDLGKVTMIKTADLKVLVG---KPYRDDDRDE 535
Db 1112 ---NEGTLSPNFPNSYNDTHECIYKITEACKGHIHRTSRFQEGDTLKVYDGDKSS 1168
QY 536 K---TIQSLQISAILHPNYDPIILDADIAILKLDKARISTRVOPICLAASRDLSFTQ 592
Db 1169 RPLGFTTKNELGLNLSTNSHLWLEFN-----TNGSDTDQGFQ 1207
QY 593 ESHITVAGNVNLADVRSPGFKNDTLR---SGVSWVWDSLLCEEQHDHGIPVSVTDNNF 648
Db 1208 ---LYTSD-LVKCEDGIPVNGYRIRDEGHFTDTVLVYSCNPGVAMHG-----SNLT 1258
QY 649 CAS-----WEPTAPSDICTAETGG---IAVS-----FPGRAPSP-EPRHMLGLVSWYDKT 696
Db 1259 CLSGDRRVWDKPLPS--CIAECGGQIHAATSGRILSPGYPAPYDNNLHCTWIIIEADPGKT 1316
QY 697 CS 698
Db 1317 IS 1318

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## RESULT 12

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CSM1_MOUSE
ID CSM1_MOUSE STANDARD; PRT; 3564 AA.
AC Q92L3; Q8BUV1; Q8BYQ3;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE CUB and eushi multiple domains protein 1 precursor.
GN CSM1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6;
RX MEDLINE=21365705; PubMed=11472063;
RA Sun P.C., Uppaluri R., Schmidt A.P., Pashia M.E., Quant E.C.,
RA Sunwoo J.B., Gollin S.M., Scholnick S.B.;
RT "Transcript map of the 8p23 putative tumor suppressor region.";
RL Genomics 75:17-25(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 3), AND SEQUENCE OF 3250-3564 FROM N.A.
RP (ISOFORM 2).
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851;

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RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami H., Schonbach C., Gojobori T.,
RA Baldairelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriell L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Ciochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer J.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Meglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Negashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hata A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q92L3-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q92L3-2; Sequence=VSP_009037;
CC Note=No experimental confirmation available;
CC Name=3;
CC IsoId=Q92L3-3; Sequence=VSP_009036;
CC Note=No experimental confirmation available;
CC -1- SIMILARITY: Belongs to the CSM1 family.
CC -1- SIMILARITY: Contains 14 CUB domains.
CC -1- SIMILARITY: Contains 28 Sushi (SCR) domains.
CC
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CC
CC -----
CC EMBL; AY017475; AAGS4083.1;
CC EMBL; AK038679; BAC30095.1; ALT_INIT.
CC EMBL; AK082377; BAC38482.1;
CC MGD; MGI:2137383; Gmtdi.
CC InterPro; IPR000859; CUB.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00431; CUB; 14.
CC Pfam; PF00084; sushi; 28.
CC SMART; SM00032; CCP; 28.
CC SMART; SM00042; CUB; 14.
CC PROSITE; PS01180; CUB; 14.
CC Repeat; Signal; Transmembrane; Sushi; Alternative splicing.
FT SIGNAL 1 29
FT CHAIN 30 3564
FT DOMAIN 30 3487
FT TRANSMEM 3488 3508
FT DOMAIN 3509 3564
FT DOMAIN 32 140
FT DOMAIN 145 202
FT DOMAIN 208 312
FT DOMAIN 349 406

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FT DOMAIN 411 522 CUB 3. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 527 580 SUSHI 3. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 584 692 CUB 4. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 697 754 SUSHI 4. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 758 866 CUB 5. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 873 926 SUSHI 5. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 930 1040 CUB 6. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 1045 1100 SUSHI 6. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 1104 1212 CUB 7. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 1217 1273 SUSHI 7. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 1277 1386 CUB 8. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 1391 1447 SUSHI 8. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 1451 1559 CUB 9. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 1564 1621 SUSHI 9. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 1625 1733 CUB 10. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 1741 1798 SUSHI 10. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 1802 1910 CUB 11. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 1915 1970 SUSHI 11. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 1974 2082 CUB 12. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 2087 2142 SUSHI 12. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 2146 2257 CUB 13. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 2258 2315 SUSHI 13. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 2319 2430 CUB 14. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 2432 2490 SUSHI 14. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 2495 2552 SUSHI 15. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 2557 2617 SUSHI 16. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 2622 2675 SUSHI 17. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 2680 2733 SUSHI 18. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 2738 2791 SUSHI 19. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 2796 2854 SUSHI 20. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 2859 2912 SUSHI 21. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 2920 2973 SUSHI 22. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 2978 3032 SUSHI 23. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 3037 3092 SUSHI 24. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 3097 3150 SUSHI 25. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 3155 3208 SUSHI 26. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 3216 3270 SUSHI 27. (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 3275 3330 SUSHI 28. (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 1015 1015 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1034 1034 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1184 1184 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1197 1197 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 1454 1454 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1572 1572 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1644 1644 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1792 1792 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1805 1805 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1882 1882 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2018 2018 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2149 2149 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2184 2184 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2358 2358 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2394 2394 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2400 2400 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2445 2445 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2470 2470 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2503 2503 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2605 2605 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2750 2750 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2761 2761 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2795 2795 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2894 2894 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 2963 2963 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 3022 3022 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 3056 3056 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 3086 3086 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 3228 3228 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 3260 3260 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 3339 3339 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 3379 3379 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 3386 3386 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 102 3564 Missing (in isoform 3).  
 FT VARSPLIC 3332 3347 /FTID=VSP 009036.  
 FT VARSPLIC 3347 /FTID=VSP 009037.  
 SQ SEQUENCE 3564 AA; 387865 MM; 70824C55B0674609 CRC64;  
 Query Match 8.3%; Score 329; DB 1; Length 3564;  
 Best Local Similarity 21.3%; Pred. No. 2.8e-16;  
 Matches 159; Conservative 95; Mismatches 226; Indels 266; Gaps 33;  
 QY 48 YQIECVCP-----GKREVVGYTIP--C---CRNEECDCSLIHPGCTIFENCK 92  
 DB 692 FQNECHDFGIPNGRRFGRFLGSSVSFCHDDGFVKTOGSEITCIIQDG----- 743  
 QY 93 SCRNGSWGOTLDDFFVYKGYCAECRAGWYGDGCMRGQVLRAPKQIILLESYP-----L 146  
 DB 744 ---NVWSSSTV-----PCGHLTASSGVILPPGFWPGYKDSL 782  
 QY 147 NAHCEWTIHAKGFWIQLRFVMSLEFDYMCQYDVYVVDGDNRCQIIRKVCGERPAP 206  
 DB 783 N--CEWVIEAKPGHSIKITDFRQTEVN---YDLEVRDGPSTSSPLIGEVHGTQAPQ 836  
 QY 207 IQSIGSSHLVHFSGSKNFDGFHAIYEITACSSSPCFHDTGTCVLDKAGSYKCACLAGY 266  
 DB 837 LISTGNMYLLFTDSSRASVGLIHESVT----- 867  
 QY 267 TGORCNLLERNCSDPGPGVNGYQKITGGPLNGRHAKIGTVVSFFCNNSVVLGNEK 326  
 DB 868 -----LESDSLDPGIPVNGQR-----HGSNFGIRSTVTFCODPGYTLSDDEP 910  
 QY 327 RTCOQNGEWSGKOPICIKAC----- 346  
 DB 911 LVCEKQHNHALPSCDALCGGYIHGKSGTVLSPGPPDFYNSLNTWTIEVSHGKVQM 970  
 QY 347 -----REPKISDLVRR---RVLPQVQV-----SRETPLH 372  
 DB 971 NFHTPHLESSHDYLLITEDGSFSEPVARLTGSLVPHTIKAGLFGNFTAQLRFISDFSISY 1030  
 QY 373 QLYSAFQKQKQSAPTKAPALPFGDLPMGYQH-LHTQLOVEICISFFYRLGSSRTCLR 431  
 DB 1031 EGFNITFAEYDLE--PCDDPGVPAFRRIGFGFGVDTLAFTCFQG-YRLEGATKLTCLG 1087  
 QY 432 TGG--WSGRAPCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSLHKGAWFLVC 489  
 DB 1088 GGRVWSAPLPRCAECG-----ASV-----KG----- 1110  
 QY 490 SGALVNERTVW---VAAH-----CV-----TDLGKVTMIKTADLVKVLGKFYRDDDRDEK 536  
 DB 1111 ----NEGTLSPNPPSHDNNHECIYKETEAGKGIHLRARTFQLFEGDTLKVYDGKDS 1165  
 QY 537 TQSLOISAIILHPNDPILLADTAIILKDKARISTRVQVICLA-ASRDLSTSFQESH 595  
 DB 1166 SRSRL---GVFTRSEFPMGLVNLSTNYLLEFNFTNGSDTAQGFQLTYSFDL-VKCEDPG 1221  
 QY 596 ITVAGNVNLADVRSFGKNDTLRSVVSVVDSILCEOEHGIPVSVTDNNMFCAS---- 651  
 DB 1222 IPNYGYR-----IRDDGHFTDTV-----VLYS--CNPYAMHG-----SSTLTCLSGDRR 1264  
 QY 652 -WEPTAPSDICTAETGGIAAVSFPGR 676  
 DB 1265 VNDKPMPS--CVABCGGLVHAATSGR 1288

RESULT 13  
 ST14\_HUMAN  
 ID ST14\_HUMAN STANDARD; Q9H350; Q9HB36; Q9HCA3;  
 AC Q9Y5Y6; Q9BS01; Q9H350; Q9HB36; Q9HCA3;  
 DT 16-OCT-2001 (Rel. 40, Created)



```
FT CONFLICT 674 674 A -> V (IN REF. 3).
SQ SEQUENCE 855 AA; 94769 MW; 26143132C01F99C9 CRC64;

Query Match 8.3%; Score 328; DB 1; Length 855;
Best Local Similarity 21.4%; Pred. No. 5.7e-17;
Matches 143; Conservative 70; Mismatches 224; Indels 230; Gaps 27;

QY 128 CGOVLRAPIKGOI-----LLSEYPLNAHCEWTIIHAKPGFVQLRPFVMSLSLEFDYM-----176
DB CGGLRAKAGTNSPYYPGHPYDICTWNIENPHNQHVKVR-----KFFVLLLEPGVPA 394
QY 177 --COYDVEVRDGDNRDGGIIKRVGCNERPAPQISGSSHLVLFHSDGSKNPDGFHAIYE 234
DB CGGLRAKAGTNSPYYPGHPYDICTWNIENPHNQHVKVR-----KFFVLLLEPGVPA 394
QY 395 GTCPKDYVEING-----EKYCGERSQFVTSNSKIVTFHSDQSYDTDTGFLAEY- 444
QY 235 EITACSSSPCFHDTGTC-----VLDKAGSYKCAACLAGY-----266
DB 445 -LSYSDSDPCPGFTGTCIRKELRCDCGWADCTDHSDELNCSDCAGHQTCKNFKCP 503
QY 267 -----TGRCENLBERNCSDPGPVNGYQKITGGFLNGHAKIGTVVSPFNNSYV 320
DB 504 LFWVCDVNDGNSDEQGCSCP-----AQTFRCSNGKC 537
QY 321 LSG-----NEKRTCOQNGESGKQPIKACREPKISDLVRRVLPVQVQSRETFPLHOLYS 376
DB 538 LSKSQOCNGKDDCGDSDSEACPKVNVVTC-----567
QY 377 AAFSKQKLOSAPTKXPALPFGDLPNGYQHLHTOLQYECISPPFYRLGSSRRRTCLRTGKWS 436
DB 568 -----TK-----HT--YRCLNGL-----CLSKGN-- 584
QY 437 GRAPSCIPCGKIENTAPKTQ-----GLR-----WPWQAAYRRTS 473
DB 585 -----PECDEKEDCSGSDKDCGLRASFTRQARVVGTDADGEWEPQVSLHALGQ 637
QY 474 GVHDGSLHGAFLVCSGALVNERTVVAACHVYDGLKVTMIKTLADLVKVLGKFRDDDR 533
DB 638 G-----H-----ICASLISNVLWSAAHCHYIDRFGFYSPDPTWTFPLG-LHDSQR 684
QY 534 DEKTIQSLQISAILHPNYOPILLDADAILKLLDKARISTRVQIPICLAASRLDLSFQE 593
DB 685 SAPGVQERRLKRILSHPFNDFTFDYDIALLEKPAEYSWVRPCLP--DASHVFEPA 741
QY 594 SH-ITVAGNVNLDVRSPPGPNFDTLSGVVSVVDSLLCERQHDHGIPVSVTNNMCASW 652
DB 742 GKAIWVTGW---GHTQYGGTGALILQKGEIRVINQTTCNL-----LPQQITPRMMCVGF 793
QY 653 EPTAPSDICTAETGG-IAAVSFPGRASPEPRHMLGLVSVSYDKTCSHRLSTAFPTKVLPF 711
DB 794 -LSGVDSOCGSDGSLUSSVEADGRI-----FQAGVVSNG-DGCAQRNKPQVYTRPLPF 845
QY 712 KDWIERN 718
DB 846 RDWIKEN 852

RESULT 14
PRTC_MOUSE STANDARD; PRT; 461 AA.
AC P33587; O35498;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).
DE PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC TISSUE=Liver;
RX MEDLINE=92316897; PubMed=1618739;
RT Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
RL "Isolation and characterization of a mouse protein C cDNA.";
RN J. Biochem. 111:491-495(1992).
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=98152576; PubMed=9493582;
RT Jallbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
RN Castellino F.J.;
RA "Nucleotide structure and characterization of the murine gene encoding
RT anticoagulant protein C.";
RN Thromb. Haemost. 79:310-316(1998).
RP SEQUENCE OF 274-434 FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=8043441;
RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
RT "A comparative study of partial primary structures of the catalytic
RN region of mammalian protein C.";
RA Br. J. Haematol. 86:590-600(1994).
CC -!- FUNCTION: Protein C is a vitamin K-dependent serine protease that
CC regulates blood coagulation by inactivating factors Va and VIIIa
CC in the presence of calcium ions and phospholipids.
CC -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -!- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a
CC tetradecapeptide from the amino end of the heavy chain; this
CC reaction, which occurs at the surface of endothelial cells, is
CC strongly promoted by thrombomodulin.
CC -!- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
CC residues allows the modified protein to bind calcium.
CC -!- MISCELLANEOUS: Calcium also binds, with stronger affinity to
CC another site, beyond the GLA domain. This GLA-independent binding
CC site is necessary for the recognition of the thrombin-
CC thrombomodulin complex.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC
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63 CDFEZAQIFQNVEDTLAFWI-----KYFDGDCSAPPDLHQCDSCCCGHGTCT-DGIGS 111

258 YKACIAGYTGQRCENTLEERNCSDPGGPVNGYQKITGGPGL-----INGRHAKITGVV 311

117 FSCSCDKGWEKGFQOELRFQDC:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 160

312 SFFCNNSVYLSGNEKR-----TCQNGSEWSGKQPICIKACREPKISDLVRRVRLPMQV 364

161 ----CAPGVELADDDHWRCKSVTNFFCGKLGRIEK:::|:::|:::|:::|:::|:::|:::| 196

365 QSRETPHLQLYSAAFSKQKLOSAPTKKPALPFGDLPWGQHLHTQLQYECISPFYRRRLGS 424

197 -KRDIDL-----EDELDPD-:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 210

425 SRRTCLRTCKWSGRAPSCPICGKIENITAPKTQGLRWPQRAIYVRTSGVHDGSLHKA 484

211 -----RIVNGTUTK-QG-DSPMQAAIL-----DSKKK- 235

485 WFLVSGALVNERTVVAAHCVTDLGVKVTMIKTADLKVLGKFRVDDDDDEKTIQSLQIS 544

236 --LACGGVLIHTSWLVTAACHVEGTKKLT-----VRLGEY--DLRRDHWELDLDIK 283

545 AILHPNVDPIILLDADINAILLKDKARISTRVQPICL-----AASRDLSITSFQESHITVAG 600

284 EILVHPNTRSSNDIALLELAQPATLSKTIIPVCLPNNGLAQOELTQAGQETVVT--G 341

601 MNVLADVRSPGFKNDTL-----RSGVSVSDSLCEQHEHDGIPVSVTDNMFC 649

342 WGYQSDRIKGRNERTFILTRIPLVARNCEVEMKV-----VSENMLC 387

650 ASWEPAPSDICTAETGGIAAVSPGGRASPEPRHMLMGLVSWDYKTCSHRLSTA-FTKV 708

388 AGIIGNT-RDACDGSDDGPMVVPFRG-----TWFLVGLVSWG--EGCGHTNNYGIYTKV 438

709 LPFKDWI 715:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 715

439 GSYLXWI 445:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 445

RESULT 15

CSM2\_HUMAN STANDARD; PRT: 3487 AA.

ID\_CSM2\_HUMAN Q7ZA08; Q8N963; Q96003; Q9H4V7; Q9HAV8; Q9H4V9; Q9H4W0; Q9H4W1;

AC Q9H4W2; Q9H4W3; Q9H4W4; Q9HCY5; Q9HCY6; Q9HCY7;

DT 15-MAR-2004 (Rel. 43, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE CUB and sushi multiple domains protein 2.

GN CSM2 OR KIAA1884

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.

RA MEDLINE=22788796; PubMed=12906867;

RX Lau W.L., Scholnick S.B.;

RT "Identification of two new members of the CSM2 gene family.";

RL Genomics 82:412-415(2003).

[1]

RP SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 2969-3487 (ISOFORM 1).

RC TISSUE=Brain, and Teratocarcinoma;

RC Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,

RA Wakedo H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,

RA Irie K., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,

RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,

RA Yamaehita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,

RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahara K.,

RA Masuho Y., Nagai K., Isegai T.;

RT "NED0 human cDNA sequencing project.";

RL Submitted (Jul-2003) to the EMBL/GenBank/DBJ databases.

RN [3]

```

RP SEQUENCE FROM N.A.
RA Wallis J., Brown A.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Tochiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitney M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurich A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 2542-3487 FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=21456161; PubMed=11572484;
RA Nagase T., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XXI.
RT The complete sequences of 60 new cDNA clones from brain which code for
RT large proteins."
RL DNA Res. 8:179-187(2001).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q72408-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q72408-2; Sequence=VSP_009038, VSP_009039, VSP_009040,
CC VSP_009041, VSP_009042;
CC Note=No experimental confirmation available;
CC Name=3;
CC IsoId=Q72408-3; Sequence=VSP_009043, VSP_009044, VSP_009045,
CC VSP_009046;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Weakly expressed in most tissues, except in
CC brain. Expressed at intermediate level in brain, including
CC cerebellum, substantia nigra, hippocampus and fetal brain.
CC Overexpressed in some head and neck cancer cell lines.
CC -1- SIMILARITY: Belongs to the CSMD family.
CC -1- SIMILARITY: Contains 14 CUB domains.
CC -1- SIMILARITY: Contains 26 Sushi (SCR) domains.
CC -1- CAUTION: Ref.3 sequence differs from that shown due to a
CC frameshift in position 939 that shortens the protein by 1021
CC residues in its N-terminus. It is unknown whether the sequence
CC shown exists or whether Ref.3 is right, shortening the sequence in
CC its N-terminus.
CC -1- CAUTION: Ref.3 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC -----
CC EMBL; AY210418; AAC34701.1; --
CC EMBL; AK095627; BAC04593.1; ALT_INIT.

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FT	CARBOHYD	34	34	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	51	51	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	581	581	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	680	680	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	949	949	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	983	983	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1009	1009	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1028	1028	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1158	1158	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1178	1178	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1194	1194	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1393	1393	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1566	1566	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1638	1638	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1786	1786	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1799	1799	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1876	1876	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	2012	2012	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	2185	2185	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	2190	2190	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	2223	2223	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	2394	2394	N-LINKED (GLCNAC. . .)	(POTENTIAL).
Query Match 8.1%; Score 318; DB 1: Length 3487;					
Best Local Similarity 22.6%; Pred. No. 1.8e-15;					
Matches 159; Conservative 70; Mismatches 236; Indels 240; Gaps 28;					
QY	57	GKREVVGYTIPCCRNENECDSLIHPGCTIPENCKSCRNGS-WGGTLDLDDFYVKFYCAE	115		
DB	675	GKK---GFNITFTFRHNECPD---PGVPV-----NGKRFQDLSQLGSSISFLCDE	719		
QY	116	CRAGWYGGDCMR-----CGQVLRAPKGOILLESYP-----LNAH	149		
DB	720	GFLGTQGETITCVLKEGVSVMNSAVLRCEAPCGGHLTSPSGTILSPGPGFYKDALS--	777		
QY	150	CEWTIRAKPGFVQLRFVMSLEFDYMCQDYVEVRDGDNRDGOIIRKVCGNERPAPIOS	209		
DB	778	CAWVIAQPGYPIKITFDKTEVN---YDLEVRDGRYTSAPLIGVHGTQVQFPLIS	833		
QY	210	IGSSLHLVPHSDGSKNPFDFHAIYEITACSSPCFHDGTCVLDKAGSYKCACLAGYTQ	269		
DB	834	TSNYLLFSTDKSHSDIGQLRYETIT-----	861		
QY	270	RCENLLEERNCSPPGPGVNGYQKITGGPGLINGRHAKIGTVIVSPFCNNSVVLGNEKRTC	329		
DB	862	-----LQSDHCLDPGIPVNGQR-----HGNDYVGVALVTFCDSGYTILSDGEPLFC	907		
QY	330	QNGWMSGKQPICIKAC-----REPKISDLVRRR-----	358		
DB	908	EPNFQHSRALPSCALCGGFIQSSGTLSPGPPDFYPNNLNCWTIETSHGKGVFFTFH	967		
QY	359	-----VLPQVQSRFTPLHQL-----Y	375		
DB	968	TFHLESGHDYLLITENGSTFQPLRLTQSLRSLPAPISAGLYGNFTAQVRFISDFMSYEGF	1027		
QY	376	SAAFSKQLQSAPTKKPALPGPLPGYOH-LHTQLQYECISPFYRLGSSRTCL--RT	432		
DB	1028	NITFSEYDLE--PCEBEPFAYSIRKGLQGVGDTLTFSCF-PGYRLEGATITCLGRR	1084		
QY	433	GKWSGRAPSCIPICGK-----IENITAPKTQGLRWPWQAAI	468		
DB	1085	RLWSSPLPRCAECGNSVTGCTQLLSPNPPVNNNNHCEIYSIQTPGKGIQ--LKARA	1142		
QY	469	YRTSG-----VHDGSLHKGAWFLVCS-----GALVNERTVVVAHCVTD-----	508		
DB	1143	FELSEGDLVKYDGNNSARLLGVSHSEMVGVTLSSTSSSLWLDFTDAENTSKGFELH	1202		
QY	509	LGVVTMIKTADLVVLGKF--YRDDRDREKTIQSLQISAILIHENYDPIILLADIAILKLL	567		
DB	1203	FSSFELIKCEDPGT--PKFGYKVHDEGHFAGSSVFSFC---DFGYS---LRGSEELICLS	1254		
QY	568	DKARISTRVQVICLAASRDLSSTFSQESHITVAGWNLADVRSFGF	612		

Db 1255 GERTWDRPLPTCVA-----ECGGTVRG-EVSGQVLSPGY 1288

Search completed: August 18, 2004, 16:24:06  
Job time : 19 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:21:34 ; Search time 21 Seconds  
(without alignments)  
3297.995 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945

Sequences: 1 MELGCWTQLGLTFLQLLIS.....LSTAFTKVLFPKDWIERNMK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 700 summaries

Database :

PIR\_78.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	949	24.1	181	2 T08805	hypothetical prote
2	672	17.0	1019	2 A38738	coagulation factor
3	482	12.2	699	1 I54763	Ra-reactive factor
4	403.5	10.2	705	1 C1HURB	complement subcomp
5	400.5	10.2	686	1 A59271	Ra-reactive factor
6	378.5	9.6	695	1 S05008	complement subcomp
7	354	9.0	1524	2 T30337	polyprotein - Afri
8	340.5	8.6	694	2 JC6554	complement subcomp
9	334	8.5	688	1 C1HUS	complement subcomp
10	331.5	8.4	1019	1 A56318	enteropeptidase (E
11	330.5	8.4	1034	1 A53663	enteropeptidase (E
12	320	8.1	461	1 JX0210	protein C (activat
13	317.5	8.0	1035	1 A43030	enteropeptidase (E
14	314.5	8.0	475	1 EXCH	coagulation factor
15	313	7.9	855	2 JC7731	membrane-bound arg
16	310.5	7.9	461	1 KXHU	protein C (activat
17	299.5	7.6	443	2 I46932	coagulation factor
18	293.5	7.4	407	1 KFB07	coagulation factor
19	292	7.4	461	1 S18994	protein C (activat
20	285.5	7.2	452	1 A30351	coagulation factor
21	283.5	7.2	482	1 AXRT	coagulation factor
22	282	7.1	456	1 KXBO	protein C (activat
23	281.5	7.1	558	2 JC5878	plasma hyaluronan
24	281	7.1	492	1 EXBO	coagulation factor
25	280.5	7.1	264	2 I38136	chymotrypsin-like
26	280	7.1	562	1 UKHU7	t-plasminogen acti
27	278.5	7.1	466	1 KPHU7	coagulation factor
28	278	7.0	488	1 EXHU	coagulation factor
29	278	7.0	1113	2 J50315	low-density lipopr

t-plasminogen acti  
t-plasminogen acti  
hepatocyte growth  
thrombin (EC 3.4.2  
plasma hyaluronan-  
t-plasminogen acti  
t-plasminogen acti  
thrombin (EC 3.4.2  
coagulation factor  
t-plasminogen acti  
u-plasminogen acti  
u-plasminogen acti  
u-plasminogen acti  
t-plasminogen acti  
chymotrypsin B - A  
coagulation factor  
serine proteinase  
29K serine protein  
u-plasminogen acti  
oviductin (EC 3.4.  
complement factor  
thrombin (EC 3.4.2  
tollid-BMP-1 like  
coagulation factor  
procollagen C-endo  
coagulation factor  
chymotrypsin (EC 3  
plasma kallikrein  
procollagen C-endo  
trypsin (EC 3.4.2  
complement factor  
haptoglobin - blac  
thrombin (EC 3.4.2  
thrombin (EC 3.4.2  
plasmin (EC 3.4.21  
thrombin (EC 3.4.2  
plasma kallikrein  
procollagen C-endo  
trypsin (EC 3.4.21  
haptoglobin precur  
chymotrypsin (EC 3  
trypsin (EC 3.4.2  
trypsin (EC 3.4.2  
procollagen C-endo  
mast cell tryptase  
apolioprotein(a)  
chymotrypsin (EC 3  
hepsin (EC 3.4.21.  
plasma kallikrein  
haptoglobin precur  
thrombin (EC 3.4.2  
haptoglobin precur  
Notch homolog Motc  
notch-1 protein -  
plasmin (EC 3.4.21  
trypsin (EC 3.4.21  
haptoglobin - chim  
trypsin (EC 3.4.21  
trypsin (EC 3.4.21  
development protei  
trypsin (EC 3.4.21  
brain-specific ser  
t-plasminogen acti  
coagulation factor  
coagulation factor  
pancreatic elastas  
chymotrypsin (EC 3



103	223.5	5.7	274	2	S35339	trypsin (EC 3.4.21)	176	199.5	5.1	2555	2	A40043	notch protein homo
104	223.5	5.7	348	1	HPHUR	haptoglobin-relate	177	198.5	5.0	229	1	TRBTR	trypsin (EC 3.4.21)
105	222.5	5.6	417	1	S00845	hepsin (EC 3.4.21)	178	198.5	5.0	232	1	KOPG	tissue kallikrein
106	222.5	5.6	434	1	A35005	u-plasminogen acti	179	198.5	5.0	237	2	S53378	serine proteinase
107	222.5	5.6	790	1	PLPG	plasmin (EC 3.4.21)	180	198	5.0	250	2	S68424	allergen Der f III
108	222	5.6	269	2	A26823	pancreatic elastase	181	198	5.0	270	2	B99934	pancreatic elastase
109	222	5.6	275	2	B35863	tryptase (EC 3.4.2)	182	198	5.0	760	1	C2MS	classical compleme
110	221.5	5.6	2531	2	S18188	notch protein homo	183	197.5	5.0	250	2	T01779	trypsin (EC 3.4.21)
111	221	5.6	231	2	S31778	trypsin (EC 3.4.21)	184	197.5	5.0	258	2	I36947	haptoglobin Hpp -
112	220.5	5.6	274	2	A45754	tryptase (EC 3.4.2)	185	196.5	5.0	269	2	C36823	pancreatic elastase
113	220.5	5.6	1057	1	A39288	dorsal-ventral pat	186	196.5	5.0	570	2	A48836	fibropellin C prec
114	220	5.6	275	2	A35863	tryptase (EC 3.4.2)	187	196.5	5.0	767	2	T30018	hypothetical prote
115	219.5	5.6	235	2	H42696	thrombin (EC 3.4.2)	188	196.5	5.0	2524	2	A35844	notch protein - Af
116	219.5	5.6	271	2	A25528	pancreatic elastase	189	196	5.0	3623	2	T08618	intrinsic factor-B
117	219.5	5.6	761	1	BBMS	complement factor	190	195.5	5.0	271	2	I46580	factor IX - pig (f
118	219	5.6	343	1	A57014	proctasin (EC 3.4.)	191	195	4.9	432	1	S18932	u-plasminogen acti
119	218	5.5	271	2	S41308	serine proteinase (	192	194.5	4.9	246	1	T8RT1	trypsin (EC 3.4.21)
120	217.5	5.5	243	2	A56338	venom proteinase	193	194	4.9	261	2	A35606	tissue kallikrein
121	217	5.5	239	2	A27207	tissue kallikrein	194	194	4.9	267	2	S40006	trypsin (EC 3.4.21)
122	217	5.5	268	2	S68825	pancreatic elastase	195	193.5	4.9	249	2	A55634	granzyme M (EC 3.4
123	217	5.5	273	2	A47246	tryptase (EC 3.4.2)	196	193.5	4.9	347	1	HPRT	haptoglobin precu
124	217	5.5	603	2	S28941	coagulation factor	197	193.5	4.9	2471	2	A91128	cell-fate determin
125	217	5.5	2703	1	A24420	notch protein - fr	198	193	4.9	240	1	CBQO3	procarboxypeptidas
126	216.5	5.5	236	2	I42696	thrombin (EC 3.4.2)	199	193	4.9	246	1	DSHU	complement factor
127	216.5	5.5	346	2	I36942	haptoglobin - chlm	200	191.5	4.9	247	1	A35852	trypsin (EC 3.4.21)
128	216.5	5.5	2616	1	PLHU	nudel protein prec	201	191.5	4.9	281	2	T13596	trypsin homolog -
129	216	5.5	810	1	TRDG	plasmin (EC 3.4.21)	202	191.5	4.9	830	2	A30359	P-selectin precurs
130	215.5	5.5	247	1	S50666	trypsin (EC 3.4.21)	203	190.5	4.8	579	2	JG7629	membrane-type friz
131	215.5	5.5	248	2	S50666	trypsin (EC 3.4.21)	204	190.5	4.8	768	2	A42755	P-selectin precurs
132	215	5.4	241	2	S39048	trypsin (EC 3.4.21)	205	190.5	4.8	1064	2	A40136	fibropellin fa - 8
133	215	5.4	268	2	S68826	pancreatic elastase	206	189.5	4.8	266	2	S54146	trypsin (EC 3.4.21)
134	214.5	5.4	247	2	S13813	tryptase (EC 3.4.21)	207	189.5	4.8	1737	2	T00209	MEGF8 protein - hu
135	214.5	5.4	366	2	JE0105	testicular serine	208	189	4.8	246	2	Q1472	trypsin (EC 3.4.21)
136	214.5	5.4	593	2	S45281	coagulation factor	209	189	4.8	247	2	S05494	trypsin (EC 3.4.21)
137	214	5.4	275	2	C35963	tryptase (EC 3.4.2)	210	189	4.8	253	2	A53968	serine proteinase
138	213.5	5.4	225	2	D42696	thrombin (EC 3.4.2)	211	189	4.8	258	4	S70439	pancreatic elastase
139	213.5	5.4	232	2	T30201	Notch homolog prot	212	189	4.8	267	4	A56615	probable pancreati
140	212	5.4	260	2	I56559	neupsein - mouse	213	189	4.8	646	2	U0473	P-selectin precurs
141	212	5.4	455	2	A61545	plasmin (EC 3.4.21)	214	188.5	4.8	282	2	I84621	coagulation factor
142	211	5.3	237	2	S68702	tryptase (EC 3.4.2)	215	188	4.8	263	2	S15686	tissue kallikrein
143	211	5.3	276	2	A38654	mast cell proteina	216	187.5	4.8	250	2	S55493	serine proteinase
144	210.5	5.3	1220	2	A56136	jagged protein pre	217	187.5	4.8	259	2	I38363	trypsin (EC 3.4.21)
145	210	5.3	2437	2	S42612	transmembrane prot	218	187.5	4.8	304	2	S33496	trypsin (EC 3.4.21)
146	209	5.3	433	1	UKMS	u-plasminogen acti	219	187	4.7	246	2	Q1471	trypsin (EC 3.4.21)
147	208.5	5.3	258	2	I36945	haptoglobin Hp - c	220	187	4.7	261	2	S45303	tissue kallikrein
148	207.5	5.3	239	2	G42696	thrombin (EC 3.4.2)	221	187	4.7	271	2	S29239	chymotrypsin (EC 3
149	207.5	5.3	269	2	B26823	pancreatic elastase	222	186	4.7	1594	2	T30549	hensin - rabbit
150	207	5.2	238	1	TRW5Y	trypsin-like prote	223	185.5	4.7	711	1	A47136	macrophage-stimula
151	206.5	5.2	246	1	TRR2	trypsin (EC 3.4.21)	224	185.5	4.7	927	1	JQ0948	A5 antigen precurs
152	206.5	5.2	256	2	T10109	serine proteinase	225	185	4.7	256	1	NGMSA	7S nerve growth fa
153	206	5.2	430	1	A24702	apoptein(a) (EC	226	183.5	4.7	1372	2	T25933	hypothetical prote
154	206	5.2	4548	1	S00657	mastocytoma protei	227	183	4.6	265	1	KQRTP	serine proteinase
155	205.5	5.2	269	2	B32410	plasmin (EC 3.4.21)	228	183	4.6	392	1	A30100	trypsin (EC 3.4.21)
156	205.5	5.2	460	2	B61545	testicular serine	229	182.5	4.6	482	2	JC5092	trypsin (EC 3.4.21)
157	204.5	5.2	367	2	JE0104	complement C2 prec	230	182.5	4.6	722	2	I48324	serine proteinase
158	204.5	5.2	752	1	C2HU	Notch B protein -	231	182.5	4.6	2531	2	T31070	notch homolog - se
159	204.5	5.2	1203	2	A49175	trypsin (EC 3.4.21)	232	182	4.6	261	1	TRMSM5	tissue kallikrein
160	203.5	5.2	247	1	B25852	complement factor	233	181.5	4.6	247	1	TRMSCL	granzyme B (EC 3.4
161	203.5	5.2	263	1	I55608	coagulation factor	234	181.5	4.6	247	2	S12764	trypsin (EC 3.4.21)
162	203.5	5.2	285	2	I48144	coagulation factor	235	181.5	4.6	258	2	A45161	serine proteinase
163	203.5	5.2	309	2	B49878	coagulation factor	236	181.5	4.6	437	1	S18407	acrosin (EC 3.4.21)
164	203.5	5.2	3623	2	T09456	intrinsic factor-B	237	181	4.6	261	1	NGMSG	7S nerve growth fa
165	203	5.1	403	2	C82228	probable trypsin v	238	181	4.6	418	2	A37344	acrosin (EC 3.4.21)
166	202	5.1	240	2	S39047	trypsin (EC 3.4.21)	239	181	4.6	1291	2	T21694	hypothetical prote
167	202	5.1	2321	2	S78549	notch3 protein - h	240	180.5	4.6	248	2	S55067	trypsin (EC 3.4.21)
168	201.5	5.1	246	1	ICUP	trypsin (EC 3.4.21)	241	180.5	4.6	275	2	I46712	factor IX - rabbit
169	200.5	5.1	226	1	KCUP	bradykinin (EC 3.4	242	180.5	4.6	437	2	JX0172	acrosin (EC 3.4.21)
170	200.5	5.1	231	1	TRPGR	trypsin (EC 3.4.21)	243	180	4.6	254	2	S49329	trypsin-like prote
171	200.5	5.1	810	2	B30848	plasmin (EC 3.4.21)	244	180	4.6	261	2	S01971	tissue kallikrein
172	199.5	5.1	247	2	A27547	trypsin (EC 3.4.21)	245	180	4.6	275	2	S40005	trypsin (EC 3.4.21)
173	199.5	5.1	257	2	S33772	tissue kallikrein	246	179.5	4.6	243	2	A35871	trypsin (EC 3.4.21)
174	199.5	5.1	258	2	G02959	haptoglobin - rhes	247	179.5	4.6	259	1	WMMS28	complement factor
175	199.5	5.1	275	2	S40007	trypsin (EC 3.4.21)	248	179.5	4.6	274	2	I47078	coagulation factor

249	179.5	4.6	728	2	I50719	C-Delta-1 - chicke	322	161.5	4.1	250	2	S31384	trypsin (EC 3.4.21
250	179.5	4.6	1047	2	A55617	masquerade precurs	323	161.5	4.1	261	2	S40162	cathepsin G (EC 3.
251	179	4.5	266	1	BLPG	pancreatic elastas	324	161.5	4.1	265	2	T15451	hypothetical prote
252	179	4.5	612	2	B42755	E-selectin precurs	325	161.5	4.1	832	2	A31246	neurogenic repetit
253	178.5	4.5	402	2	JH0403	procollagen I C-pr	326	161.5	4.1	880	2	S00670	complement C3d/Eps
254	177.5	4.5	248	2	A43520	natural killer cel	327	161.5	4.1	1025	1	A43526	hypothetical prote
255	177.5	4.5	420	2	A55283	notch4 - mouse	328	161	4.1	1827	2	T34288	coagulation factor
256	177.5	4.5	1964	2	T09059	notch4 - mouse	329	160.5	4.1	661	1	KFHU13	granzyme A (EC 3.4
257	177	4.5	268	2	J01473	pancreatic elastas	330	160	4.1	262	1	A31372	fibrillin-1 precur
258	177	4.5	473	2	A56175	adhesive plaque pr	331	160	4.1	3002	2	A47221	protein Fl1C7.4 fi
259	177	4.5	747	2	I51579	complement factor	332	159.5	4.0	1722	2	E89753	tissue kallikrein
260	176.5	4.5	1091	1	PL0009	complement C3d/Eps	333	159	4.0	244	2	A42884	gamma-actinin (EC 3.
261	176	4.5	261	1	S11336	tissue kallikrein	334	159	4.0	261	2	A28062	fibrillin-2 precur
262	176	4.5	261	2	A29745	tissue kallikrein	335	159	4.0	2907	2	A57278	mast cell proteina
263	176	4.5	264	2	S32794	trypsin-like prote	336	158.5	4.0	247	2	S59135	homocytic protein d
264	176	4.5	2318	2	S45306	notch 3 protein -	337	158.5	4.0	385	2	S53718	gene Delta protein
265	175.5	4.4	274	2	S40004	trypsin-related pr	338	158.5	4.0	833	2	S19087	hypothetical prote
266	175	4.4	270	2	A29934	pancreatic elastas	339	158	4.0	610	2	T16761	fibrillin-2 precur
267	175	4.4	421	1	S11674	acrosin (EC 3.4.21	340	158	4.0	2918	2	A54105	hypothetical prote
268	174.5	4.4	232	2	S32398	serine proteinase	341	157.5	4.0	579	2	A56740	sperm-egg recognit
269	174.5	4.4	246	1	TRDGC	trypsin (EC 3.4.21	342	157.5	4.0	907	2	T27317	hypothetical prote
270	174	4.4	259	2	A29746	tissue kallikrein	343	157	4.0	261	2	JE0236	tissue kallikrein
271	174	4.4	261	1	KQMS1	tissue kallikrein	344	157	4.0	610	2	A35046	E-selectin precurs
272	174	4.4	1295	2	A32901	glpi protein precu	345	156.5	4.0	252	2	A36172	procytotoxic T-lym
273	173.5	4.4	548	2	D82175	probable trypsin v	346	156.5	4.0	275	2	JC8506	tumor necrosis fac
274	173	4.4	229	1	TRDFS	trypsin (EC 3.4.21	347	156.5	4.0	1429	2	S06434	homocytic protein 1
275	173	4.4	768	2	I53821	p-selectin - rat	348	156.5	4.0	3635	2	T10053	laminin alpha 5 ch
276	172.5	4.4	248	1	PRMSC2	granzyme C (EC 3.4	349	156	4.0	259	1	KQRTTN	tonin (EC 3.4.21.-
277	172.5	4.4	277	2	S35340	trypsin (EC 3.4.21	350	156	4.0	261	2	A29586	tissue kallikrein
278	172.5	4.4	431	2	S47538	acrosin (EC 3.4.21	351	156	4.0	702	2	T16832	hypothetical prote
279	172.5	4.4	449	2	A55362	procollagen I C-pr	352	155.5	3.9	213	2	S17537	fibrinolytic prote
280	172	4.4	254	2	S65465	trypsin-like prote	353	155.5	3.9	485	2	S36772	E-selectin - bovin
281	172	4.4	261	2	A24378	tissue kallikrein	354	155.5	3.9	533	2	JC7985	brain-specific CUB
282	172	4.4	415	1	A34170	acrosin (EC 3.4.21	355	155	3.9	250	2	S15685	kallikrein, glandu
283	171.5	4.3	230	2	A27802	hypodermin C (EC 3	356	155	3.9	2489	2	I73012	complement C3b/C4b
284	171.5	4.3	262	1	KQHU	tissue kallikrein	357	154.5	3.9	252	2	A34877	C4b-binding protei
285	171.5	4.3	2403	2	A59386	sanko - human	358	154	3.9	689	2	S65551	factor H - bovine
286	171	4.3	257	2	B45061	granzyme A (EC 3.4	359	153.5	3.9	251	2	JC2125	chymase (EC 3.4.21
287	171	4.3	260	2	A45061	granzyme A (EC 3.4	360	153.5	3.9	387	2	B49125	Notch A protein -
288	171	4.3	266	1	ELRT1	pancreatic elastas	361	153.5	3.9	551	2	I46709	endothelial leukoc
289	171	4.3	273	2	S40003	trypsin-related pr	362	153.5	3.9	1786	1	MMWSB1	laminin beta-1 cha
290	171	4.3	2139	2	A35672	crumbs protein - f	363	153	3.9	152	2	A53274	complement factor
291	170	4.3	248	2	S33756	granzyme-like prot	364	153	3.9	254	1	TRWV3Y	trypsin-like prote
292	170	4.3	266	2	JC4850	trypsin-like prote	365	153	3.9	2871	2	A55567	fibrillin-1 - bovi
293	169.5	4.3	251	2	T10262	mast cell serine p	366	152.5	3.9	248	1	S01007	granzyme F (EC 3.4
294	169.5	4.3	261	1	S35711	semenogelase (EC 3	367	152.5	3.9	264	2	S65663	granzyme 3 (EC 3.4
295	169.5	4.3	421	2	S29599	acrosin (EC 3.4.21	368	152.5	3.9	385	2	A54785	preadipocyte facto
296	169.5	4.3	214	2	T16833	hypothetical prote	369	152.5	3.9	422	1	KXHUZ	plasma protein Z p
297	169	4.3	214	2	S17680	fibrinolytic prote	370	152	3.9	281	1	A61021	Granzyme B (EC 3.4
298	169	4.3	246	2	S64707	chymase (EC 3.4.21	371	152	3.9	686	2	JC7569	Delta-4 protein -
299	169	4.3	259	2	B31136	tissue kallikrein	372	151.5	3.8	261	2	A40332	tissue kallikrein
300	169	4.3	504	2	S56745	mucin (clone pgM31	373	151.5	3.8	716	1	A40332	macrophage-stimula
301	168.5	4.3	248	2	S33755	granzyme-like prot	374	151.5	3.8	977	2	I52657	seizure-related pr
302	168	4.3	597	2	S71352	metalloproteinase	375	151	3.8	249	1	A35842	chymase (EC 3.4.21
303	168	4.3	2014	2	I36936	complement recepto	376	151	3.8	261	2	A41020	tissue kallikrein
304	167.5	4.2	261	1	A32297	semenogelase (EC 3	377	151	3.8	1620	2	T27283	hypothetical prote
305	167.5	4.2	383	2	S53716	delta-like homocyt	378	150.5	3.8	248	2	S43259	granzyme-like prot
306	167	4.2	247	2	S45113	granzyme-like prot	379	150.5	3.8	277	2	A41735	hyaluronate-bindin
307	167	4.2	260	2	A37938	tissue kallikrein	380	150.5	3.8	285	2	T35195	probable serine pr
308	166	4.2	265	2	T10495	chymotrypsin (EC 3	381	150.5	3.8	685	2	JC7570	Delta-4 protein -
309	165	4.2	2043	2	T18524	scavenger receptor	382	150.5	3.8	1053	2	S46199	probable complemen
310	164.5	4.2	449	1	NBHUS	complement factor	383	150	3.8	263	1	WMVZSP	apolipoprotein H h
311	164.5	4.2	1231	1	NBHUS	complement factor	384	150	3.8	267	1	ELHUL	leukocyte elastase
312	164	4.2	230	2	I48695	mast cell proteina	385	150	3.8	601	2	B36346	fibrulin 1 precurs
313	164	4.2	613	2	S15468	complement C3b/C4b	386	150	3.8	770	2	T00203	LDL receptor-relat
314	164	4.2	2871	2	A55624	fibrillin-1 precur	387	150	3.8	3712	2	S18253	laminin alpha-1 ch
315	163	4.1	868	2	T40239	hypothetical prote	388	149.5	3.8	236	1	A32121	snake venom factor
316	162.5	4.1	276	2	A27290	TSG-6 homolog P84	389	149.5	3.8	259	1	TRSMG	trypsin (EC 3.4.21
317	162.5	4.1	1290	2	A57190	ebnerin precursor	390	149.5	3.8	13288	2	T03099	mucin, submaxillar
318	162.5	4.1	2083	2	T42721	CRP-ductin-alpha p	391	149	3.8	216	1	KYVH20	chymotrypsin (EC 3
319	162	4.1	261	1	EGMSB	tissue kallikrein	392	149	3.8	683	2	C36346	fibrulin 1 precurs
320	161.5	4.1	226	2	S69370	duodenase - bovine	393	149	3.8	770	2	T00204	LDL receptor relat
321	161.5	4.1	248	2	S01006	cytotoxic T-lympho	394	149	3.8	1408	2	S16148	gene serrate prote

395	148	3.8	218	1	KYH2C	chymotrypsin (EC 3	468	134	3.4	3034	2	T14119	seven-pass transme
396	148	3.8	668	2	A46013	coagulation factor	469	133.5	3.4	154	2	S35207	proteinase 7 - buf
397	148	3.8	1469	2	B36665	slit protein 2 pre	470	133.5	3.4	1687	2	S35207	EGF repeat transme
398	148	3.8	1480	2	A36665	slit protein 1 pre	471	133.5	3.4	3507	2	T34513	hypothetical prote
399	147.5	3.7	244	2	A34910	mast cell proteina	472	133	3.4	810	2	T10756	Nel-homolog protei
400	147.5	3.7	244	2	A46721	chymase (EC 3.4.21	473	132.5	3.4	331	2	T27906	hypothetical prote
401	147.5	3.7	597	1	S53711	C4BP alpha chain p	474	132	3.3	246	2	A38678	mast cell proteina
402	147.5	3.7	1786	1	MMHUB1	laminin beta-1 cha	475	132	3.3	372	2	JC5377	L-selectin precurs
403	147.5	3.7	4391	2	A38096	perlecan precursor	476	132	3.3	558	2	S57953	C4BP protein alpha
404	147	3.7	236	2	A28566	T-cell suppressor	477	132	3.3	2109	1	I50421	aggregran precursor
405	147	3.7	259	2	D23863	tissue kallikrein	478	132	3.3	3871	2	T22812	hypothetical prote
406	147	3.7	262	1	JC4803	venombin A (EC 3.4	479	131.5	3.3	302	1	WMBE1E	secretory compleme
407	147	3.7	716	1	JC5061	macrophage-stimula	480	131.5	3.3	1268	2	S52781	neurocan - mouse
408	147	3.7	1557	2	T28811	hypothetical prote	481	130.5	3.3	1257	2	S28764	neurocan precursor
409	147	3.7	3084	1	MMMSA	laminin alpha-1 ch	482	130.5	3.3	3672	2	T23433	hypothetical prote
410	146.5	3.7	236	1	B32121	snake venom factor	483	130.5	3.3	3704	2	T37316	probable laminin a
411	146.5	3.7	3707	2	S18252	heparan sulfate pr	484	129.5	3.3	233	1	JG0169	venombin A (EC 3.4
412	146	3.7	263	2	T28450	hypothetical prote	485	129.5	3.3	376	2	JC4892	L-selectin precurs
413	145	3.7	256	1	TRPF	trypsin-like prote	486	129.5	3.3	381	1	B36359	decay-accelerating
414	145	3.7	263	1	C36838	complement control	487	129.5	3.3	440	2	A63359	decay-accelerating
415	145	3.7	372	2	A32375	L-selectin precurs	488	129	3.3	235	1	S65621	venombin AB (EC 3.
416	145	3.7	782	2	A61625	tenascin-like prot	489	128.5	3.3	255	2	A27122	cathepsin G (EC 3.
417	144.5	3.7	246	2	B38578	mast cell proteina	490	128.5	3.3	321	2	T33161	hypothetical prote
418	144.5	3.7	303	2	T13598	trypsin homolog -	491	128	3.2	219	1	TRPGA2	azurocidin - pig
419	144.5	3.7	360	2	T42321	complement control	492	127.5	3.2	5147	1	LJFFTM	cadherin-related t
420	144	3.7	283	2	B72152	Bi8L protein - var	493	127	3.2	1531	2	T42218	slit-1 protein hom
421	144	3.7	685	2	S78040	fibulin, splice fo	494	127	3.2	258	2	S62220	tryptase 2 - rat
422	143.5	3.6	247	2	S23504	chymase (EC 3.4.21	495	127	3.2	1609	1	MMHUB2	laminin gamma-1 ch
423	143	3.6	3075	2	S14458	laminin alpha-1 ch	496	127	3.2	1751	1	MMHUMH	laminin alpha-2 ch
424	142.5	3.6	260	2	S26043	chymase (EC 3.4.21	497	127	3.2	3106	1	S53868	laminin alpha-2 ch
425	142	3.6	272	2	JC4170	trypsin-like prote	498	126.5	3.2	1025	2	T42626	secreted leucine-r
426	141.5	3.6	310	2	S41055	metalloproteinase	499	126	3.2	265	2	J50260	serine proteinase
427	141.5	3.6	385	1	A34015	L-selectin precurs	500	126	3.2	265	2	A38894	serine proteinase
428	141	3.6	225	2	S45356	probable serine pr	501	126	3.2	330	2	I56100	complement factor
429	141	3.6	246	2	A32692	cytotoxic T-lympho	502	126	3.2	642	2	S53433	plasma protein S p
430	140.5	3.6	246	1	A46504	chymase (EC 3.4.21	503	125.5	3.2	254	2	S35585	chymotrypsin-like
431	140.5	3.6	1234	1	NBMSH	complement factor	504	125.5	3.2	265	2	I48679	neutrophil elastase
432	140.5	3.6	2406	2	A54148	odz protein - frui	505	125.5	3.2	597	1	NBUC4	C4b-binding protei
433	140.5	3.6	2515	2	S47008	tenascin-like prot	506	125	3.2	152	2	S35209	serine proteinase
434	140	3.5	396	1	KXBOZ	plasma protein Z -	507	125	3.2	323	1	S09702	L-selectin precurs
435	139.5	3.5	258	1	S44184	chymotrypsin (EC 3	508	125	3.2	1790	1	MMFFB1	laminin beta-1 cha
436	139.5	3.5	288	2	T33224	hypothetical prote	509	124.5	3.2	248	2	A33412	cytotoxic T-lympho
437	139.5	3.5	319	2	I51569	UVS-2 protein - Af	510	124.5	3.2	548	2	T16642	hypothetical prote
438	139	3.5	1820	2	A55494	latent transformin	511	124	3.1	330	2	T46256	hypothetical prote
439	138.5	3.5	244	2	S26042	chymase (EC 3.4.21	512	124	3.1	710	1	I51283	hepatocyte growth
440	138.5	3.5	247	1	KYHUCM	chymase (EC 3.4.21	513	124	3.1	883	2	S49126	brevican precursor
441	138.5	3.5	705	2	S34968	fibulin, splice fo	514	124	3.1	1221	2	A49457	fibulin-2 precurs
442	138.5	3.5	1111	2	T26972	hypothetical prote	515	124	3.1	1523	2	T13953	MEGF5 protein - ra
443	137.5	3.5	191	2	S54115	complement factor	516	124	3.1	1584	2	T22674	hypothetical prote
444	137.5	3.5	808	2	D35069	complement factor	517	124	3.1	2180	2	T29764	hypothetical prote
445	137	3.5	288	2	S57960	C4BP protein beta	518	123.5	3.1	151	2	S35205	proteinase 5 - buf
446	137	3.5	372	2	S23936	L-selectin precurs	519	123.5	3.1	259	1	S49129	chymotrypsin (EC 3
447	137	3.5	2823	2	T23064	hypothetical prote	520	123.5	3.1	370	2	S22124	L-selectin precurs
448	137	3.5	2823	2	F87908	protein T22A3.8 li	521	123.5	3.1	699	2	T33375	hypothetical prote
449	137	3.5	3102	2	T43291	laminin alpha chai	522	123.5	3.1	1184	2	A55184	fibulin-2 precurs
450	136.5	3.5	247	1	PRRTG	mast cell proteina	523	123	3.1	248	2	S49323	chymotrypsin (EC 3
451	136.5	3.5	1274	2	T42017	cysteine rich prot	524	123	3.1	308	2	JC7125	epidermal growth f
452	136	3.4	360	1	WMBS2E	membrane-bound com	525	123	3.1	340	2	I56234	decay-accelerating
453	136	3.4	676	2	A45900	complement C3b rec	526	123	3.1	798	2	T22793	hypothetical prote
454	136	3.4	1574	2	T13954	MEGF6 protein - ra	527	123	3.1	2844	2	S28291	hypothetical prote
455	136	3.4	1607	1	MMMSB2	laminin gamma-1 ch	528	122.5	3.1	1081	2	T31329	receptor tyrosine
456	135.5	3.4	226	2	JM0151	myonase (EC 3.4.-	529	122	3.1	152	2	S35206	serine proteinase
457	135.5	3.4	372	2	T29359	hypothetical prote	530	122	3.1	198	2	I46002	C4BP beta chain -
458	135.5	3.4	452	2	A35068	complement factor	531	122	3.1	676	1	KXHUS	plasma protein S p
459	135.5	3.4	469	1	NBMSCA	C4b-binding protei	532	122	3.1	1810	1	A32230	tenascin precursor
460	135	3.4	159	2	I84615	coagulation factor	533	122	3.1	1955	1	AGCH	agrin precursor -
461	135	3.4	343	2	G35070	apolipoprotein H-r	534	121.5	3.1	245	2	A48598	kallikrein-like se
462	135	3.4	345	1	NBRU	apolipoprotein H p	535	121.5	3.1	416	2	T20448	hypothetical prote
463	135	3.4	3051	2	S42373	hypothetical prote	536	121.5	3.1	610	1	I46001	C4b-binding protei
464	134.5	3.4	601	2	T22025	hypothetical prote	537	121.5	3.1	576	2	T42215	zonadhesin - mouse
465	134.5	3.4	601	2	D89711	protein F40E10.4 [	538	121	3.1	647	2	A43902	tenascin - easteat
466	134	3.4	232	1	A54361	venombin A (EC 3.4	539	121	3.1	1627	2	S65464	pregnancy-associat
467	134	3.4	2824	2	T22759	hypothetical prote	540	121	3.1	2409	1	A60979	versican precursor

541	120.5	3.1	247	2	564708	chymase (EC 3.4.21)	614	112	2.8	228	1	S35689	venombin A (EC 3.4
542	120.5	3.1	252	2	T46247	hypothetical prote	615	112	2.8	918	2	JC4361	scavenger receptor
543	120.5	3.1	345	1	JN0465	apolipoprotein H p	616	112	2.8	1125	1	S57846	protein-tyrosine k
544	120.5	3.1	497	2	JC2054	complement regulat	617	112	2.8	1353	1	JH0675	restriccin precurs
545	120.5	3.1	646	2	S38819	plasma protein S -	618	112	2.8	1639	1	MMFEB2	laminin gamma-1 ch
546	120.5	3.1	689	2	T42760	fibulin, splice fo	619	112	2.8	3562	2	A47171	chondroitin sulfat
547	120.5	3.1	712	2	T42990	fibulin 1, splice	620	112	2.8	4307	2	T20721	hypothetical prote
548	120.5	3.1	728	1	A60185	hepatocyte growth	621	111.5	2.8	159	2	S35202	proteinase 2 - buf
549	120.5	3.1	1394	2	A35626	transforming growt	622	111.5	2.8	370	2	JC7592	spinal cord-derive
550	120.5	3.1	1801	1	NMRTS	laminin beta-2 cha	623	111.5	2.8	651	2	T19477	hypothetical prote
551	120	3.0	257	1	JC2479	venombin B (EC 3.4	624	111.5	2.8	1328	2	T43060	agrin - electric r
552	120	3.0	363	2	B45900	complement C3d/Eps	625	111.5	2.8	1797	2	A55677	tenascin beta-2 cha
553	120	3.0	493	2	JC5621	epidermal growth f	626	111.5	2.8	2019	1	JQ1322	tenascin precursor
554	120	3.0	589	2	T43210	fibulin-ID precurs	627	111.5	2.8	2531	2	T16743	hypothetical prote
555	120	3.0	912	2	A54423	brevican precursor	628	111.5	2.8	4351	2	T00252	MEGF1 protein - ra
556	120	3.0	1548	2	S34593	serine proteinase	629	111	2.8	231	2	A60468	venombin A (EC 3.4
557	120	3.0	1643	2	T14274	versican precursor	630	111	2.8	915	2	T21773	hypothetical prote
558	120	3.0	2397	1	A55535	versican precursor	631	110.5	2.8	234	1	S20407	venombin A (EC 3.4
559	120	3.0	3381	2	T42389	versican precursor	632	110.5	2.8	237	1	NBRT	apolipoprotein H p
560	119.5	3.0	161	2	T48158	coagulation factor	633	110.5	2.8	408	2	T22801	hypothetical prote
561	119.5	3.0	482	2	A34924	complement C3b/C4b	634	110.5	2.8	583	2	A29154	growth arrest-spec
562	119.5	3.0	675	1	KXB05	plasma protein S p	635	110.5	2.8	678	2	B48089	hypothetical prote
563	119.5	3.0	835	2	JP0076	nel protein - chic	636	110.5	2.8	692	2	T32980	hypothetical prote
564	119.5	3.0	1247	1	NMUND	nidogen precursor	637	110.5	2.8	961	1	TSHUP4	thrombospondin 4 p
565	119.5	3.0	1506	2	T30886	integrin precursor	638	110.5	2.8	1217	1	EGMSMG	epidermal growth f
566	119	3.0	258	2	A57290	venom plasminogen	639	110.5	2.8	1894	2	JC4980	plexin I precursor
567	119	3.0	513	2	D88991	protein apx-1 [imp	640	110	2.8	266	2	T19292	hypothetical prote
568	118.5	3.0	674	2	I55476	growth potentiatin	641	110	2.8	1124	1	I58388	protein-tyrosine k
569	118.5	3.0	728	1	JH0579	hepatocyte growth	642	110	2.8	1905	2	I51553	Plexin - African c
570	118.5	3.0	728	1	A35644	hepatocyte growth	643	109.5	2.8	198	2	S06176	cytotoxic T-lympho
571	118	3.0	133	2	T21114	spermathecin AMN -	644	109.5	2.8	2215	2	T00348	LR11 protein - mou
572	118	3.0	196	2	T08808	hypothetical prote	645	109	2.8	661	2	T42754	hypothetical prote
573	118	3.0	293	2	B26637	neurogenic repetit	646	109	2.8	1808	2	T15099	hypothetical prote
574	118	3.0	838	2	T20125	hypothetical prote	647	109	2.8	2610	2	T20968	hypothetical prote
575	118	3.0	883	2	S57653	brevican precursor	648	108.5	2.8	236	1	A41456	venombin A (EC 3.4
576	117.5	3.0	188	2	B23240	tissue kallikrein	649	108.5	2.8	2825	2	T14271	Doc4 protein, stre
577	117.5	3.0	259	2	T21011	hypothetical prote	650	108	2.7	221	1	TRHUZ	azurocidin precurs
578	117.5	3.0	642	2	S53434	plasma protein S p	651	108	2.7	1450	2	T30273	hypothetical prote
579	117.5	3.0	996	2	J20237	apolipoprotein E r	652	108	2.7	1700	2	S08167	Balbani ring 3 pr
580	117.5	3.0	1160	2	F88369	protein unc-52 [im	653	108	2.7	2476	2	T34022	zonadhesin - pig
581	117.5	3.0	2295	2	C88369	protein unc-52 [im	654	107.5	2.7	640	2	T19346	hypothetical prote
582	117.5	3.0	3375	2	T19821	hypothetical prote	655	107.5	2.7	670	2	I65967	disintegrin-like m
583	116.5	3.0	256	1	PRH03	proteinase 3 (EC 3	656	107.5	2.7	3566	1	A40701	tenascin-X precurs
584	116.5	3.0	377	2	I54479	membrane cofactor	657	107.5	2.7	4544	1	S02392	alpha-2-macroglobu
585	116.5	3.0	378	2	B50186	Wnt inhibitory fac	658	107	2.7	280	2	G02741	skeletal muscle LI
586	116.5	3.0	384	2	S01896	membrane cofactor	659	107	2.7	497	2	T27827	hypothetical prote
587	116.5	3.0	1170	2	A53612	laminin B1k chain	660	106.5	2.7	192	2	E70414	hypothetical prote
588	116	2.9	1376	2	G00043	osteonidogen - hum	661	106.5	2.7	362	2	JC5194	membrane cofactor
589	115.5	2.9	440	2	A43519	complement recepto	662	106.5	2.7	369	2	JC5138	hypothetical prote
590	115.5	2.9	1474	2	D88550	protein ZC84.6 [im	663	106.5	2.7	616	2	T29234	hypothetical prote
591	115.5	2.9	1680	2	A43434	furin (EC 3.4.21.7	664	106.5	2.7	755	2	A44315	hypothetical prote
592	115	2.9	279	2	JG0164	LIM protein, FHL4	665	106	2.7	417	2	T33376	hypothetical prote
593	115	2.9	1207	1	EGHU	epidermal growth f	666	106	2.7	657	2	T00859	hypothetical prote
594	114.5	2.9	270	2	T37278	complement factor	667	106	2.7	927	2	T21772	epidermal growth f
595	114.5	2.9	349	2	G02913	sperm CD46 - human	668	106	2.7	1133	1	EGRT	hypothetical prote
596	114.5	2.9	369	2	I57998	membrane cofactor	669	106	2.7	1142	2	T30272	hypothetical prote
597	114.5	2.9	1798	2	S53869	laminin beta-2 cha	670	106	2.7	1522	2	H88380	protein T22F7.3 [i
598	114	2.9	255	1	A28169	venombin A (EC 3.4	671	106	2.7	1805	2	T21888	hypothetical prote
599	114	2.9	741	2	T46488	hypothetical prote	672	106	2.7	2195	2	T42464	hypothetical prote
600	114	2.9	846	2	A30889	integrin beta chai	673	105.5	2.7	346	2	T46914	hypothetical prote
601	114	2.9	1069	2	T42681	hypothetical prote	674	105.5	2.7	596	2	A45664	variant-specific a
602	113.5	2.9	293	2	T22919	hypothetical prote	675	105.5	2.7	673	2	A48089	growth arrest-spec
603	113.5	2.9	502	2	T20130	hypothetical prote	676	105	2.7	860	1	QRHULD	LDL receptor precu
604	113.5	2.9	558	2	T17324	hypothetical prote	677	105	2.7	1107	2	T15884	hypothetical prote
605	113.5	2.9	574	2	B88465	protein B0244.8 [i	678	105	2.7	1746	1	S19694	tenascin precursor
606	113.5	2.9	879	1	ORRTLD	LDL receptor precu	679	105	2.7	2201	2	A32160	tenascin-C - human
607	113.5	2.9	1712	2	A38261	masking protein pr	680	104.5	2.6	345	1	NBMS	apolipoprotein H p
608	112.5	2.9	161	2	I62744	coagulation factor	681	104.5	2.6	1360	2	T33522	hypothetical prote
609	112.5	2.9	264	2	T28942	pancreatic elastas	682	104	2.6	345	1	NBBO	apolipoprotein H p
610	112.5	2.9	370	2	JC7591	spinal cord-derive	683	104	2.6	360	1	A55198	transcription fac
611	112.5	2.9	677	2	C42125	trophozoite cystei	684	104	2.6	379	2	A59180	Wnt inhibitory fac
612	112.5	2.9	1228	2	A57384	multimerin, endoth	685	104	2.6	473	2	T32326	hypothetical prote
613	112.5	2.9	1797	2	T11889	hypothetical prote	686	104	2.6	2101	2	S57245	insulin receptor (



Qy 456 -KTQGLRWPQAIIYRRTSGVHDGSLHKGAWFLVCSGALVNRVTVAHVCTDGLGKVTM 514  
 Db 767 NSTEIGQWPAQAGISRWLA-----DHNWFLQCGGSLNKKWIVTAHCVTSATAEI 819  
 Qy 515 IKTADLVVGLKFPDRDRDEKTIQSLQISAILHNNYDPIILLDADTALIKLADKARIST 574  
 Db 820 IDPSQFKYLGKYYRDRSDDDYVQVREALIEIHVNPNDPGLNFDLALQLKTPVTLTT 879  
 Qy 575 RVOPICLAARDLSTSPQESHI-----TVAGWNVLADVRSPGKNDTLRSVVVVDLSL 628  
 Db 880 RVOPICLPT-DITT--REHLREGTLAVTGWG---LNENNTYSEMIQQAIVPVVAAS 930  
 Qy 629 LCEQEDHGHIPVSTONMFCASWEPAPSDICTAETGGIAAVSPGASPERHLMGL 688  
 Db 931 TCEBGYKEADLPVTNMFMCAGYK-KGRYDACSDDSGG--PLVAFDDSRSTRRWVLEGI 987  
 Qy 689 VSMGYDKTCSH-RLSTAFKTVLPFKDWIER 717  
 Db 988 VSMGSPGCGKANQYGGFTKVNFLSWIRQ 1017

RESULT 3  
 I54763  
 Na-Reactive factor (EC 3.4.21.-) 1 precursor - human  
 A/Alternate names: mannose binding protein-associated serine proteinase 1 (MASP-1)  
 C/Species: Homo sapiens (man)  
 C/Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 16-Jun-2000  
 C/Accession: I54763; JN0883  
 R/Sato, T.; Endo, Y.; Matsumura, M.; Fujita, T.  
 Int. Immunol. 6, 665-669, 1994  
 A/Title: Molecular characterization of a novel serine protease involved in activation of  
 A/Reference number: I54763; MUID:94289349; PMID:8018603  
 A/Accession: I54763  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-699 <SAT>  
 A/Cross-references: GB:028593; NID:9790963; PIDN:BAA05928.1; PID:9471128  
 R/Takada, F.; Takayama, Y.; Hataue, H.; Kawakami, M.  
 Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993  
 A/Title: A new member of the C1s family of complement proteins found in a bactericidal f  
 A/Reference number: JN0883; MUID:94059062; PMID:8240317  
 A/Accession: JN0883  
 A/Molecule type: mRNA  
 A/Residues: 1-234, 'E', 236-284, 'G', 286-498, 'K', 500-542, 'K', 544-642, 'S', 644-699 <TAK>  
 A/Cross-references: DBJ:DL7525; NID:9433712; PIDN:BAA04477.1; PID:9433713  
 A/Experimental source: liver  
 C/Comment: This is a serum bactericidal factor that activates complement C4 and C2 compo  
 C/Genetics:  
 A/Geno: GDB:MASP1; GDB:CRAPF; CRAPF1; PRSS5; MASP  
 A/Cross-references: GDB:361104; GDB:330954; OMIM:600521  
 A/Map position: 3q27-3q28  
 C/Suprafamily: complement subcomponent C1r; C1r/C1s repeat homology; complement factor H  
 C/Keywords: beta-hydroxyasparagine; complement pathway; duplication; glycoprotein; hydro  
 F/1-17/Domain: signal sequence #status predicted <SIG>  
 F/18-448/449-699/Product: Ra-reactive factor #status predicted <MAT>  
 F/19-135/Domain: C1r/C1s repeat homology <C1r1>  
 F/143-181/Domain: EGF homology <EGF>  
 F/185-294/Domain: C1r/C1s repeat homology <C1R2>  
 F/301-362/Domain: complement factor H repeat homology <FHL>  
 F/367-432/Domain: complement factor H repeat homology <FH2>  
 F/449-631/Domain: trypsin homology <TRY>  
 F/479,479,407/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F/73-91,143-157,153-166,168-181,185-212,242-260,301-349,329-362,367-414,397-432,436-572,  
 F/159/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
 F/448-449/Cleavage site: Arg-Ile (autolytic) #status predicted  
 F/490,552,646/Active site: His, Asp, Ser #status predicted

Query Match 12.2%; Score 482; DB 1; Length 699;  
 Best Local Similarity 24.9%; Pred. No. 1.2e-24;  
 Matches 178; Conservative 93; Mismatches 215; Indels 228; Gaps 39;  
 Qy 69 CRNEENEDSLIHPGCTIPENCCKSRNGSGTGLDDPYYKGFYCAECRAGWY---GGD 124

Db 143 CKEREDEELSCDHY-----CHN-----YIGGYCS-CRFGYILHTDNR 180  
 Qy 125 C-MRCQVLRAPKGOILL-----ESYPLNAHCWETIHAKEPGFVIQIRFVWLSLEFDYM-- 176  
 Db 181 CRVECDNLFTQRTGVTSPDPFNPYPKSKSECLYTIIEBEGFMVNLQFEDI---FDIQDH 237  
 Qy 177 ----COYDVVEVDGNRGQIIRKVCNERPAPIOSIGSSLLHVLPHSDGSKNFDFHAI 232  
 Db 238 PEVPCPYDIKIKVGP-----KVLGPFCEGKAPETISTQSHSVLLILPHSDNSAENRWRL- 292  
 Qy 233 YEBITACSSPPCHDGTCLVDKAGSYKCACTAGYTCQRCENLEERNCSDPGPGPVNGYQK 292  
 Db 293 -----SYRAA-----GNECPCL-----QP-PVH----- 309  
 Qy 293 ITGGPGLINGRAHAKIGTVVSFF-----CNNSY-VLSGNEKR-----TCQOENGWSGKQ 339  
 Db 310 ----GKIPSOAKY-----FFKQDVLSCDTGYKVLKDNVEMDTFQIECLDKGTWSNKI 359  
 Qy 340 PIC-IKACHEPKISDLVRRVLPVQVSRETPLHQLYSAAFSKQKLOSAPTKKPALPFGD 398  
 Db 360 PTCKIVDCRAP-----OLOYECISPFYRRILGSSR--RTCLRTGKWS---GRA-PSC 442  
 Qy 399 LPMGYQHLHT-----OLOYECISPFYRRILGSSR--RTCLRTGKWS---GRA-PSC 442  
 Db 373 LEHGLTFTSTRNLTKYKSEIKYSCQEPYKMLNNTGIYTCQAQWVWNVKVLGRSLPTC 432  
 Qy 443 IPICG-----KIENITAPKTQGLRWPQAIIYRRTSGVHDGSLHKGAWFLVCSGA 492  
 Db 433 LPVCGLPKFSRKLWARIFN-GRPAQKGT-PTIAML-----SHLNGQPF--CGGS 478  
 Qy 493 LVNERTVVAACHV---TDLGKVT-----MIKTADLKVLGKPYRDDRDEKTIQSLQIS 544  
 Db 479 LIGSSWIVTAACHLQSLDPGDTLDRSDLSFDFKILGLKHW--LRSDENEQHLGVK 536  
 Qy 545 AILHNPYDPIILLADIAILKLDKARISTRVOPICLAASRDLSFSQE-SHITVAGWNV 603  
 Db 537 HTLHRQYDNTENDVALVELLESPLNAAFVNPICLPBPQ-----QEGAWIVSWGK 591  
 Qy 604 LADVRSPGKNDTLRSVSVVSDLSLCEQEDHGHIPVSTDNMFCAWEPAPSDICTA 663  
 Db 592 QFLQRFPP-----ETLMEIPIVDHSTQKAYAP--LKQKVTDRDMICAG-EKEGKDKACAG 644  
 Qy 664 ETGIAAVSPGASPERHLMGLVSVSYDKTCSHRLSTAFKTVLPFKDWIER 717  
 Db 645 DSGGPMVTLNRERG-----QMYLVGTVSGWDDCKGKORYG-VYSYIHHNKDWIOR 693

RESULT 4  
 C1HURB  
 Complement subcomponent C1r (EC 3.4.21.41) precursor [validated] - human  
 C/Species: Homo sapiens (man)  
 C/Date: 15-Nov-1984 #sequence\_revision 30-Jun-1991 #text\_change 28-Jul-2003  
 C/Accession: A24170; A29768; A29769; S02422; A00916; A37820; S68830  
 R/Leytus, S.P.; Kurachi, K.; Sakariassen, K.S.; Davie, E.W.  
 Biochemistry 25, 4855-4863, 1986  
 A/Title: Nucleotide sequence of the cDNA coding for human complement C1r.  
 A/Reference number: A24170; MUID:87026566; PMID:3021205  
 A/Accession: A24170  
 A/Molecule type: mRNA  
 A/Residues: 1-705 <LEY>  
 A/Cross-references: GB:M14058; NID:G179643; PIDN:AAA51851.1; PID:G179644  
 R/Journet, A.; Tosi, M.  
 Biochem. J. 240, 783-787, 1986  
 A/Title: Cloning and sequencing of full-length cDNA encoding the precursor of human compl  
 A/Reference number: A29768; MUID:87156625; PMID:3030286  
 A/Accession: A29768  
 A/Molecule type: mRNA  
 A/Residues: 1-151, 'L', 153-705 <JOU>  
 A/Cross-references: GB:X04701; NID:G29538; PIDN:CXA28407.1; PID:G29539  
 R/Arlaud, G.J.; Willis, A.C.; Gagnon, J.  
 Biochem. J. 241, 711-720, 1987  
 A/Title: Complete amino acid sequence of the A chain of human complement-classical-pathwa  
 A/Reference number: A29769; MUID:87241248; PMID:3036070



A;Accession: A29769  
 A;Molecule type: protein  
 A;Residues: 18-166, 'X', 168-463 <ARL>  
 A;Note: 152-Leu was also found  
 R;Arnaud, G.J.; van Dorsselaer, A.; Bell, A.; Mancini, M.; Aude, C.; Gagnon, J.  
 FEBS Lett. 222, 129-134, 1987  
 A;Title: Identification of erythro-beta-hydroxyasparagine in the EGF-like domain of human  
 A;Reference number: S02422; MUID:88005128; PMID:2820791  
 A;Accession: S02422  
 A;Molecule type: protein  
 A;Residues: 152-186 <AR3>  
 A;Note: 152-Leu was also found  
 R;Arnaud, G.J.; Gagnon, J.  
 Biochemistry 22, 1758-1764, 1983  
 A;Title: Complete amino acid sequence of the catalytic chain of human complement subcomp  
 A;Reference number: A00916; MUID:83204782; PMID:6303394  
 A;Accession: A00916  
 A;Molecule type: protein  
 A;Residues: 464-705 <AR2>  
 R;Thielens, N.M.; Aude, C.A.; Lacroix, M.B.; Gagnon, J.; Arlaud, G.J.  
 J. Biol. Chem. 265, 14469-14475, 1990  
 A;Title: Ca(2+) binding properties and Ca(2+)-dependent interactions of the isolated NH-  
 A;Reference number: A37820; MUID:90354439; PMID:2387866  
 A;Accession: A37820  
 A;Molecule type: protein  
 A;Residues: 18-26; 'L', 153-160; 'XX', 252-255 <TH1>  
 R;Pelloux, S.; Thielens, N.M.; Hudry-Clergeon, G.; Petillot, Y.; Filhol, O.; Arlaud, G.J.  
 FEBS Lett. 386, 15-20, 1996  
 A;Title: Identification of a cryptic protein kinase CK2 phosphorylation site in human co  
 A;Reference number: S68830; MUID:96221263; PMID:8635594  
 A;Accession: S68830  
 A;Molecule type: protein  
 A;Residues: 133-137; 187-211; 610-613 <PEL>  
 A;Experimental source: plasma  
 C;Comment: C1r is a dimer of identical chains, each of which is activated by cleavage in  
 A chain, while fragment gamma remains disulfide-bonded to the B chain to form C1r II.  
 C;Comment: This protein is a serine protease that combines with C1q and C1s to form C1,  
 n, activate C2 and C4.  
 C;Genetics:  
 A;Gene: GDB:C1R  
 A;Cross-references: GDB:119729; OMIM:216950  
 A;Map position: 12p13-12p13  
 C;Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement factor H  
 C;Keywords: acute phase; beta-hydroxyasparagine; calcium binding; complement pathway; du  
 F;1-17/Domain: signal sequence #status predicted <SIG>  
 F;18-463/Product: complement C1r chain A #status experimental <ACH>  
 F;146-189/Domain: EGF homology <EGF>  
 F;193-302/Domain: C1r/C1s repeat homology <C1R2>  
 F;297-463/Product: C1r gamma fragment #status experimental <GFR>  
 F;309-371/Domain: complement factor H repeat homology <FH1>  
 F;376-447/Domain: complement factor H repeat homology <FH2>  
 F;464-705/Product: complement C1r chain B #status experimental <BCH>  
 F;464-697/Domain: trypsin homology <TRY>  
 F;71-89, 146-165, 165-174, 176-189, 193-220, 268, 309-358, 338-371, 376-429, 406-447, 451-577,  
 F;125, 221, 514, 581/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F;167/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental  
 F;206/Binding site: phospho (Ser) (covalent) (by casein kinase II) #status experimental  
 F;463-464/Cleavage site: Arg-11e (autolytic) #status experimental  
 F;502, 557, 654/Active site: His, Asp, Ser #status predicted

Query Match 10.2%; Score 403.5; DB 1; Length 705;  
 Best Local Similarity 22.9%; Pred. No. 2.2e-19;  
 Matches 178; Conservative 96; Mismatches 259; Indels 245; Gaps 41;

QY 44 ECCEYDQIEC-----VC-----PGKREVVGVTIPCC-----RNEEED 77  
 Db 69 EGCYDVVKISADKSLGRFCGLGSLGNPPCKEFMSQGNKMLTFTDFSEEN--G 126  
 QY 78 SCLIHPCGTIF-----ENKSCRNSGWSGTLD-----DFYVKGVCACRAGW----- 120  
 Db 127 TIMFYKGLAYQAVDLDECASRSKSGEDPQCQCHLCHNYVGGYFCSC-CPRGYELQED 185

QY 121 ---YGGDCMRCQVLRAPKQI-LLE---SYPLNAHCWTTHAKPGFVQIRFVNLSEF 173  
 Db 186 RHSCQAE--SSELYTEASGVYSSLEYPSPDLRCNYSIRVERGLTLHLKFLF---PF 240  
 QY 174 P-----YWCQDYVVEVDGDNRGQIIKRVCGNERPAPIQSIGSSLLHVLHSDGSKNFD 227  
 Db 241 DDDHQVHCVPDQIQI-----YANGKNIGFCGKQRPDLDTSSNAVDLFFTDSSGDSR 296  
 QY 228 GFHAIY-BEITACSSSPCFHDGTCVLDKAGSYKACACLAGYTGQRCENLLBERNCSDPGGP 286  
 Db 297 GWKLYTTEIIKCPQPKLDEFTIIONLQPOVQ---PRDYFIATCK----- 339  
 QY 287 VNGYQKITGGPGLINGRAKIGTVVSPFCNNSVYLSGNEKTCQONGSWSGKQPTC-IKA 345  
 Db 340 -GGYQLIEGNQVL-----HSFT-----AVCDDGTWHRAMPRECKIKD 375  
 QY 346 CREPKISDLVRRRLPMQVSRETPLHQLYSAAFSKQLQSAPTKKPALPFGDL-----PM 401  
 Db 376 CQPR-----NLPNGDPYTTM 393  
 QY 402 GYQHLHTQVEICISPFYR---RLGSSRR---TCLRTGKWSG-----RAPSCIPICGK 448  
 Db 394 GVNTYKARIQYYCHEPYKMQTRAGSRESEQGVYTTAAGIWKNEQKGEKIPRCCLPVCGK 453  
 QY 449 IEN-----ITAPKTOGLRPMQAAIYRTSGVHDSGLHKGAWFLVCSGALVNERTVV 500  
 Db 454 PNVPEQRIIGGOKAKGNFPQVQ-----FTNIHG-----GGALLGDRWIL 498  
 QY 501 VAAHCVTDLGKVTMIKTADLKVLGKGYRDDRDEKTIQSLQ-----ISAILHPNY-- 552  
 Db 499 TAAHTLYPKEHAQ-SNASLDVFLG-----HTNVEELMKLGNHPIRRVSVHPDVRQ 548  
 QY 553 -DPILLDDADIAILKLLDKARISTRVQPTCLAAARDLSTSPQESHI-TVAGNNVLAD---- 606  
 Db 549 DESVNFEGDIALLENSVTLGNLLPICLP---DNDFYDLGLMGVYSGFGVMEKIAH 605  
 QY 607 ---VRSFGKNDTLRSVGSVDSLLCEEQEDHGIPVSVTDNNMFCASWEPTASDICT 662  
 Db 606 DLRFVRLP-----VANPQACENMLGRKRMDFSQNMFCAG-HPSLKQDACQ 651  
 QY 663 ABTGGIAAVSPFGRASPRWHLMLGWSYDKTCSHRLSTAFKTLVLPFKMWERNMK 720  
 Db 652 GDSGGVFAVRDPN----TDRVATGIVSGIG--CS-RGYFTYTKVLYNVVDWIKEME 702

RESULT 5  
 A59271  
 Ra-reactive factor (EC 3.4.21.-) 2 precursor - human  
 N;Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)  
 C;Species: Homo sapiens (man)  
 C;Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 16-Jun-2000  
 C;Accession: A59271  
 R;Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaebler, W.J.; Laursen, S.B.; Poulsen, K.;  
 Nature 386, 506-510, 1997  
 A;Title: A second serine protease associated with mannan-binding lectin that activates co  
 A;Reference number: A59271; MUID:97242412; PMID:9087411  
 A;Accession: A59271  
 A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-686 <JEN>  
 A;Cross-references: GB:Y09926; NID:g4007626; PIDN:CAA71059.1; PID:g4007627  
 A;Experimental source: tissue liver  
 A;Note: submitted to GenBank, December 1996  
 C;Genetics:  
 A;Gene: GDB:MASP2  
 A;Cross-references: GDB:6071500  
 A;Map position: lp36.2-lp36.3  
 C;Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement factor H  
 C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine pr  
 F;1-15/Domain: signal sequence #status predicted <SIG>  
 F;16-444, 445-686/Product: Ra-reactive factor 2 #status predicted <MAT>  
 F;19-134/Domain: C1r/C1s repeat homology <C1R1>



F;142-180/Domain: EGF homology <EGF>  
F;184-293/Domain: C1r/C1s repeat homology <C1R2>  
F;300-361/Domain: complement factor H repeat homology <FH1>  
F;366-430/Domain: complement factor H repeat homology <FH2>  
F;445-679/Domain: trypsin homology <TRY>  
F;72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,  
F;158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
F;444-445/Cleavage site: Arg-tle (autolytic) #status predicted  
F;483,532,633/Active site: His, Asp, Ser #status predicted

Query Match 10.2%; Score 400.5; DB 1; Length 686;  
Best Local Similarity 22.7%; Pred. No. 3.4e-19;  
Matches 173; Conservative 78; Mismatches 245; Indels 267; Gaps 34;

QY 128 CGQVLR--APK-----GQILLESYP-----LNACCEWTHAKPGFVIQIRFVMSLEFDY 175  
DB 11 CGSVATPLGPKPEPVFGRGLASPGFPOEYANDQERRWTLTAPPGYRLRLYFTFDFLELSH 70  
QY 176 MCQYDVEVRDGNRDGQIIKRVGNB-----RPAP-----IQSIGSSHLVLFHSDGS--KN 225  
DB 71 LCBYDFVKLSG-----AKVLATLGGQESTDTERAPGKDTFYSLGSSLDITFRSDYSNEKP 126  
QY 226 FDGPHALY--EETACSSP-----CPHDGTCVLDKAGSKYKACACLAGYTCQR-----CENL 274  
DB 127 FTGFEAFYAEADDECOVAGEAPTCDH--CHNLGGFYCSCRAGYVLRNKRKTCAL 183  
QY 275 -----LEE----- 277  
DB 184 CSGQVFTORGELSSPYPRYPKLSCTYSISLEEGFVILDVFESFDVETHPETLCPY 243  
QY 278 -----RNCSDP 283  
DB 244 DFLKIOTDREHGFCKTLPHRIETKSNVTITFTVDESDDHTGKIHNTSTAHCYPY 303  
QY 284 GGPVNGYQKITGGGLNGHAK--ICTVVSFFCNNSY-VLSG-----NEKRTCCQNGEW 335  
DB 304 MAPNGH-----VSPQAKVILKDSIFCETGYELQHLPLKSFVAVCQKDSW 354  
QY 336 SGKQPIC- IKACREPKITSLVRRVRLPMQVQSRETPHLQLYSAAFSKQLQSAPTKKPAL 394  
DB 355 DRPMFACSIVDCGPP--DDLPSGRV-----EYITGP----- 383  
QY 395 PFGDLPNGYQHLTLQLOVEICISPY-RLGSSRRRTCLRTKWSG-----RAPSCIPCCK 448  
DB 384 -----GVTTYKAVIQYCEETFTYMKVNDGKYVCEADGFTWSSKGEKSLPCEPVCG 436  
QY 449 IENITAPKTOGLR-----WPWQAIIYRRRTSGVHDGSLHKGAWFLVCGSGALVNERTVVA 502  
DB 437 SARTTGGRIYGGQAKGDFPWQVLLIGTT-----AAGALLYDNWVLT 481  
QY 503 AHCVTDLGKVTMIKTADLKVLGKPYRDRDRDEKTIQSLQ-----ISAILHPNY-DP 554  
DB 482 AHAYVE-----QKHDASALDIRMG-----TLKRLSPHYTQAWSEAVFIHEGYTHD 526  
QY 555 ILLDADIALKLLDKARISTRVOPICLAASRDLSFSQESHITVAGNVLADVRSPGFKN 614  
DB 527 AGFPNDIALIKLNKNVINSNITPICLRKEAESFMRTDDIGTASGWG-----LQRFGLA 582  
QY 615 DTLRSGVSVVDSLLCBEQHEHGHIP-VSVTDNNMFCASWEPTAPSDICTAETGGIAAVSF 673  
DB 583 RNLWYVDIPVDHQKCTAAAYEKPPYPRGSVTANMLCAGLE-SGGKDCRGDSGG--ALVF 639  
QY 674 PGRASPEPRWHLMLGNSVDKTCSHRLSTAFKVLFPFKWIE 716  
DB 640 --LDSETERFVVGIVSGWGMNCGEAGQYGVYTKVINYIPWIE 680

RESULT 6

S05008  
complement subcomponent C1s (EC 3.4.21.42) precursor [similarity] - golden hamster  
C;Species: Mesocricetus auratus (golden hamster)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 28-Jul-2003  
C;Accession: S05008

R;Kinoshita, H.; Sakiyama, H.; Tokunaga, K.; Imajob-Ohmi, S.; Hamada, Y.; Isono, K.; Saki  
FEBS Lett. 250, 411-415, 1989  
A;Title: Complete primary structure of a calcium-dependent serine proteinase capable of c  
A;Reference number: S05008; MUID:89325606; PMID:2753140  
A;Accession: S05008  
A;Molecule type: mRNA  
A;Residues: 1-695 <KIN>  
A;Cross-references: EMBL:X16160; NID:g49621; PIDN:CAA34286.1; PID:g49622  
A;Note: part of this sequence, including the amino ends of both the heavy and light chain  
C;Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement factor H  
C;Keywords: beta-hydroxyasparagine; calcium binding; duplication; glycoprotein; hydrolase  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;17-133/Domain: C1r/C1s repeat homology <C1R1>  
F;22-444/Product: serine proteinase heavy chain #status experimental <HCH>  
F;141-177/Domain: EGF homology <EGF>  
F;181-293/Domain: C1r/C1s repeat homology <C1R2>  
F;300-360/Domain: complement factor H repeat homology <FH1>  
F;365-428/Domain: complement factor H repeat homology <FH2>  
F;445-682/Domain: trypsin homology <TRY>  
F;446-695/Product: serine proteinase light chain #status experimental <LCH>  
F;71-89,141-153,149-162,164-177,181-208,240-257,300-347,327-360,365-410,392-428,432-556,  
F;155/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
F;180,413/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;482,536,638/Active site: His, Asp, Ser #status predicted

Query Match 9.6%; Score 378.5; DB 1; Length 695;  
Best Local Similarity 21.8%; Pred. No. 1e-17;  
Matches 168; Conservative 81; Mismatches 227; Indels 293; Gaps 35;

QY 137 GQILL-----ESYPLNAHCEWTHAKPGFVIQIRFVMSLEFDYVYVEVRDGNRDG 192  
DB 27 GEILSPNYQAYPNEKMTDIEVPEGFGVRLYFTLHDMELSENCEYDSVQIISGGVEEG 86  
QY 193 QIIKRVCGNERP-----API-----QSIGSSHLVLFHSDGS--KNFDGFHALY-----EET 237  
DB 87 -----RLCGORTSKNANSPIVEEFQIPYNKLVIFRSDFSNEERFTGFAAYAAIDVNECT 142  
QY 238 ACSSSCFHDGTCVLDKAGSKYKACLAGY-----RNCSDP----- 266  
DB 143 DFTDVPSCSHFNFI---GGYFCSPPEYFLHDDMRNCGVNSGNVFTALIGISSPNYP 199  
QY 267 ---TQRCEN--LLEE-----RNCSDP----- 283  
DB 200 NPYENSRCYQILLEGQVWVVIQREDFDVEPADSQNCQDLSLLFAAKNRQGFPPCGN 259  
QY 284 -----GGVNGYQKITGGP----- 297  
DB 260 GPFPLTIETHSNTLDIVFTQDLTEQKQKWLRYHGDPIPCPEKITANSVWAPEKARYVF 319  
QY 298 -----GLINGRAKIGTVVSFFCNNSYVLSGNEKRTCCQNGEWSGK---QPICIKACR 347  
DB 320 KDVWKISCDVGFPAEAVGNVGSTFFYS-----TCQNGQWNSRLRCQPV---DCG 366  
QY 348 EPKISDLVRRVRLPMQVQSRETPHLQLYSAAFSKQLQSAPTKKPALPFGDLPNGYQHLH 407  
DB 367 IPE-----PIQNGKVDDEPNTLFGSV----- 387  
QY 408 TQLOYSICISPY-----RLGSSRRRTCLRTKWSG-----RAPSCIPCCKIENITAPKTQ 458  
DB 388 --IHYSCPEYTYMEHAHGGGYR-CAANGSWYNDLIGLIELPKCVFCG-----VPT 437  
QY 459 GLRWPQAAIYRRTSGVHDGSLHKGAW-----FLVCGSGALVNERTVVAACHVTDLGKVT 513  
DB 438 PFR-----IQKIFGGFPAKIQSPFWQVFFEPFRAGGALIGEHWLTAAHVVEGSDPS 491  
QY 514 M-IKTADLKVLGKPYRDRDRDEKTIQSLQISAILHPNYDP-----ILLDADIALK 565  
DB 492 MYVGSTSVRM-----ENLANVQKLTDRVIIHPGKPGDLSLSTRNFDNDIALVR 541  
QY 566 LLDKARISTRVOPICLAASRDLSFSQESH---ITVAGW-----NVLDVRSPGFKNDT 616  
DB 542 LKDPVWKGPTVSPICLFGT---SSEYSEGDGLISGMGRTERRNIVIQLR----- 590

QY 617 LRSQGVVVDLSL-----LCEQEHEDHGIPSVSTDMNMFASWEPTAPSDICTAETGIAAV 671  
 DB 591 ---GAKLPVTSLEKCRQVKEENPKARADDVFTSNMICAEGKV---DSCQGDGCAFAL 644  
 QY 672 SPGRASPEPRHMLGLVSWSDKTSRHLSTAFYKVLPPKDWIERNMK 720  
 DB 645 PVFN--VRDPKFVYAGLVSWG--KKCG--TYGIYTKVRKNKDWILQTMQ 687

RESULT 7  
 T30337  
 polypeptide - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 03-Feb-2003  
 C:Accession: T30337  
 R:Yang, J.C.; Lindsey, L.L.; Hedrick, J.L.  
 A:Description: cDNA cloning of ovocytinase, a chymotrypsin-like protease released from X.  
 A:Reference number: Z20829  
 A:Accession: T30337  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1524 <YAN>  
 A:Cross-references: EMBL:U81290; NID:G2981640; PID:G2981641; PIDN:AAC24717.1  
 C:Superfamily: tryosin related polypeptide; trypsin homology

Query Match 9.0%; Score 354; DB 2; Length 1524;  
 Best Local Similarity 22.3%; Pred. No. 1.1e-15;  
 Matches 166; Conservative 101; Mismatches 260; Indels 216; Gaps 39;

QY 55 CRGKREVGY-----TIPCRNEECDSCLHPGCTIFENCKSRNGSGTLDFFYK 109  
 DB 214 CHAVLEPIGHVLDLTMCLGAPPEGGMDACQDGGPFV--CRR-RSGVW---FLA 263  
 QY 110 GFVCAB---CRAGW-----YGGDCMRCGGVLRAP 135  
 DB 264 G--CVSMGLGCGRSGWAKQIIRSQSGSPALFRRVSVLDLFRPPKLTGCGSSKGRITGK 321  
 QY 136 KGOI---LLESYPLNACWTHAKPGFVQLRFLVMSLEFDMYQYDVVRDGNRGG 192  
 DB 322 NGTVRYPLSGNYSINVCRWMLAVQAKTIEIRFLQDIEDHATCTFVLSFTVNE--- 377  
 QY 193 QIHKVCGNERPAPIOSIGSLHLVPHSDGSKNPGFHAIEITACSSSPCFHDGTCVL 252  
 DB 378 KMIRKVGSTIPLSLIVRKNVTTFPSDGTGTFGRGFEIQFALPTKASAC--GSAKIL 435  
 QY 253 DKAGSYKACLAGYTGRCENLLEERNCSDP-----GGPVNGYQKITGGPGLIN 301  
 DB 436 KKKG-----MISPNYDPYPRKLTCSMIIEAPENHIVKLKFEDEFNVE 478  
 QY 302 GRHAKIGTVSPFCNNYSYVLSGNEKRTCCQNGEWSGKQPCIKACREPKISDLVRR---R 358  
 DB 479 YGHGCIYDAVE-----VYDGAEEK-----QLIARLCGY 506  
 QY 359 VLPQVQVQSE-----TFLHQLYSAFSAKQLQSAATKPK-ALPFGDLPNGYQHLHQ 409  
 DB 507 TLPLPISSENWMLIRFKTDMENSYG--FKWFSVPVKEKFSPLPDDTPT-ISMHLPR 563  
 QY 410 ---LQYECISPFYRRLGSSRRCLRTGKWSGRAPSCIP-ICGKIENITAPKTQGLRWPMQ 465  
 DB 564 AIALDVCGMAPM-----TPKN-----WLPRIVGEE--ASPNS-----WPMQ 598  
 QY 466 AAI-YRTSGVHDSLHGKAFVLCGALVNRVTVVAAHCVTDLQKVTMTAD---LK 521  
 DB 599 VQIFLRT-----PH-----CEGAIISQWILTAHAC-----IRAAEPSYWT 635  
 QY 522 VVLGKPYRDDR--DSKTIQSLQISAILHPNVDPILLDADIALKLDKARISTRVQPI 579  
 DB 636 VIAG-----DHNRLMNSTQIRNIKIIRHDNYSYNDIALLYLEPDLNDFVRV 691  
 QY 580 CLAAASRLSTSFQESHITVAGNVLADVRSPGKNDLRSVGVVSDLSLCEQEHEDHG 639  
 DB 692 CLPEPEVLV--PASVCVVTGWTAEADGQALGLOQLQ---LPILDSIICNTSYSG-- 744

QY 640 PVSVDNMFCAWBTAPSDICTAETGIAAVSPFGRASPEPRHMLGLVSWSDKTSCH 699  
 DB 745 --ELTDHMLCAGFPSPSKKADACQDGGPLVCQ-----NEKEQFSIYGLVSWG--EGCG- 794  
 QY 700 RLST--AFTKVLPPKDWIERNMK 720  
 DB 795 RVSRPGVYTKVRLFFFTWIONTOQ 817

RESULT 8  
 JC6554  
 Complement subcomponent C1s (EC 3.4.21.42) precursor [similarity] - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 28-Jul-2003  
 C:Accession: JC6554  
 R:Sakai, H.; Nakashima, S.; Yoshimura, S.; Nishimura, Y.; Sakai, N.; Nozawa, Y.  
 A:Title: Molecular cloning of a cDNA encoding a serine protease homologous to complement  
 A:Reference number: JC6554; MUID:98192519; PMID:9524231  
 A:Accession: JC6554  
 A:Molecule type: mRNA  
 A:Residues: 1-694 <SAK>  
 A:Cross-references: DBJ:U88250; NID:G3080541; PIDN:BAA25797.1; PID:G3080542  
 C:Comment: This protein is involved in glial cell differentiation and cartilage remodeling  
 C:Genetics:  
 A:Gene: r-gsp  
 C:Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement factor H  
 C:Keywords: differentiation; glycoprotein; hydrolase; serine proteinase  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:17-133/Domain: C1r/C1s repeat homology <C1R>  
 F:22-694/Product: serine protease homolog #status predicted <MAT>  
 F:141-177/Domain: EGF homology <EGF>  
 F:300-360/Domain: complement factor H repeat homology <FHR>  
 F:444-681/Domain: trypsin homology <TRY>  
 F:180, 412/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:481, 535, 637/Active site: His, Asp, Ser #status predicted

Query Match 8.6%; Score 340.5; DB 2; Length 694;  
 Best Local Similarity 21.2%; Pred. No. 3.6e-15;  
 Matches 167; Conservative 98; Mismatches 244; Indels 277; Gaps 40;

QY 44 ECCEYDQTECVCPGKRE-----VVGVTIPCCR-----NEE--- 73  
 DB 69 ENCAVDSVQIISGLIEERLCQSSKSPNSFTVEFQFPYRLQVQVTSFDSNEERTG 128  
 QY 74 -----NECDCLHPGCTIFENCKSRNGSGTLDFFYKPYCAECRAGWYGG 123  
 DB 129 FAAYSAVDVNECTDFTDVP--CSHF-----CNN-----FTGGYFCS-CPPEYFLH 171  
 QY 124 DCMR-----CGQVLRAPKQIILLES-----YPLNACWTHAKPGFVQLRFLVMSLEP 173  
 DB 172 DDMRTGVCNCGDVFALIGEASPNYPNPENPENSRCYQIRLQEGF--RLVLTIRREDF 229  
 QY 174 DVMQYDVVEVRDGNR-----DQIIRKVCGERPAP--IOSIGSLHLVPHSDG 222  
 DB 230 D-----VEPADSEGNCHDSLTAQKQVQPGYCGNGFGPGLITKTSNTLDIVFQIDL 282  
 QY 223 SKNFDGFHAY-----EETACS-----SPPCFHDGTCVLDKAGSYKACLAGYTG 268  
 DB 283 TGQNGKWLRYHGDPIPCPKSISANSIWEPEKAKYFKD-----VVKITC----- 327  
 QY 269 QRCENLLEERNCSDPGPNVYQKITGGPGLINGEHALGITVVSFFCNSYVLSGNEKRT 328  
 DB 328 -----VDGFEVVEGVNG-----STSPY-----ST 346  
 QY 329 COQNGESGK---OPICIKAREPKISDLVRRRRLVPMQVQSRPTPLHQLYSAFSAKQL 384  
 DB 347 COSNQNSRLQCPV--PCGVPE-----PIENGKVEDPDTVFGSV----- 387  
 QY 385 QAPATKPKALPFGDLPNGYQHLTQLOVEICISPFY--RRLGSSRRRTCLRTGKWSG----- 437  
 DB 388 -----IHYTCBEPYTYMEQEBEGEYHCAANGSVWVDQLGV 422



Qy 267 TQRCENL-----ERNCS-----PGPVNGYQKIT 294  
 Db 198 ENSRCEYQIRLEKGFQVVTLRREDFVEAADSAGNCLDSLVFVAGDRQFGPCGH-----253  
 Qy 295 GGPCLIN-----GRHAK--I 307  
 Db 254 GFGPLNIETKSNALDIIFQDLDGKKGKWLRYHGDPMPCPKEDTNSVWEPAKAYVP 313  
 Qy 308 GTVVSPFCNNY-VLSG-----NEKRTCCQNGWSGK-----QPTICAKREPKISDLVRR 357  
 Db 314 RDVVQITCLDGFVEVEGRVGTSPYSTCQNGKWSNKLKCPV-----DCGIP-----362  
 Qy 358 RVLPMQVQSRTPHLQLYSAFSAFKQKLSAPTKP-ALPFGDLPMGQHLHQLQYECIS 416  
 Db 363 -----ESIENGKVEDPESTLFGSV-----IRYCEE 388  
 Qy 417 PFY--RRLGSSRRRLCTLTKGWSGRA-----PSCPICGKIENITAPKTQGLRWPMQAAIY 469  
 Db 389 PYYMENGSGGEYHCAGNSGVNEVLGPELPKCPVCG-----VP-----REPFEEK--435  
 Qy 470 RRTSGVHDSLHKGAWFLV-----CSGALVNERTVVVAACHVTDLGVTKVTKTADLKVIL 524  
 Db 436 QRIIGSGDADIKNPFQVFFDNPMWAGGALINEYVWLTAAHVVEGNREPTW-----YV 487  
 Qy 525 GKPYRDDDRDEKTIQSLQISAILHPNVDPIIL-----DADIAILKLDKARISTRVQ 577  
 Db 488 GSTSVQTSRLAKS--KMLTPPEHVFTHPGWKULEPEVPEGRNTFNDNLALVRLKDPVPMGPTVS 546  
 Qy 578 PICLAARDLSTSPQESHITVAGNVNLDVRSFGKND-----TLRSGVSVVVDLSLLCEQH 634  
 Db 547 PICLPGTSSDYNLMDGLGLISGW-----RTE--KRDRAVRLKAARLPVAPLRKCKEVK 599  
 Qy 635 EDHGIPVS-----VTNMFCAWNEPTAPSDICTAETGGIAAVSFPGRASPERPHLMGL 688  
 Db 600 VEK--PTADAEAYVFTENMTCAGGE--KGMDSCKGDSGGAFAVQDP---NDKTKFYAAGL 652  
 Qy 689 VSNVSYDKTCSHRLTAFTKVLPPKDWTERNNK 720  
 Db 653 VSWG--PQCG--TYGLTRVKNYVDWIMKTMQ 680  
 RESULT 10  
 A56318  
 A;Description: cleaves activation peptide from trypsinogen to produce active trypsin  
 N;Alternate names: enterokinase  
 C;Species: Homo sapiens (man)  
 C;Date: 19-May-1995 #sequence\_revision 09-Aug-1996 #text\_change 28-Apr-2003  
 C;Accession: A56318; B43090  
 R;Kitamoto, Y.; Veille, R.A.; Donis-Keller, H.; Sadler, J.E.  
 Biochemistry 34, 4562-4568, 1995  
 A;Title: cDNA sequence and chromosomal localization of human enterokinase, the proteolytic  
 A;Reference number: A56318; MUID:95234679; PMID:7718557  
 A;Accession: A56318  
 A;Molecule type: mRNA  
 A;Residues: 1-1019 <KIT>  
 A;Crosso-references: GB:U09860; NID:G746412; PIDN:AAC50138.1; PID:G746413  
 R;Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994  
 A;Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease compo  
 A;Reference number: A43090; MUID:94329561; PMID:8052624  
 A;Accession: B43090  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 749-1019 <KIT>  
 A;Crosso-references: GB:U09860  
 C;Comment: The mechanism of association with the membrane of the intestinal brush border  
 (noted below) or with amino-terminal myristoylation of the heavy chain.  
 C;Genetics:  
 A;Gene: GDB:BRSS7  
 A;Crosso-references: GDB:384083; OMIM:226200  
 A;Map position: 21q21-21q21  
 C;Complex: Mature enteropeptidase is variously reported to contain two (heavy and light)  
 ed by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involv

ducts.  
 C;Function: cleaves activation peptide from trypsinogen to produce active trypsin  
 A;Pathway: intestinal digestive hydrolase cascade  
 C;Superfamily: enteropeptidase; Clr/Cls repeat homology; LDL receptor ligand-binding repe  
 C;Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen  
 F;1-784/Product: enteropeptidase heavy chain #status predicted <HCH>  
 F;22-38/Domain: transmembrane #status predicted <TM>  
 F;184-221/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
 F;342-504/Domain: NAM homology <NAM>  
 F;526-631/Domain: Clr/Cls repeat homology <Clr>  
 F;643-677/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
 F;678-783/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRCF  
 F;785-1015/Product: enteropeptidase light chain #status predicted <LCH>  
 F;785-1015/Domain: trypsin homology <TRY>  
 F;116,147,179,328,388,440,470,503,534,630,682,706,725,848,887,909,949/Binding site: c  
 F;772-896,810-826,910-977,941-956,967-995/Disulfide bonds: #status predicted  
 F;825,876,971/Active site: His, Asp, Ser #status predicted  
 Query Match 8.4%; Score 331.5; DB 1; Length 1019;  
 Best Local Similarity 22.9%; Pred. No. 2.2e-14;  
 Matches 136; Conservative 90; Mismatches 225; Indels 143; Gaps 27;  
 Qy 143 SYPLNAHCWTHAKPGFVIQLRFVMLSLFDFVMCOYDVYVRDGDNRDQIIRKVCNE 202  
 Db 545 SYPLNAFCVWLNNAQKNIQLHF-----QEFLENINDVVEIRDGEADSLAVTG--598  
 Qy 203 RPAPIQISGSLH-----VLPHSDGSKNF-DGFHAIYEEITACSSSPCFHGTCTV 251  
 Db 599 -PGPVKQDFSTTRMTVLLITNDVLARGFGFKANFTTGYHLGIPE-----PC-----643  
 Qy 252 LDKAGSYKC---ACLA-----GYTCQRCENLEERCSDPGPVNGYQKITGGPGLNG 302  
 Db 644 --KADHFQCKNGECVPLVNLCDGHL--HCEBDSDEAD-----VRFNGTNNNGLVRF 693  
 Qy 303 RHAKIGTVVSVFFCNNSYVLSGNEKRTCCQNGEWSGKQPIKACRPKISDLVRRVRLPM 362  
 Db 694 RIQSIW-----HTACAENWTTQISNDVC-----QLLGL 721  
 Qy 363 QVQSRTPHLQLYSAFSAFKQKLSAPTKPAPLPGDLPNGYQHLHQLQYECISPPYRRL 422  
 Db 722 GSGNSSKPIFTDGGPF--VKLNTAPD-----GHLILTPSQCLQDSLRL 765  
 Qy 423 GSSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDSLHK 482  
 Db 766 QCNHKS-----GKCLAAQDITPKI--VGSNAKEGAWPMVVGILY-----YGR--807  
 Qy 483 GAWFLVCSGALVNERTVVVAACHVTDLGVTKVTKTADLKVLGKFYRDDDRDEKTIQSLQ 542  
 Db 808 ----LLCGASLVSSDWLVSAHCV--YGR--NLEPSKWTAILGLHMKSNLSTPQTVPRL-858  
 Qy 543 ISAILHPNVDPIILDADIAILKLDKARISTRVQPICLAASRDLSSTFQESHITVAGWN 602  
 Db 859 IDEIVINPHNRRKNDIAMWHLEPKVNVTDYIQPICLPEENQVPPGR--NCSTAGWG 916  
 Qy 603 VLADVSPGKNDTLASGVSVVVDLSLCESEHEDHGI PVSVTDNMFCAWNEPTAPSDICT 662  
 Db 917 T---VVYQGTANILQEAADVPLLSNERCCQPEY-----NITENMICAGYE-BGGIDSCQ 968  
 Qy 663 AETGGIAAVSFPGRASPERPHLMGLVSVWSYDKTCSHRLSTAFKTLVLPKDWIE 716  
 Db 969 GDSGG-----PLMCQNNRWFLAGVTSFGYKCALPNR-PGVYARVSRFTWFIQ 1015  
 RESULT 11  
 A53663  
 A;Description: enteropeptidase (EC 3.4.21.9) precursor [validated] - pig  
 N;Alternate names: enterokinase  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 07-Oct-1994 #sequence\_revision 09-Aug-1996 #text\_change 28-Apr-2003  
 C;Accession: A53663  
 R;Matsushima, M.; Ichinose, M.; Yahagi, N.; Kakei, N.; Takeda, S.; Miki, K.; Kurokawa, T  
 J. Biol. Chem. 269, 19976-19982, 1994

A/Title: Structural characterization of porcine enteropeptidase.

A/Reference number: A53663; MUID:94327548; PMID:8051081

A/Accession: A53663

A/Molecule type: mRNA

A/Residues: 1-1034 <M>

A/Cross-references: GB:D30799; NID:G505122; PID:BAA06459.1; PID:G505123

A/Note: Parts of this sequence, including the amino ends of three chains isolated from the intestine of the porcine brush border membrane, were used for the structural characterization of the heavy chain.

C/Comment: The mechanism of association with the membrane of the heavy chain (heavy and light) is not clear. Mature enteropeptidase is variously reported to contain two (heavy and light) chains, or a single chain. Possibly, conversion from membrane-bound to soluble forms involves a disulfide bond.

C/Function: cleaves activation peptide from trypsinogen to produce active trypsin

A/Pathway: intestinal digestive hydrolase cascade

C/Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding repeat

C/Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen

F/22-38/Domain: transmembrane #status predicted <TM>

F/52-117/Product: enteropeptidase mini chain #status predicted <MCH>

F/118-799/Product: enteropeptidase heavy chain #status predicted <HCH>

F/199-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F/357-519/Domain: MAM homology <MAM>

F/541-646/Domain: C1r/C1s repeat homology <C1R>

F/658-692/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F/693-798/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRC>

F/800-1034/Product: enteropeptidase light chain #status predicted <LCH>

F/800-1029/Domain: trypsin homology <TRY>

F/116-147/Domain: trypsin homology <TRY>

F/787-911-825-841-925-992-956-971-982-1010/Disulfide bonds: #status predicted

F/840-891-986/Active site: His, Asp, Ser #status predicted

Query Match 8.4%; Score 330.5; DB 1; Length 1034;

Best Local Similarity 22.9%; Pred. No. 2.6e-14;

Matches 137; Conservative 86; Mismatches 224; Indels 151; Gaps 27;

QY 143 SYPLNACEWTIAKPGFVLQIRFVMSLFEDYMCQDYVEVRDGDNRDGOIIRKVCNCE 202

DB 560 NYNQAFVFNWLNKQKKNQLHPE-----EPDENIADVVEIRDEEDSILLAVYTG-- 613

QY 203 RPAPIQSIGSS---LHVLPHSDGS-----KNF-DGFHAIYBEITACSSSPCFHD---- 247

DB 614 -PGVEDVFSTNRMVTLFTNDALTAKGFKANFTTGYHLGPE-----PKEDNFQC 665

QY 248 --GTCVLDKAGSYKACLAGYTGRCENLLEERNCSDFGPGVNGYQKITGGPGLNGRHA 305

DB 666 ENGECVL-----LVNLCDFGSHCKDGSDEAHCVPLNGTANNGLVQPRIQ 711

QY 306 KIGTVVSFFCNNSYVLGSGNEKRTCCQNGSWGSKQPIKACREPKISDLVRRVRLPMQV 365

DB 712 SIW-----HTACAEWTTQTSDVC-----QLLGLGTG 739

QY 366 SRETPLHQLYSAAFSKQKLOSAPTKPALPGDLPMGYQHLHTQLQYECISPFYRRLGSS 425

DB 740 NSSMPFFSSGGPPE--VKLNTAPNGSLILTASE-----QCFEDSLILLQCN 783

QY 426 RRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLR-----WPQAAIYRRSIVHDS 479

DB 784 HKSC--GK-----KQVAQVSPKIVGNDREGAWPWVALY-----YNGQ 822

QY 480 LHKGAWFLVCSGALVNRVTVAACHCVTDLGKVTMIKTADLVKVLGKFYRDDRDDEKTIQ 539

DB 823 -----LLCGASIVSRDLVSAACHV--YGR--NLSPSKWAILG-LHMTSNLTSQIV 870

QY 540 SLQISAILHPNYPDILLADIAIILKLDKARISTRVQPICLAASRDLSFQESHITV 598

DB 871 TRLIDEIVINPHYNNRRKDSIAMMHELFKNVYDYIOPICLPEENQV---FPDGRICSI 927

QY 599 AGNVLADVSPGPNKDTLISGVSVSDSLICEQHEHDHGIPVSVTDNMFECASHEPTAPS 658

DB 928 AGMKVITYQGSPPA---DILEADYPLLISNEKCOQOMPEY-----NITENMMCAQYE-BGGI 979

QY 659 DICTAETGGIAAIVFPGRASPEPRWHLMLGWSYDKTCSHRLSTAPTKVLPFKDWIE 716

DB 980 DSCQDGGG-----FLMCLENRFLLAGVTSFGYQCALPNR-PGVVARVPKFTWFIQ 1030

RESULT 12

JX0210

protein C (activated) (EC 3.4.21.69) precursor - mouse

N/Alternate names: vitamin K-dependent serine proteinase

C/Species: Mus musculus (house mouse)

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000

C/Accession: JX0210

R/Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.

J. Biochem. 111, 491-495, 1992

A/Title: Isolation and characterization of a mouse protein C cDNA.

A/Reference number: JX0210; MUID:92316897; PMID:1618739

A/Accession: JX0210

A/Molecule type: mRNA

A/Residues: 1-461 <TAB>

A/Cross-references: GB:D10445; NID:G220385; PIDN:BAA01235.1; PID:G220386

A/Experimental source: liver

C/Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that reg

S. C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutami

F/1-33/Domain: signal sequence #status predicted <SIG>

F/27-85/Domain: Gla domain homology <GLA>

F/34-41/Domain: propeptide #status predicted <PRO>

F/42-196/Domain: product: protein C #status predicted <PRC>

F/42-196/Domain: light chain #status predicted <PCL>

F/91-130/Domain: EGF homology <EG1>

F/139-174/Domain: EGF homology <EG2>

F/199-461/Domain: heavy chain #status predicted <PCH>

F/199-211/Domain: activation peptide #status predicted <ACT>

F/212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>

F/212-445/Domain: trypsin homology <TRY>

F/47-48-55-57-60-61-66-67-70-76/Modified site: gamma-carboxyglutamic acid (Glu) #status I

F/112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

F/121-130-139-150-146-159-161-174-182-319-338-354-373-387-426/Disulfide bonds: #statu

F/214-290-355/Binding site: carbohydrate (Aen) (covalent) #status predicted

F/253-299-402/Active site: His, Asp, Ser #status predicted

Query Match 8.1%; Score 320; DB 1; Length 461;

Best Local Similarity 23.9%; Pred. No. 5.4e-14;

Matches 145; Conservative 70; Mismatches 174; Indels 218; Gaps 29;

QY 152 WTI-----HAKPGF-----VIQLRFVMSLFEDYMCQDYVEVRDGDNRDGOIIRK 198

DB 14 WGSIIPAHDPDPVFSSESSEHAHQVLRVRRANSFL-----EMRPG-SLERECHEEI 62

QY 199 CGNERPAPI-QSIGSSILHVLPHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGS 257

DB 63 CDFEAAQEIFQVEDTIAFWI-----KYFDGQCSAPPDLHQDCSPCCGHGTCL-DGIGS 116

QY 258 YKACLAGYTGRCENLLEERNCSDFGPGVNGYQKITGGPGL-----INGRHAKIGTVV 311

DB 117 FSCSDKMGWEGKFCQQLRFQDC-----RVNNGGCLHYCLEESNGRCA----- 160

QY 312 SFCNNNSYVLGSGNEK-----TCQNGSWGSKQPIKACREPKISDLVRRVRLPMQV 364

DB 161 ---CAPGYELADHMRCKSTVNPFCGKLGRIEK-----KKIL----- 196

QY 365 QSRETPHLQLYSAAFSKQKLOSAPTKPALPGDLPMGYQHLHTQLQYECISPFYRRLG 424

DB 197 -KDDTDL-----EDELPPD----- 210

QY 425 SRETCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSVHDSGLHKA 484

DB 211 -----RVNGLTLTK-QG-DSPWQAILL-----DSKKK-- 235

QY 485 WFLVCSGALVNRVTVAACHCVTDLGKVTMIKTADLVKVLGKFYRDDRDDEKTIQSIQ 544

DB 236 --LACGVLHTSWVLTAACHVEGTGKLT-----VRLGEY--DLRRRDHWDLDLDIK 283

QY 545 AILHPNYPDILLADIAIILKLDKARISTRVQPICL-----AASRDLSFQESHITVAG 600



Db 284 EILVHPNRYTRSSDNDIALRLAQAATLSKTIPIVCLPNNGLAQOELTQAGQETVVT--G 341  
QY 601 WNVLVADVRSPGKNDTL-----RSGVVSVVDSLLCEQEDHGIPVSVTDNMFC 649  
Db 342 MGVSORIKDGRNRRTFIITRIPLVARNECEVMKNV-----VSENMULC 387  
QY 650 ASWEPTAPSDICTAETGGIAAASVPPGRASPERWHLMLGLVMSYDKTCSHRLSTA-FTKV 708  
Db 388 AGIIGNT-RDACDGSQGPVWFFRG-----TWPLVGLVSG--EGCGHTNNYGIYTKV 438  
QY 709 LPFKDWT 715  
Db 439 GSYLKW 445

RESULT 13  
A43090  
N;Alternate names: enterokinase  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 28-Apr-2003  
C;Accession: A43090; A48874; A61436  
R;Kitamoto, Y.; Yuan, Q.; Wu, Q.; McCourt, D.W.; Sadler, J.E.  
Proc. Natl. Acad. Sci. U.S.A. 91, 7598-7592, 1994  
A;Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease compo  
A;Reference number: A43090; MUID:94329561; PMID:8052624  
A;Accession: A43090  
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1035 <KIT>  
A;Cross-references: GB:U09859; NID:G746410; PIDN:ABA40026.1; PID:G746411  
A;Experimental source: small intestine  
R;Lavallio, E.R.; Rehentulla, A.; Racie, L.A.; DiBlasio, E.A.; Ferenz, C.; Grant, K.L.;  
J. Biol. Chem. 268, 23311-23317, 1993  
A;Title: Cloning and functional expression of a cDNA encoding the catalytic subunit of b  
A;Reference number: A48874; MUID:94043122; PMID:8226855  
A;Accession: A48874  
A;Molecule type: mRNA  
A;Residues: 801-1035 <LAV>  
A;Cross-references: GB:L19663; NID:G416131; PIDN:AAA16035.1; PID:G416132  
A;Note: parts of this sequence, including the amino end of the mature protein, were conf  
R;Light, A.; Janaka, H.  
J. Protein Chem. 10, 475-480, 1991  
A;Title: The amino-terminal sequence of the catalytic subunit of bovine enterokinase.  
A;Reference number: A61436; MUID:92189715; PMID:1799406  
A;Accession: A61436  
A;Molecule type: protein  
A;Residues: 801-807, 'Y', 809-827 <LIG>  
C;Comment: The mechanism of association with the membrane of the intestinal brush border  
embrane attachment using a signal-anchor sequence.  
C;Comment: Conversion from membrane-bound to soluble forms may involve further processin  
C;Complex: mature enteropeptidase is variously reported to contain two (heavy and light)  
lflde linked  
C;Function:  
A;Description: cleaves propeptide from trypsinogen to produce active trypsin  
A;Pathway: intestinal digestive hydrolase cascade  
C;Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding ref  
C;Keywords: glycoprotein; hydrolase; intestine; serine proteinase; transmembrane protein  
F;22-38/Domain: transmembrane #status predicted <TMM>  
F;52-117/Product: enteropeptidase mini chain #status predicted <MCH>  
F;118-800/Product: enteropeptidase heavy chain #status predicted <HCH>  
F;199-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
F;358-520/Domain: MAM homology <MAM>  
F;542-647/Domain: C1r/C1s repeat homology <C1r>  
F;659-693/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
F;694-799/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRC  
F;801-1035/Product: enteropeptidase light chain #status predicted <LCH>  
F;801-1030/Domain: trypsin homology <TRY>  
F;116-147, 170, 194, 233, 263, 264, 404, 456, 486, 519, 550, 646, 698, 722, 741, 762, 864, 903, 965/Bindin  
F;788-912, 826-842, 926-993, 957-972, 983-1011/Diulfide bonds: #status predicted  
F;841.892.987/Active site: His, Asp, Ser #status predicted

Query Match 8.0%; Score 317.5; DB 1; Length 1035;

Best Local Similarity 24.6%; Pred. No. 1.9e-13;  
Matches 146; Conservative 80; Mismatches 225; Indels 143; Gaps 30;

QY 143 SYPLNAHCETIHAHKGPFVIOQLRFVMLSLEFDYMCQDYVVRDGDNRDGOIIRKVCNE 202  
Db 561 SYPNOAFICIMLNIAQKQKNIQLHF-----QEPDENIADVIRDEGDDSLFLAYTGG-- 614  
QY 203 RPAPIQSIGSS---LHLVLFHSDGSKNFDGFHAIYEEITACS--SSPCFHDG--TCVLDKAGS 257  
Db 615 -PGPVNDVFSTTRMTVLFTIDNMLAKQGFKANFTTGYGLGIPKPECKEDNFQC---KDG- 669  
QY 258 YKACLAGYTGORCENLEERNCSDPGGPVNGYQKITGGPGLINGRHAHAKITGVVSFFCNN 317  
Db 670 -ECIPLVNL-----CDGPFHCKDGSDEAHCVRLEFNGTTDSSGLVQFRIOSIWHV----- 717  
QY 318 SYVLSGNEKRTCCQNGEWSGKQPIKICAKREPDKISDLVRRRVLPQVQVSRETPLHQLYSA 377  
Db 718 -----ACAEN--WT-----TQISDDVCQLL----- 735  
QY 378 AFSKOKLOSAPTCKPALPFGDLPMGYQHLHTQLQVEICISPFYRRLGSSRRRTCLRTGKWSG 437  
Db 736 -----GLGTGSSSVTFTSTGGGP--YVNLNT-----APNGSLILTPSQOCL- 775  
QY 438 RAPSCIP- ----CGK--IENITAPKTQG-----LRWPOAAIYRRTSGVHDSLHKG 483  
Db 776 --DSLILQCNVSKCGKKLVQEVSPKIVGSDSREGAWPVVADY-----FDDQ----- 823  
QY 484 AFWLVCSGALVNERTVVVAACHCVTDLGGKVTMIKTADLVKLVGKGYRDDRDEKTIQSLQI 543  
Db 824 ---QVCGASLVSRDLVSAACHV--YGR--NWEPSEKMAVLG-LHMASNLITSPQIETRLI 875  
QY 544 SAILIHPNDPILDDADIAILKLDKARISTRVQPICLAASRDLSFQESH--TVAGWN 602  
Db 876 DQIVINPHYNKRNKNDLMMHLEMKVNTYDIQICLPEENQV---FPPGRCISAGNG 932  
QY 603 VLADVRSFGKNDTLRSVGVSVDLSLCEQEDHGIPVSVTDNMFCASWEPTAFSDICT 662  
Db 933 ALI-----YOGSTADVLQEADVPLLSNEKCCQMPET-----NITENMVCAGYE-AGGVDSQ 984  
QY 663 AETGGIAAVSPFGRASPERWHLMLGLVMSYDKTCSHRLSTAFTKVLPPFKOWIE 716  
Db 985 GDSGG-----PLMCQENNRLLAGVTSFGYQCALPNR-PGVYARVPRTTEWQ 1031

RESULT 14  
EXCH  
coagulation factor Xa (EC 3.4.21.6) precursor - chicken  
N;Alternate names: virus-activating proteinase  
C;Species: Gallus gallus (chicken)  
C;Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text\_change 16-Jul-1999  
C;Accession: S15838; S20380; S20381  
R;Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Nag  
FEBS Lett. 283, 281-285, 1991  
A;Title: Primary structure of the virus activating protease from chick embryo. Its ident  
A;Reference number: S15838; MUID:91257322; PMID:2044767  
A;Accession: S15838  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-475 <SUZ>  
A;Cross-references: DBJ:ID00844; NID:G222869; PIDN:BA00724.1; PID:G222870  
R;Gotoh, B.; Yamauchi, F.; Ogasawara, T.; Nagai, Y.  
FEBS Lett. 296, 274-278, 1992  
A;Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsabl  
A;Reference number: S20380; MUID:92164779; PMID:1537403  
A;Accession: S20380  
A;Molecule type: protein  
A;Residues: 41-55 <GO2>  
A;Accession: S20381  
A;Molecule type: protein  
A;Residues: 241-246, 'X', 248-251, 'X', 253-261 <GOT>  
C;Function:  
A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pre  
A;Pathway: blood coagulation

A:Accession: J07731  
A:Molecule type: mRNA  
A:Residues: 1-855 <KIS>  
A:Cross-references: DDBJ:AB049189  
A:Experimental source: strain Male, 7-week-old  
R:Satomi, S.; Yamasaki, Y.; Tezuka, S.; Hitomi, Y.; Iwanaga, T.; Fushiki, T.  
Biochem. Biophys. Res. Commun. 287, 995-1002, 2001  
A>Title: A role for membrane-type serine protease (MT-SPI) in intestinal epithelial turn-over of specific proteins or peptides on the brushborder membranes. It also participates in lateral migration and/or cell loss.  
A:Reference number: J07775; PMID:1157363  
A:Contents: Small intestine  
C:Genetics:  
A:Gene: mt-spi  
A:Map position: basolateral cell surface  
C:Superfamily: membrane-bound arginine-specific serine proteinase  
C:Keywords: protein digestion

Query Match      7.9%; Score 313; DB 2; Length 855;  
Best Local Similarity    21.4%; Pred. No. 3.1e-13;  
Matches 151; Conservative 76; Mismatches 227; Indels 250; Gaps 33;

QY                 82 HPG--CTIPENCKSRNGSGTLLDPFVKGFGYCAECRAGWVGDCMCGQLRAPKGQI 139  
                 ||||| : | : | : | : | : | : | : | :  
Db                 324 HPGEATPFPLPM-----SSCGLLSE---AQTFSSP-----YYPG----- 358  
  
QY                 140 LLESYLNAHCEWTIHAKPGFVIQLRFVLMSLEFDYM----COYDYVEVRDGNRDGOII 195  
                 ||||| : | : | : | : | : | : | : | :  
Db                 359 ---HYPPNINCTWNIKVPNNRNKVFKLFYLDPNIPGVGSCTKYDYEING----- 406  
  
QY                 196 KRVCGNERPAPIOSSLHVLFHSCKSPDGPHAYEEITACSSSPC-----PHDGTTC 250  
                 ::::| : | : | : | : | : | : | : | :  
Db                 407 EKFCGERSQPVVVSNNSKIIVFHSHDSHTDTGFLAEY--LSYSDNDPCPGFMCKTGRC 464  
  
QY                 251 VL-----DRAGSKYKCACLGY---TGORCNELL-----BERNGS 281  
                 : | : | : | : | : | : | : | :  
Db                 465 IRKDRLCDGWADCPDYSDERHCRCNATHFWCKNQFCFLFWCVDSVND CGDGSDEEGCS 524  
  
QY                 282 DPGGPNGYQKITGGPGLINGRIHAKIGTVVSFFCNSVYL-----SGNEKRTCQQNGEWSG 337  
                 ||||| : | : | : | : | : | : | : | :  
Db                 525 CPAG-----SFKCSNGKCLPQSQCNCNKDKDCGDGSDAS 558  
  
QY                 338 KPICITIKACREPKISDLVRRRLVMQSVRETPLHLYSAAFSKQKLOSAPTKKPALPG 397  
                 : | : | : | : | : | : | : | :  
Db                 559 CDNVAVSC-----PEK----- 567  
  
QY                 398 DLPMGYQHLTQLQEYCISPFRRLGSSRRFTCLRTKWGSRAPSCIPC GKIENTAPT KT 457  
                 : | : | : | : | : | : | : | :  
Db                 568 -----TKTYRC-----QNGLCLKNGN-----PEC---DGKDKCSDGDB 599  
  
QY                 458 Q-----GLR-----HPQAARIYRTSGVDHDSLHGAWFLVC SGALVN 495  
                 : |||| : | : | : | : | : | : | : | :  
Db                 600 KNDCGLRSFTKOARVVGGVGNADGEPWPQWSLHALQG-----H-----LC GAS LIS 647  
  
QY                 496 ERTVVAAHCVTDLGKVTMIKTAD---LKVVLGKFYRDDREKTIQSIQISAILLHPNY 552  
                 : | : | : | : | : | : | : | :  
Db                 648 PDWLVSAAHCFQD---ETIFKYS DHTWWTA FLG-LLDQSKRSASGVQE HKLR II THPSF 703  
  
QY                 553 DPILLADIAILKLDKVARISTRVQPICLAASRLDSTFQESHITVAGNNVADV RSPGF 612  
                 ||||| : | : | : | : | : | : | : | :  
Db                 704 NDFTFDYDIALLLEKPAYS TVVRPICLPDNTHVFVPAGKA--IWVTGH---GHTKEGGT 758  
  
QY                 613 KNDTLRSGVVVSDSLCEEHQEDHGPVSVTDNMFCASWBPTAPS DIC TAETGG -IAAV 671  
                 : | : | : | : | : | : | : | :  
Db                 759 GAILIQGETRVINQTTCHEL-----LPQOI TP RMVC VGF -LSGGVDS CQGS GG P LSSV 812  
  
QY                 672 SFPCRASP EPRHLMGI V SVSYDKTSCHRLST-AFTKVL PF KWIE 716  
                 ||||| : | : | : | : | : | : | : | :



Db 813 EKDRI-----EQAGVWSWG--EGCAQRNKPQYTRIPEVRDIX 850

Search completed: August 18, 2004, 16:25:30  
Job time : 26 00cs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: August 18, 2004, 16:14:22 ; Search time 20 seconds  
(without alignments)  
1858.535 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945

Sequence: 1 MELGCWTQLGLTFLQLLLIS.....LSTAFKVLFPKDWIERNMK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 700 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/2/iaa/5A COMB.pap.\*

2: /cgn2\_6/ptodata/2/iaa/5B COMB.pap.\*

3: /cgn2\_6/ptodata/2/iaa/6A COMB.pap.\*

4: /cgn2\_6/ptodata/2/iaa/6B COMB.pap.\*

5: /cgn2\_6/ptodata/2/iaa/PCTUS COMB.pap.\*

6: /cgn2\_6/ptodata/2/iaa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	665	16.9	1019	1	US-08-296-014A-4
2	665	16.9	1019	2	US-08-596-405-4
3	665	16.9	1019	2	US-08-877-820-4
4	665	16.9	1019	4	US-09-287-368-4
5	665	16.9	1083	1	US-08-296-014A-2
6	665	16.9	1083	2	US-08-596-405-2
7	665	16.9	1083	2	US-08-877-820-2
8	665	16.9	1083	4	US-09-287-368-2
9	327	8.3	855	2	US-09-087-337-2
10	327	8.3	855	4	US-09-644-600-2
11	327	8.3	855	4	US-09-654-600A-2
12	321	8.1	460	6	5270178-16
13	317.5	8.0	798	1	US-08-200-900A-2
14	317.5	8.0	798	5	PCT-US94-00616-2
15	311.5	7.9	461	6	5460953-3
16	310.5	7.9	409	3	US-09-065-872-2
17	310.5	7.9	409	4	US-09-667-570A-2
18	310.5	7.9	410	3	US-09-065-872-1
19	310.5	7.9	410	4	US-09-667-570A-1
20	310.5	7.9	419	1	US-08-295-411-1
21	310.5	7.9	419	2	US-08-955-471-1
22	310.5	7.9	419	4	US-09-667-570A-3
23	310.5	7.9	419	4	US-10-182-263-1
24	310.5	7.9	419	5	PCT-US92-10242-1
25	310.5	7.9	460	2	US-08-756-506-2
26	310.5	7.9	460	2	US-08-756-506-4
27	310.5	7.9	461	4	US-10-182-263-2

28	310.5	7.9	461	6	5225537-2	Patent No. 5225537
29	310	7.9	419	4	US-10-182-263-6	Sequence 6, Appl
30	309	7.8	419	4	US-10-182-263-3	Sequence 3, Appl
31	309	7.8	419	4	US-10-182-263-5	Sequence 5, Appl
32	309	7.8	461	6	5270178-2	Patent No. 5270178
33	308	7.8	419	4	US-10-182-263-4	Sequence 4, Appl
34	307	7.8	460	6	5270178-15	Patent No. 5270178
35	305	7.7	460	6	5270178-13	Patent No. 5270178
36	305	7.7	461	6	5270178-14	Patent No. 5270178
37	302.5	7.7	461	6	5270178-17	Patent No. 5270178
38	302.5	7.7	461	6	5270178-18	Patent No. 5270178
39	288.5	7.3	902	4	US-09-644-600-10	Sequence 10, Appl
40	288.5	7.3	902	4	US-09-654-600A-10	Sequence 10, Appl
41	282	7.1	527	6	5520913-1	Sequence 53, Appl
42	281	7.1	487	1	US-08-469-486-53	Sequence 53, Appl
43	281	7.1	487	2	US-08-469-658-53	Sequence 53, Appl
44	281	7.1	488	4	US-09-367-777-44	Sequence 44, Appl
45	281	7.1	488	4	US-09-367-791A-27	Sequence 27, Appl
46	281	7.1	492	1	US-08-469-486-2	Sequence 2, Appl
47	281	7.1	492	2	US-08-469-658-2	Sequence 2, Appl
48	280	7.1	527	1	US-07-609-510B-16	Sequence 16, Appl
49	280	7.1	527	2	US-08-811-949-39	Sequence 39, Appl
50	280	7.1	527	5	PCT-US91-01025A-2	Sequence 2, Appl
51	280	7.1	527	6	5185259-8	Patent No. 5185259
52	280	7.1	562	2	US-08-811-949-43	Sequence 43, Appl
53	280	7.1	562	2	US-08-560-098A-50	Sequence 50, Appl
54	280	7.1	562	2	US-08-883-795A-38	Sequence 38, Appl
55	280	7.1	562	4	US-09-703-695A-4	Sequence 4, Appl
56	280	7.1	562	6	5185259-3	Patent No. 5185259
57	280	7.1	562	6	5200340-2	Patent No. 5200340
58	280	7.1	562	6	5344773-2	Patent No. 5344773
59	278.5	7.1	466	1	US-07-882-202A-4	Sequence 4, Appl
60	278.5	7.1	466	1	US-08-021-615A-4	Sequence 4, Appl
61	278.5	7.1	466	1	US-08-321-777-4	Sequence 4, Appl
62	278.5	7.1	466	3	US-09-009-217-14	Sequence 14, Appl
63	278.5	7.1	466	3	US-09-009-656-14	Sequence 14, Appl
64	278.5	7.1	466	5	PCT-US93-04493-4	Sequence 4, Appl
65	278	7.0	448	5	PCT-US92-10068-1	Sequence 1, Appl
66	276.5	7.0	655	1	US-08-148-910-12	Sequence 12, Appl
67	276.5	7.0	655	1	US-08-448-937A-12	Sequence 12, Appl
68	276	7.0	448	1	US-08-295-411-3	Sequence 3, Appl
69	276	7.0	448	2	US-08-955-471-3	Sequence 3, Appl
70	276	7.0	448	5	PCT-US92-10242-3	Sequence 3, Appl
71	275.5	7.0	406	1	US-08-295-411-5	Sequence 5, Appl
72	275.5	7.0	406	5	PCT-US92-10242-5	Sequence 5, Appl
73	275.5	7.0	406	5	PCT-US92-10242-5	Sequence 5, Appl
74	275.5	7.0	444	1	US-08-475-845-2	Sequence 2, Appl
75	275.5	7.0	444	2	US-08-327-690-2	Sequence 2, Appl
76	275.5	7.0	444	2	US-08-660-289-2	Sequence 2, Appl
77	275.5	7.0	444	2	US-08-537-807-2	Sequence 2, Appl
78	275.5	7.0	444	2	US-08-871-003-2	Sequence 2, Appl
79	275.5	7.0	444	3	US-08-464-233-2	Sequence 2, Appl
80	275.5	7.0	444	3	US-09-189-607-2	Sequence 2, Appl
81	275.5	7.0	444	3	US-09-378-907-2	Sequence 2, Appl
82	275.5	7.0	444	5	PCT-US94-05779-2	Sequence 2, Appl
83	275	7.0	562	6	5244676-5	Patent No. 5244676
84	272	6.9	488	1	US-08-487-037-1	Sequence 1, Appl
85	271.5	6.9	244	1	US-08-361-395-1	Sequence 1, Appl
86	270.5	6.9	415	1	US-08-295-411-2	Sequence 2, Appl
87	270.5	6.9	415	1	US-08-955-471-2	Sequence 2, Appl
88	270.5	6.9	415	5	PCT-US92-10242-2	Sequence 2, Appl
89	268.5	6.8	406	1	US-08-293-778-24	Sequence 24, Appl
90	264.5	6.7	415	1	US-08-073-531B-1	Sequence 1, Appl
91	264.5	6.7	415	2	US-08-766-288-1	Sequence 1, Appl
92	263	6.7	431	4	US-09-101-272G-1	Sequence 1, Appl
93	263	6.7	431	6	5188829-1	Patent No. 5188829
94	262.5	6.7	461	3	US-08-742-877-2	Sequence 2, Appl
95	262.5	6.7	461	4	US-09-053-871A-21	Sequence 21, Appl
96	262.5	6.7	461	4	US-10-133-907-5	Sequence 5, Appl
97	262.5	6.7	461	6	5521070-2	Patent No. 5521070
98	261.5	6.6	415	4	US-09-118-748-2	Sequence 2, Appl
99	260.5	6.6	437	1	US-08-487-037-2	Sequence 2, Appl
100	260	6.6	477	2	US-08-560-098A-51	Sequence 51, Appl

101	258.5	6.6	411	1	US-08-087-163-1	Sequence 1, Appl	174	238.5	6.0	437	2	US-08-811-949-57	Sequence 57, Appl
102	258.5	6.6	411	1	US-08-286-748B-18	Sequence 18, Appl	175	238	6.0	237	3	US-08-163-919A-3	Sequence 3, Appl
103	258.5	6.6	411	1	US-08-153-799-18	Sequence 18, Appl	176	238	6.0	237	5	PCT-US94-14073-3	Sequence 3, Appl
104	258.5	6.6	411	3	US-09-181-816-1	Sequence 1, Appl	177	236.5	6.0	274	2	US-08-978-404B-5	Sequence 5, Appl
105	257.5	6.5	430	6	5219569-2	Patent No. 5219569	178	236.5	6.0	355	1	US-08-137-116-1	Sequence 1, Appl
106	256.5	6.5	411	4	US-09-403-736-2	Sequence 2, Appl	179	236.5	6.0	355	1	US-08-217-618-1	Sequence 1, Appl
107	256.5	6.5	430	1	US-07-942-157A-3	Sequence 3, Appl	180	236.5	6.0	355	1	US-08-427-640-2	Sequence 2, Appl
108	255.5	6.5	434	4	US-09-618-259-11	Sequence 11, Appl	181	236.5	6.0	355	1	US-08-427-640-6	Sequence 6, Appl
109	254.5	6.5	437	1	US-08-487-037-3	Sequence 3, Appl	182	236.5	6.0	355	1	US-08-217-617A-1	Sequence 1, Appl
110	254	6.4	261	6	5270178-21	Patent No. 5270178	183	236.5	6.0	355	1	US-08-217-616-1	Sequence 1, Appl
111	251	6.4	261	6	5270178-5	Patent No. 5270178	184	236.5	6.0	355	2	US-08-811-949-45	Sequence 45, Appl
112	250.5	6.3	229	2	US-08-557-146-13	Sequence 13, Appl	185	236.5	6.0	355	2	US-08-811-949-47	Sequence 47, Appl
113	250.5	6.3	229	2	US-09-154-344-13	Sequence 13, Appl	186	236.5	6.0	355	3	US-08-794-528-1	Sequence 1, Appl
114	250.5	6.3	411	2	US-08-560-098A-48	Sequence 48, Appl	187	236.5	6.0	355	6	5223256-1	Patent No. 5223256
115	249.5	6.3	986	4	US-09-285-385C-19	Sequence 19, Appl	188	236.5	6.0	356	1	US-08-437-640-4	Sequence 4, Appl
116	249	6.3	251	3	US-08-944-483-47	Sequence 47, Appl	189	236.5	6.0	378	4	US-09-553-498-10	Sequence 10, Appl
117	248.5	6.3	250	3	US-08-944-483-51	Sequence 51, Appl	190	236.5	6.0	378	4	US-09-618-869-10	Sequence 63, Appl
118	248.5	6.3	261	6	5270178-19	Patent No. 5270178	191	236.5	6.0	472	2	US-08-811-949-63	Sequence 19, Appl
119	248.5	6.3	261	6	5270178-20	Patent No. 5270178	192	236.5	6.0	871	3	US-08-245-041-19	Sequence 3, Appl
120	248.5	6.3	262	1	US-07-720-189-1	Sequence 1, Appl	193	236.5	6.0	1013	2	US-08-866-650-3	Sequence 3, Appl
121	248	6.3	230	3	US-08-944-483-62	Sequence 62, Appl	194	236.5	6.0	1013	2	US-09-021-287-3	Sequence 3, Appl
122	248	6.3	231	2	US-09-027-337-6	Sequence 6, Appl	195	236.5	6.0	1013	3	US-09-240-473-3	Sequence 3, Appl
123	248	6.3	231	4	US-09-644-600-6	Sequence 6, Appl	196	236.5	6.0	1350	3	US-09-245-041-17	Sequence 17, Appl
124	248	6.3	231	4	US-09-654-600A-6	Sequence 6, Appl	197	236	6.0	355	2	US-08-811-949-53	Sequence 53, Appl
125	247	6.3	764	2	US-08-177-109A-2	Sequence 2, Appl	198	235	6.0	355	2	US-08-811-949-59	Sequence 59, Appl
126	246.5	6.2	764	2	US-08-687-706-2	Sequence 2, Appl	199	235	6.0	270	2	US-08-978-404B-8	Sequence 8, Appl
127	246.5	6.2	259	3	US-08-944-483-52	Sequence 52, Appl	200	233.5	5.9	252	3	US-08-944-483-72	Sequence 72, Appl
128	246.5	6.2	295	3	US-08-338-368-2	Sequence 2, Appl	201	233.5	5.9	253	2	US-09-027-337-8	Sequence 8, Appl
129	246.5	6.2	376	2	US-08-558-269-10	Sequence 10, Appl	202	233.5	5.9	253	4	US-09-644-600-8	Sequence 8, Appl
130	246.5	6.2	376	3	US-09-410-882-10	Sequence 10, Appl	203	233.5	5.9	253	4	US-08-654-600A-8	Sequence 8, Appl
131	246.5	6.2	579	1	US-08-295-411-4	Sequence 4, Appl	204	233.5	5.9	383	2	US-08-558-269-6	Sequence 6, Appl
132	246.5	6.2	579	2	US-08-955-471-4	Sequence 4, Appl	205	233.5	5.9	383	2	US-09-410-882-6	Sequence 6, Appl
133	246.5	6.2	579	3	US-09-117-708-14	Sequence 14, Appl	206	233.5	5.9	546	6	5200340-6	Patent No. 5200340
134	246.5	6.2	579	5	PCT-US92-10242-4	Sequence 4, Appl	207	232.5	5.9	1013	2	US-08-866-650-5	Sequence 5, Appl
135	246.5	6.2	615	1	US-07-998-972A-3	Sequence 3, Appl	208	232.5	5.9	1013	2	US-09-021-287-5	Sequence 5, Appl
136	246.5	6.2	615	1	US-08-462-261-3	Sequence 3, Appl	209	232.5	5.9	1013	3	US-08-991-408-2	Sequence 2, Appl
137	246.5	6.2	615	1	US-08-462-261-3	Sequence 3, Appl	210	232.5	5.9	1013	3	US-08-991-408-2	Sequence 2, Appl
138	246.5	6.2	615	5	PCT-US92-11357-3	Sequence 3, Appl	211	233.5	5.9	1013	4	US-09-412-473-5	Sequence 2, Appl
139	246.5	6.2	622	3	US-08-952-967-8	Sequence 8, Appl	212	232.5	5.9	1013	4	US-09-285-385C-20	Sequence 20, Appl
140	246	6.2	812	4	US-08-991-761A-7	Sequence 7, Appl	213	232	5.9	638	2	US-08-681-151-3	Sequence 3, Appl
141	245	6.2	228	1	US-08-278-091-10	Sequence 10, Appl	214	231.5	5.9	389	2	US-08-811-949-65	Sequence 65, Appl
142	245	6.2	228	1	US-08-483-859-10	Sequence 10, Appl	215	231.5	5.9	417	4	US-08-820-002-4	Sequence 4, Appl
143	245	6.2	228	2	US-08-472-173-10	Sequence 10, Appl	216	231	5.9	365	1	US-08-093-741-83	Sequence 83, Appl
144	245	6.2	228	2	US-08-487-167-10	Sequence 10, Appl	217	231	5.9	365	1	US-08-720-012-83	Sequence 83, Appl
145	245	6.2	228	2	US-08-482-816-10	Sequence 10, Appl	218	231	5.9	393	2	US-08-560-098A-44	Sequence 44, Appl
146	245	6.2	228	2	US-08-296-149-10	Sequence 10, Appl	219	231	5.9	393	3	US-08-967-024C-24	Sequence 24, Appl
147	245	6.2	228	2	US-08-801-499-10	Sequence 10, Appl	220	231	5.9	393	3	US-08-967-024C-25	Sequence 25, Appl
148	245	6.2	228	2	US-08-615-271-10	Sequence 10, Appl	221	231	5.9	1012	4	US-09-285-385C-4	Sequence 4, Appl
149	245	6.2	228	3	US-09-074-660-10	Sequence 10, Appl	222	230.5	5.8	302	3	US-09-220-731-26	Sequence 26, Appl
150	245	6.2	228	3	US-09-074-659-10	Sequence 10, Appl	223	230.5	5.8	302	4	US-09-242-999-22	Sequence 22, Appl
151	245	6.2	228	3	US-09-106-468-10	Sequence 10, Appl	224	230	5.8	248	3	US-08-944-483-63	Sequence 63, Appl
152	245	6.2	228	3	US-09-106-466A-10	Sequence 10, Appl	225	230	5.8	387	3	US-09-032-215-8	Sequence 8, Appl
153	245	6.2	228	3	US-09-106-467-10	Sequence 10, Appl	226	230	5.8	387	3	US-09-032-215-13	Sequence 13, Appl
154	244.5	6.2	269	4	US-09-715-99A-2	Sequence 2, Appl	227	229	5.8	242	3	US-09-004-731-36	Sequence 36, Appl
155	242.5	6.1	416	2	US-09-000-846-2	Sequence 2, Appl	228	229	5.8	242	3	US-08-749-699-36	Sequence 36, Appl
156	242	6.1	730	3	US-08-872-757-2	Sequence 2, Appl	229	229	5.8	242	4	US-09-004-729-36	Sequence 36, Appl
157	242	6.1	730	3	US-08-872-757-2	Sequence 2, Appl	230	229	5.8	400	3	US-09-004-731-30	Sequence 30, Appl
158	241.5	6.1	347	4	US-09-850-048A-2	Sequence 2, Appl	231	229	5.8	400	3	US-09-004-731-33	Sequence 33, Appl
159	241.5	6.1	788	1	US-08-811-949-1	Sequence 1, Appl	232	229	5.8	400	3	US-08-749-699-30	Sequence 30, Appl
160	241	6.1	354	2	US-08-572-225-1	Sequence 1, Appl	233	229	5.8	400	3	US-08-749-699-33	Sequence 33, Appl
161	241	6.1	986	3	US-08-811-949-61	Sequence 61, Appl	234	229	5.8	400	4	US-08-004-729-30	Sequence 30, Appl
162	241	6.1	986	3	US-08-872-757-4	Sequence 4, Appl	235	229	5.8	400	4	US-09-004-729-33	Sequence 33, Appl
163	240.5	6.1	986	4	US-09-850-048A-4	Sequence 4, Appl	236	228.5	5.8	235	3	US-08-807-151-3	Sequence 3, Appl
164	240.5	6.1	3571	1	US-08-427-640-8	Sequence 8, Appl	237	228.5	5.8	235	4	US-09-478-957-3	Sequence 3, Appl
165	240.5	6.1	432	2	US-09-911-842A-2	Sequence 2, Appl	238	228	5.8	591	3	US-08-991-408-4	Sequence 4, Appl
166	239.5	6.1	1015	4	US-08-560-098A-47	Sequence 47, Appl	239	228	5.8	591	4	US-09-432-473-4	Sequence 4, Appl
167	239.5	6.1	3594	4	US-09-285-385C-2	Sequence 2, Appl	240	228	5.8	809	4	US-08-991-761A-9	Sequence 9, Appl
168	239	6.1	230	4	US-09-911-842A-4	Sequence 4, Appl	241	228	5.8	812	1	US-08-248-629A-1	Sequence 1, Appl
169	239	6.1	356	2	US-09-601-318-3	Sequence 3, Appl	242	228	5.8	812	1	US-08-451-932-1	Sequence 1, Appl
170	239	6.1	389	2	US-08-681-151-1	Sequence 1, Appl	243	228	5.8	812	1	US-08-452-260-1	Sequence 1, Appl
171	238.5	6.0	437	2	US-08-811-949-67	Sequence 67, Appl	244	228	5.8	812	2	US-08-326-785-1	Sequence 1, Appl
172	238.5	6.0	437	2	US-08-811-949-51	Sequence 51, Appl	245	228	5.8	812	2	US-08-612-788-1	Sequence 1, Appl
173	238.5	6.0	437	2	US-08-811-949-55	Sequence 55, Appl	246	228	5.8	812	2	US-08-605-598B-1	Sequence 1, Appl

247	228	5.8	812	2	US-08-429-743-1	Sequence 1, Appli	320	215	5.4	791	4	US-08-991-761A-6	Sequence 6, Appli
248	228	5.8	812	2	US-08-866-735-1	Sequence 1, Appli	321	215	5.4	810	1	US-07-854-603-2	Sequence 2, Appli
249	228	5.8	812	3	US-09-066-028-1	Sequence 1, Appli	322	215	5.4	810	1	US-08-147-008B-29	Sequence 23, Appli
250	228	5.8	812	4	US-09-192-012-3	Sequence 3, Appli	323	215	5.4	810	3	US-09-086-514-1	Sequence 1, Appli
251	228	5.8	812	4	US-09-335-325-1	Sequence 1, Appli	324	215	5.4	810	4	US-09-192-012-5	Sequence 5, Appli
252	228	5.8	812	4	US-08-991-761A-12	Sequence 12, Appli	325	215	5.4	810	4	US-09-403-736-1	Sequence 1, Appli
253	228	5.8	812	5	PCT-US95-05107-1	Sequence 1, Appli	326	214	5.4	254	4	US-08-560-098A-49	Sequence 49, Appli
254	227	5.8	812	4	US-09-023-942A-26	Sequence 26, Appli	327	213.5	5.4	255	3	US-08-944-483-67	Sequence 67, Appli
255	227	5.8	812	3	US-08-705-875A-10	Sequence 10, Appli	328	213.5	5.4	256	2	US-09-027-337-3	Sequence 3, Appli
256	227	5.8	308	4	US-09-242-999-10	Sequence 10, Appli	329	213.5	5.4	256	4	US-09-644-600-3	Sequence 3, Appli
257	226.5	5.7	454	3	US-09-518-046-2	Sequence 2, Appli	330	213.5	5.4	256	4	US-09-654-600A-3	Sequence 3, Appli
258	226.5	5.7	2787	3	US-09-245-041-15	Sequence 15, Appli	331	212.5	5.4	250	4	US-09-205-258-427	Sequence 427, App
259	226	5.7	406	4	US-09-851-588-6	Sequence 6, Appli	332	212.5	5.4	282	3	US-09-025-059-1	Sequence 1, Appli
260	226	5.7	423	4	US-09-656-002-2	Sequence 2, Appli	333	212.5	5.4	289	4	US-09-386-642-14	Sequence 14, Appli
261	226	5.7	435	3	US-09-008-271A-6	Sequence 6, Appli	334	212	5.4	260	3	US-09-025-059-3	Sequence 3, Appli
262	226	5.7	437	4	US-09-851-588-8	Sequence 8, Appli	335	212	5.4	260	4	US-09-618-259-8	Sequence 8, Appli
263	224.5	5.7	235	3	US-09-944-483-65	Sequence 65, Appli	336	212	5.4	814	1	US-08-750-711-1	Sequence 1, Appli
264	224	5.7	275	2	US-09-016-366A-17	Sequence 17, Appli	337	211.5	5.4	232	1	US-08-508-448C-19	Sequence 19, Appli
265	224	5.7	275	2	US-08-978-404B-12	Sequence 12, Appli	338	211.5	5.4	418	1	US-08-508-448C-25	Sequence 25, Appli
266	224	5.7	306	2	US-08-560-098A-45	Sequence 45, Appli	339	211.5	5.4	418	4	US-09-370-838-82	Sequence 82, Appli
267	224	5.7	331	2	US-08-560-098A-46	Sequence 46, Appli	340	211.5	5.4	418	4	US-09-370-838-83	Sequence 83, Appli
268	223.5	5.7	245	3	US-08-944-483-69	Sequence 69, Appli	341	211	5.3	276	2	US-09-016-366A-15	Sequence 15, Appli
269	223	5.7	238	3	US-08-944-483-64	Sequence 64, Appli	342	211	5.3	276	2	US-08-978-404B-21	Sequence 21, Appli
270	222.5	5.6	790	4	US-08-991-761A-13	Sequence 13, Appli	343	211	5.3	300	3	US-08-705-875A-4	Sequence 4, Appli
271	222	5.6	274	2	US-09-016-366A-21	Sequence 21, Appli	344	211	5.3	300	3	US-09-320-731-21	Sequence 21, Appli
272	222	5.6	274	2	US-08-978-404B-16	Sequence 16, Appli	345	211	5.3	300	4	US-09-242-999-4	Sequence 4, Appli
273	222	5.6	407	4	US-09-734-675-4	Sequence 4, Appli	346	211	5.3	1010	3	US-08-882-046-7	Sequence 7, Appli
274	221	5.6	253	3	US-08-944-483-73	Sequence 73, Appli	347	211	5.3	1036	4	US-09-068-740A-6	Sequence 6, Appli
275	221	5.6	273	2	US-08-978-404B-6	Sequence 6, Appli	348	211	5.3	1187	4	US-09-068-740A-7	Sequence 7, Appli
276	221	5.6	300	4	US-08-705-875A-6	Sequence 6, Appli	349	211	5.3	1208	4	US-09-199-865-1	Sequence 1, Appli
277	221	5.6	300	4	US-09-242-999-6	Sequence 6, Appli	350	211	5.3	1218	2	US-08-400-159-6	Sequence 6, Appli
278	220.5	5.6	376	4	US-09-820-002-2	Sequence 2, Appli	351	211	5.3	1218	3	US-08-611-729A-6	Sequence 6, Appli
279	220	5.6	273	2	US-09-016-366A-19	Sequence 19, Appli	352	211	5.3	1218	3	US-08-882-046-2	Sequence 2, Appli
280	220	5.6	273	2	US-08-978-404B-14	Sequence 14, Appli	353	211	5.3	1218	3	US-09-214-278-7	Sequence 7, Appli
281	219.5	5.6	254	3	US-09-944-483-50	Sequence 50, Appli	354	211	5.3	1218	4	US-09-068-740A-11	Sequence 11, Appli
282	219.5	5.6	255	2	US-09-027-337-7	Sequence 7, Appli	355	211	5.3	1218	4	US-09-855-722-7	Sequence 7, Appli
283	219.5	5.6	255	4	US-09-644-600-7	Sequence 7, Appli	356	210.5	5.3	418	4	US-09-370-838-62	Sequence 62, Appli
284	219.5	5.6	255	4	US-09-654-600A-7	Sequence 7, Appli	357	210.5	5.3	1219	3	US-08-882-046-5	Sequence 5, Appli
285	218.5	5.5	244	4	US-09-601-318-4	Sequence 4, Appli	358	210	5.3	154	3	US-09-261-416-5	Sequence 5, Appli
286	218.5	5.5	244	4	US-09-601-318-5	Sequence 5, Appli	359	210	5.3	492	3	US-08-944-483-24	Sequence 24, Appli
287	218.5	5.5	244	4	US-09-601-318-6	Sequence 6, Appli	360	208.5	5.3	248	4	US-09-685-166A-895	Sequence 895, App
288	218.5	5.5	244	4	US-09-601-318-7	Sequence 7, Appli	361	208	5.3	268	1	US-08-270-584A-2	Sequence 2, Appli
289	218.5	5.5	245	3	US-09-079-970A-6	Sequence 6, Appli	362	208	5.3	268	2	US-08-765-192-2	Sequence 2, Appli
290	218.5	5.5	245	3	US-09-601-318-1	Sequence 1, Appli	363	208	5.3	268	1	US-09-199-793-2	Sequence 2, Appli
291	218.5	5.5	245	3	US-09-079-970A-5	Sequence 5, Appli	364	208	5.3	271	1	US-08-467-155A-10	Sequence 10, Appli
292	217.5	5.5	1198	3	US-09-245-041-131	Sequence 131, App	365	208	5.3	271	2	US-08-628-198-10	Sequence 10, Appli
293	217.5	5.5	1198	3	US-09-794-236-3	Sequence 3, Appli	366	208	5.3	271	3	US-09-201-038-10	Sequence 10, Appli
294	217.5	5.5	1429	3	US-09-245-041-130	Sequence 130, App	367	208	5.3	271	5	PCT-US96-07343-10	Sequence 10, Appli
295	217	5.5	239	3	US-08-944-483-61	Sequence 61, Appli	368	207.5	5.3	241	3	US-08-944-483-59	Sequence 59, Appli
296	217	5.5	268	4	US-09-613-822B-2	Sequence 2, Appli	369	206.5	5.2	255	1	US-08-650-129-5	Sequence 5, Appli
297	217	5.5	273	2	US-08-978-404B-3	Sequence 3, Appli	370	206.5	5.2	255	3	US-08-984-417-5	Sequence 5, Appli
298	217	5.5	791	1	US-08-643-219-1	Sequence 1, Appli	371	206.5	5.2	284	4	US-09-387-375-7	Sequence 7, Appli
299	217	5.5	791	3	US-08-851-350-1	Sequence 1, Appli	372	206.5	5.2	316	4	US-09-387-375-9	Sequence 9, Appli
300	217	5.5	2703	1	US-08-185-432-19	Sequence 19, Appli	373	205.5	5.2	235	3	US-08-944-483-48	Sequence 48, Appli
301	217	5.5	2703	4	US-08-899-232-4	Sequence 4, Appli	374	205.5	5.2	269	2	US-08-978-404B-10	Sequence 10, Appli
302	216	5.5	267	2	US-09-016-366A-23	Sequence 23, Appli	375	205.5	5.2	288	4	US-09-386-642-13	Sequence 13, Appli
303	216	5.5	267	2	US-08-978-404B-18	Sequence 18, Appli	376	205.5	5.2	327	4	US-09-386-629-8	Sequence 8, Appli
304	216	5.5	268	1	US-08-568-031-2	Sequence 2, Appli	377	205.5	5.2	492	3	US-09-342-749-2	Sequence 2, Appli
305	216	5.5	268	2	US-09-153-304-2	Sequence 2, Appli	378	205.5	5.2	492	4	US-09-691-840-2	Sequence 2, Appli
306	216	5.5	268	3	US-09-153-304-2	Sequence 3, Appli	379	204	5.2	260	3	US-09-070-526-2	Sequence 2, Appli
307	216	5.5	299	3	US-08-944-483-66	Sequence 66, Appli	380	204	5.2	260	4	US-09-618-259-7	Sequence 7, Appli
308	216	5.5	319	4	US-09-386-642-12	Sequence 12, Appli	381	203.5	5.2	224	3	US-08-944-483-34	Sequence 34, Appli
309	216	5.5	328	4	US-09-386-642-11	Sequence 11, Appli	382	203.5	5.2	3623	4	US-09-341-461-2	Sequence 2, Appli
310	216	5.5	790	1	US-08-469-486-54	Sequence 54, Appli	383	203	5.1	283	3	US-08-807-151-1	Sequence 1, Appli
311	216	5.5	790	2	US-08-469-486-54	Sequence 54, Appli	384	203	5.1	283	4	US-09-478-957-1	Sequence 1, Appli
312	216	5.5	810	6	5200340-8	Patent No. 5200340	385	202	5.1	2321	4	US-09-230-652-2	Sequence 2, Appli
313	215.5	5.5	317	4	US-09-386-629-7	Sequence 7, Appli	386	200.5	5.1	226	1	US-08-550-129-4	Sequence 4, Appli
314	215.5	5.5	317	4	US-09-907-794A-263	Sequence 263, App	387	200.5	5.1	226	3	US-08-984-417-4	Sequence 4, Appli
315	215.5	5.5	317	4	US-09-905-125A-263	Sequence 263, App	388	200.5	5.1	232	1	US-08-278-091-8	Sequence 8, Appli
316	215.5	5.5	317	4	US-09-902-775A-263	Sequence 263, App	389	200.5	5.1	232	1	US-08-483-859-8	Sequence 8, Appli
317	215	5.4	791	2	US-09-131-995-1	Sequence 1, Appli	390	200.5	5.1	232	1	US-08-472-173-8	Sequence 8, Appli
318	215	5.4	791	2	US-08-832-087B-1	Sequence 1, Appli	391	200.5	5.1	232	2	US-08-487-167-8	Sequence 8, Appli
319	215	5.4	791	3	US-09-132-154-1	Sequence 1, Appli	392	200.5	5.1	232	2	US-08-482-816-8	Sequence 8, Appli

393	200.5	5.1	232	2	US-08-296-149-8	Sequence 8, Appl	466	193	4.9	228	3	US-08-944-483-44	Sequence 44, Appl
394	200.5	5.1	232	2	US-08-801-499-8	Sequence 8, Appl	467	193	4.9	253	6	5223425-8	Patent No. 5223425
395	200.5	5.1	232	2	US-08-615-271-8	Sequence 8, Appl	468	193	4.9	268	3	US-09-032-215-42	Sequence 42, Appl
396	200.5	5.1	232	3	US-09-074-650-8	Sequence 8, Appl	469	192.5	4.9	225	2	US-08-557-146-12	Sequence 12, Appl
397	200.5	5.1	232	3	US-09-074-659-8	Sequence 8, Appl	470	192.5	4.9	225	2	US-09-154-344-12	Sequence 12, Appl
398	200.5	5.1	232	3	US-09-106-468-8	Sequence 8, Appl	471	192.5	4.9	281	1	US-08-467-155A-7	Sequence 7, Appl
399	200.5	5.1	232	3	US-09-106-468-8	Sequence 8, Appl	472	192.5	4.9	281	2	US-08-620-138-7	Sequence 7, Appl
400	200.5	5.1	232	3	US-09-106-467-8	Sequence 8, Appl	473	192.5	4.9	281	3	US-09-201-038-7	Sequence 7, Appl
401	200.5	5.1	247	2	US-08-956-267A-2	Sequence 2, Appl	474	192.5	4.9	281	5	PCT-US96-07343-7	Sequence 20, Appl
402	200.5	5.1	314	4	US-09-636-382A-2	Sequence 2, Appl	475	192	4.9	149	3	US-09-518-046-20	Sequence 13, Appl
403	200.5	5.1	415	4	US-09-907-794A-104	Sequence 104, App	476	191.5	4.9	224	2	US-08-766-982-13	Sequence 36, Appl
404	200.5	5.1	415	4	US-09-905-125A-104	Sequence 104, App	477	191.5	4.9	224	3	US-08-944-483-36	Sequence 36, Appl
405	200.5	5.1	415	4	US-09-902-775A-104	Sequence 104, App	478	191.5	4.9	224	3	US-09-295-219-13	Sequence 13, Appl
406	200.5	5.1	810	4	US-08-991-761A-11	Sequence 11, Appl	479	191.5	4.9	225	2	US-09-027-337-5	Sequence 5, Appl
407	200	5.1	385	4	US-09-163-951-16	Sequence 16, Appl	480	191.5	4.9	225	4	US-09-644-600-5	Sequence 5, Appl
408	200	5.1	385	4	US-09-345-881-16	Sequence 16, Appl	481	191.5	4.9	225	4	US-09-654-600A-5	Sequence 5, Appl
409	199.5	5.1	1193	2	US-08-400-159-10	Sequence 10, Appl	482	191.5	4.9	233	4	US-09-636-382A-24	Sequence 24, Appl
410	199.5	5.1	1193	3	US-08-611-729A-10	Sequence 10, Appl	483	191.5	4.9	830	1	US-08-110-158-4	Sequence 4, Appl
411	199.5	5.1	2556	1	US-08-185-432A-17	Sequence 17, Appl	484	191	4.8	250	6	5223425-4	Patent No. 5223425
412	199.5	5.1	2556	1	US-08-083-590A-20	Sequence 20, Appl	485	191	4.8	254	4	US-09-439-313-525	Sequence 525, App
413	199.5	5.1	2556	3	US-08-532-384-20	Sequence 20, Appl	486	191	4.8	254	4	US-09-636-215-525	Sequence 525, App
414	199.5	5.1	2556	4	US-08-999-232-2	Sequence 2, Appl	487	191	4.8	254	4	US-09-685-166A-525	Sequence 525, App
415	199	5.0	260	3	US-09-008-271A-7	Sequence 7, Appl	488	190	4.8	455	3	US-09-261-416-2	Sequence 2, Appl
416	199	5.0	278	3	US-08-392-828C-4	Sequence 4, Appl	489	190	4.8	284	4	US-09-386-642-54	Sequence 54, Appl
417	199	5.0	278	3	US-09-330-945-4	Sequence 4, Appl	490	189	4.8	220	4	US-09-439-313-327	Sequence 327, App
418	198.5	5.0	223	1	US-08-278-091-9	Sequence 9, Appl	491	189	4.8	220	4	US-09-352-616A-327	Sequence 327, App
419	198.5	5.0	223	1	US-08-483-859-9	Sequence 9, Appl	492	189	4.8	220	4	US-09-232-149A-327	Sequence 327, App
420	198.5	5.0	223	1	US-08-472-173-9	Sequence 9, Appl	493	189	4.8	220	4	US-09-636-215-327	Sequence 327, App
421	198.5	5.0	223	2	US-08-487-167-9	Sequence 9, Appl	494	189	4.8	220	4	US-09-685-166A-327	Sequence 327, App
422	198.5	5.0	223	2	US-08-482-816-9	Sequence 9, Appl	495	189	4.8	220	4	US-09-688-489-327	Sequence 327, App
423	198.5	5.0	223	2	US-08-296-149-9	Sequence 9, Appl	496	189	4.8	224	3	US-08-944-483-33	Sequence 33, Appl
424	198.5	5.0	223	2	US-08-801-499-9	Sequence 9, Appl	497	189	4.8	225	2	US-09-027-337-4	Sequence 4, Appl
425	198.5	5.0	223	2	US-08-615-271-9	Sequence 9, Appl	498	189	4.8	225	4	US-09-644-600-4	Sequence 4, Appl
426	198.5	5.0	223	3	US-09-074-660-9	Sequence 9, Appl	499	189	4.8	225	4	US-09-654-600A-4	Sequence 4, Appl
427	198.5	5.0	223	3	US-09-074-659-9	Sequence 9, Appl	500	189	4.8	238	6	5223425-5	Patent No. 5223425
428	198.5	5.0	223	3	US-09-106-468-9	Sequence 9, Appl	501	189	4.8	253	2	US-08-557-146-2	Sequence 2, Appl
429	198.5	5.0	223	3	US-09-106-466A-9	Sequence 9, Appl	502	189	4.8	253	2	US-08-824-874-3	Sequence 3, Appl
430	198.5	5.0	223	3	US-09-106-467-9	Sequence 9, Appl	503	189	4.8	253	2	US-09-154-344-2	Sequence 2, Appl
431	198.5	5.0	223	4	US-09-601-318-2	Sequence 2, Appl	504	189	4.8	253	3	US-08-930-188-2	Sequence 2, Appl
432	198.5	5.0	223	4	US-09-120-582-2	Sequence 2, Appl	505	189	4.8	253	3	US-09-210-084-3	Sequence 3, Appl
433	198.5	5.0	223	2	US-08-978-404B-45	Sequence 45, Appl	506	189	4.8	253	4	US-09-764-762-3	Sequence 3, Appl
434	198	5.0	242	3	US-08-944-483-57	Sequence 57, Appl	507	189	4.8	312	5	PCT-US96-04294-2	Sequence 2, Appl
435	197.5	5.0	242	3	US-08-944-483-54	Sequence 54, Appl	508	189	4.8	449	4	US-09-023-942A-4	Sequence 4, Appl
436	197.5	5.0	222	1	US-08-456-840-46	Sequence 46, Appl	509	189	4.8	449	4	US-09-636-215-617	Sequence 617, App
437	197.5	5.0	222	1	US-08-266-407A-46	Sequence 46, Appl	510	189	4.8	449	4	US-09-685-166A-617	Sequence 617, App
438	197.5	5.0	222	1	US-08-892-544-46	Sequence 46, Appl	511	188.5	4.8	290	4	US-09-386-653A-7	Sequence 7, Appl
439	197	5.0	338	4	US-08-991-761A-10	Sequence 10, Appl	512	188	4.8	248	1	US-08-744-026-1	Sequence 1, Appl
440	196.5	5.0	241	3	US-08-944-483-60	Sequence 60, Appl	513	188	4.8	248	2	US-09-102-732-1	Sequence 1, Appl
441	196.5	5.0	248	3	US-08-148-910-1	Sequence 71, Appl	514	188	4.8	248	3	US-09-261-767-1	Sequence 1, Appl
442	196.5	5.0	300	1	US-08-448-937A-1	Sequence 1, Appl	515	188	4.8	254	4	US-09-439-313-523	Sequence 523, App
443	196.5	5.0	300	1	US-08-448-937A-1	Sequence 1, Appl	516	188	4.8	254	4	US-09-636-215-523	Sequence 523, App
444	196.5	5.0	2523	1	US-08-185-432-18	Sequence 18, Appl	517	188	4.8	263	2	US-08-790-137-4	Sequence 4, Appl
445	196.5	5.0	2523	4	US-08-899-232-3	Sequence 3, Appl	518	188	4.8	263	2	US-08-824-874-5	Sequence 5, Appl
446	195.5	5.0	232	3	US-08-944-483-45	Sequence 45, Appl	519	188	4.8	263	3	US-08-807-151-5	Sequence 5, Appl
447	195.5	5.0	241	1	US-08-330-978-4	Sequence 4, Appl	520	188	4.8	263	3	US-09-210-084-5	Sequence 5, Appl
448	195.5	5.0	241	1	US-08-474-042-4	Sequence 4, Appl	521	188	4.8	263	3	US-09-210-084-5	Sequence 5, Appl
449	195.5	5.0	241	1	US-08-484-558-4	Sequence 4, Appl	522	188	4.8	263	4	US-09-478-957-5	Sequence 5, Appl
450	195.5	5.0	241	1	US-08-774-592-4	Sequence 4, Appl	523	188	4.8	263	4	US-09-764-762-5	Sequence 5, Appl
451	195.5	5.0	254	1	US-08-330-978-3	Sequence 3, Appl	524	188	4.8	333	4	US-08-991-761A-8	Sequence 8, Appl
452	195.5	5.0	254	1	US-08-474-042-3	Sequence 3, Appl	525	187.5	4.8	224	3	US-08-944-483-35	Sequence 35, Appl
453	195.5	5.0	254	1	US-08-484-558-3	Sequence 3, Appl	526	187.5	4.8	242	3	US-08-944-483-29	Sequence 29, Appl
454	195.5	5.0	254	1	US-08-774-592-3	Sequence 3, Appl	527	187.5	4.8	255	3	US-08-906-769-83	Sequence 83, Appl
455	195.5	5.0	254	1	US-08-330-978-1	Sequence 1, Appl	528	187.5	4.8	255	3	US-08-906-616-83	Sequence 83, Appl
456	195.5	5.0	306	1	US-08-474-042-1	Sequence 1, Appl	529	187.5	4.8	255	3	US-08-617-795-83	Sequence 83, Appl
457	195.5	5.0	306	1	US-08-484-558-1	Sequence 1, Appl	530	187.5	4.8	255	3	US-08-639-075A-83	Sequence 83, Appl
458	195.5	5.0	306	1	US-08-185-432-16	Sequence 16, Appl	531	187.5	4.8	255	3	US-09-012-431-83	Sequence 83, Appl
459	195.5	5.0	2471	1	US-08-185-432-16	Sequence 16, Appl	532	187.5	4.8	255	3	US-09-012-692-83	Sequence 83, Appl
460	195.5	5.0	2471	1	US-08-033-590A-19	Sequence 19, Appl	533	187.5	4.8	255	5	PCT-US95-1442A-83	Sequence 83, Appl
461	195.5	5.0	2471	3	US-08-532-384-19	Sequence 19, Appl	534	187.5	4.8	110	4	US-09-341-461-28	Sequence 28, Appl
462	195.5	5.0	2471	3	US-08-899-232-1	Sequence 1, Appl	535	186	4.7	230	1	US-08-456-840-47	Sequence 47, Appl
463	194.5	4.9	246	2	US-08-978-404B-44	Sequence 44, Appl	536	186	4.7	230	1	US-08-266-407A-47	Sequence 47, Appl
464	194.5	4.9	415	3	US-09-032-523-2	Sequence 2, Appl	537	186	4.7	230	1	US-08-266-407A-47	Sequence 47, Appl
465	194.5	4.9	415	4	US-09-802-633-2	Sequence 2, Appl	538	186	4.7	230	2	US-08-892-544-47	Sequence 47, Appl

539	186	4.7	230	2	US-08-766-982-12	Sequence 12, Appl	612	178.5	4.5	468	4	US-09-802-633-8	Sequence 8, Appl
540	186	4.7	230	3	US-09-944-483-53	Sequence 53, Appl	613	178.5	4.5	922	4	US-09-116-473-4	Sequence 4, Appl
541	186	4.7	230	3	US-09-296-219-12	Sequence 12, Appl	614	178.5	4.5	923	3	US-08-936-135-6	Sequence 6, Appl
542	186	4.7	232	2	US-08-897-340-11	Sequence 31, Appl	615	178.5	4.5	923	4	US-09-439-711C-6	Sequence 6, Appl
543	186	4.7	232	3	US-08-232-329-31	Sequence 31, Appl	616	177.5	4.5	248	2	US-08-851-974-3	Sequence 3, Appl
544	186	4.7	326	4	US-09-411-977-3	Sequence 3, Appl	617	177.5	4.5	248	2	US-09-413-390-3	Sequence 3, Appl
545	185.5	4.7	256	3	US-09-032-215-27	Sequence 27, Appl	618	177.5	4.5	1964	4	US-09-467-997-1	Sequence 1, Appl
546	185.5	4.7	261	3	US-08-163-919A-2	Sequence 2, Appl	619	177	4.5	102	3	US-09-374-135-7	Sequence 7, Appl
547	185.5	4.7	261	5	PCT-US94-14073-2	Sequence 2, Appl	620	177	4.5	110	4	US-09-341-461-29	Sequence 29, Appl
548	185.5	4.7	306	4	US-09-386-642-53	Sequence 53, Appl	621	177	4.5	110	1	US-08-378-091-11	Sequence 11, Appl
549	185.5	4.7	711	1	US-08-184-012C-8	Sequence 8, Appl	622	177	4.5	240	1	US-08-483-859-11	Sequence 11, Appl
550	185.5	4.7	711	1	US-08-334-177-2	Sequence 2, Appl	623	177	4.5	240	1	US-08-472-173-11	Sequence 11, Appl
551	185.5	4.7	711	2	US-08-666-082B-1	Sequence 1, Appl	624	177	4.5	240	2	US-08-487-167-11	Sequence 11, Appl
552	185.5	4.7	711	5	PCT-US95-13830-2	Sequence 2, Appl	625	177	4.5	240	2	US-08-482-816-11	Sequence 11, Appl
553	185.5	4.7	713	3	US-08-872-855-5	Sequence 5, Appl	626	177	4.5	240	2	US-08-296-149-11	Sequence 11, Appl
554	185	4.7	247	3	US-08-944-483-49	Sequence 49, Appl	627	177	4.5	240	2	US-08-801-499-11	Sequence 11, Appl
555	185	4.7	258	1	US-08-744-026-3	Sequence 3, Appl	628	177	4.5	240	2	US-08-615-271-11	Sequence 11, Appl
556	185	4.7	258	2	US-09-102-732-3	Sequence 3, Appl	629	177	4.5	240	3	US-09-074-650-11	Sequence 11, Appl
557	185	4.7	258	3	US-08-261-767-3	Sequence 3, Appl	630	177	4.5	240	3	US-09-106-468-11	Sequence 11, Appl
558	185	4.7	314	4	US-09-023-942A-6	Sequence 6, Appl	631	177	4.5	240	3	US-09-106-468A-11	Sequence 11, Appl
559	184	4.7	144	4	US-09-618-259-1	Sequence 1, Appl	632	177	4.5	240	3	US-09-106-467-11	Sequence 11, Appl
560	184	4.7	314	3	US-09-008-271A-3	Sequence 3, Appl	633	177	4.5	240	3	US-08-872-855-8	Sequence 8, Appl
561	184	4.7	314	4	US-09-907-794A-257	Sequence 257, App	634	177	4.5	729	3	US-08-872-855-8	Sequence 8, Appl
562	184	4.7	314	4	US-09-905-125A-257	Sequence 257, App	635	177	4.5	830	6	5378464-2	Patent No. 5378464
563	184	4.7	314	4	US-09-902-775A-257	Sequence 257, App	636	176.5	4.5	232	1	US-07-990-301A-4	Sequence 4, Appl
564	183.5	4.7	711	2	US-08-766-982-2	Sequence 2, Appl	637	176.5	4.5	901	3	US-08-936-135-22	Sequence 22, Appl
565	183.5	4.7	711	3	US-09-296-219-2	Sequence 2, Appl	638	176.5	4.5	901	4	US-09-439-711C-22	Sequence 22, Appl
566	183.5	4.7	711	4	US-09-600-991-12	Sequence 20, Appl	639	176.5	4.5	906	3	US-08-936-135-24	Sequence 24, Appl
567	183.5	4.7	722	3	US-08-981-392-12	Sequence 12, Appl	640	176.5	4.5	906	4	US-09-439-711C-24	Sequence 24, Appl
568	182.5	4.6	258	4	US-09-023-942A-8	Sequence 8, Appl	641	176.5	4.5	909	3	US-08-936-135-8	Sequence 8, Appl
569	182.5	4.6	484	2	US-08-232-433C-9	Sequence 9, Appl	642	176.5	4.5	909	3	US-08-936-135-10	Sequence 10, Appl
570	182.5	4.6	484	3	US-09-276-197-9	Sequence 9, Appl	643	176.5	4.5	909	4	US-09-439-711C-8	Sequence 8, Appl
571	182.5	4.6	720	3	US-08-872-855-4	Sequence 4, Appl	644	176.5	4.5	914	3	US-09-439-711C-10	Sequence 10, Appl
572	182	4.6	405	4	US-08-734-675-2	Sequence 2, Appl	645	176.5	4.5	914	3	US-08-936-135-12	Sequence 12, Appl
573	182	4.6	721	3	US-08-872-855-7	Sequence 7, Appl	646	176.5	4.5	914	4	US-09-439-711C-12	Sequence 12, Appl
574	182	4.6	1055	3	US-09-214-278-2	Sequence 2, Appl	647	176.5	4.5	925	4	US-09-116-473-2	Sequence 2, Appl
575	182	4.6	1055	4	US-08-855-722-2	Sequence 2, Appl	648	176.5	4.5	926	3	US-08-936-135-14	Sequence 14, Appl
576	182	4.6	1065	2	US-08-400-159-8	Sequence 8, Appl	649	176.5	4.5	926	3	US-09-439-711C-14	Sequence 14, Appl
577	182	4.6	1212	3	US-09-214-278-3	Sequence 3, Appl	650	176.5	4.5	931	3	US-08-936-135-16	Sequence 16, Appl
578	182	4.6	1212	4	US-08-855-722-3	Sequence 3, Appl	651	176.5	4.5	931	4	US-09-439-711C-16	Sequence 16, Appl
579	182	4.6	1238	3	US-09-214-278-5	Sequence 5, Appl	652	176	4.5	233	3	US-09-004-731-27	Sequence 27, Appl
580	182	4.6	1238	4	US-08-855-722-5	Sequence 5, Appl	653	176	4.5	233	3	US-08-749-699-27	Sequence 27, Appl
581	182	4.6	1257	3	US-08-611-729A-8	Sequence 8, Appl	654	176	4.5	233	4	US-09-004-729-27	Sequence 27, Appl
582	181.5	4.6	258	1	US-07-990-301A-2	Sequence 2, Appl	655	176	4.5	242	3	US-08-944-483-58	Sequence 58, Appl
583	181.5	4.6	299	1	US-08-467-155A-8	Sequence 8, Appl	656	176	4.5	266	3	US-09-004-731-24	Sequence 24, Appl
584	181.5	4.6	299	2	US-08-628-198-8	Sequence 8, Appl	657	176	4.5	266	3	US-08-749-699-24	Sequence 24, Appl
585	181.5	4.6	299	3	US-09-201-038-8	Sequence 8, Appl	658	176	4.5	266	4	US-09-004-729-24	Sequence 24, Appl
586	181.5	4.6	299	5	PCT-US96-07343-8	Sequence 8, Appl	659	175.5	4.4	921	4	US-09-439-711C-4	Sequence 4, Appl
587	181	4.6	396	4	US-09-800-729-86	Sequence 86, Appl	660	175	4.4	909	3	US-08-936-135-18	Sequence 18, Appl
588	180	4.6	260	6	5223425-10	Patent No. 5223425	661	175	4.4	909	4	US-09-439-711C-18	Sequence 18, Appl
589	179.5	4.6	205	3	US-09-020-956-176	Sequence 176, App	662	175	4.4	926	3	US-08-936-135-20	Sequence 20, Appl
590	179.5	4.6	205	3	US-09-030-607-176	Sequence 176, App	663	175	4.4	926	4	US-09-439-711C-20	Sequence 20, Appl
591	179.5	4.6	205	4	US-09-439-313-176	Sequence 176, App	664	175	4.4	931	4	US-09-583-638-4	Sequence 4, Appl
592	179.5	4.6	205	4	US-09-352-616A-176	Sequence 176, App	665	174	4.4	265	2	US-08-177-109A-57	Sequence 57, Appl
593	179.5	4.6	205	4	US-08-232-149A-176	Sequence 176, App	666	174	4.4	286	1	US-08-687-706-57	Sequence 57, Appl
594	179.5	4.6	205	4	US-09-159-812-176	Sequence 176, App	667	174	4.4	286	2	US-08-467-155A-9	Sequence 9, Appl
595	179.5	4.6	205	4	US-09-636-215-176	Sequence 176, App	668	174	4.4	286	2	US-08-628-198-9	Sequence 9, Appl
596	179.5	4.6	205	4	US-08-685-166A-176	Sequence 176, App	669	174	4.4	286	3	US-09-201-038-9	Sequence 9, Appl
597	179.5	4.6	205	4	US-09-115-453-176	Sequence 176, App	670	174	4.4	286	5	PCT-US96-07343-9	Sequence 9, Appl
598	179.5	4.6	205	4	US-09-688-489-176	Sequence 176, App	671	173.5	4.4	294	4	US-09-800-729-146	Sequence 146, App
599	179.5	4.6	259	6	5223425-2	Patent No. 5223425	672	173.5	4.4	717	3	US-08-872-855-9	Sequence 9, Appl
600	179.5	4.6	728	3	US-08-981-392-2	Sequence 2, Appl	673	173	4.4	211	3	US-09-220-731-25	Sequence 25, Appl
601	179.5	4.6	830	5	PCT-US91-05059-2	Sequence 2, Appl	674	173	4.4	211	4	US-09-242-999-20	Sequence 20, Appl
602	179	4.5	230	1	US-08-379-621-2	Sequence 2, Appl	675	172.5	4.4	449	2	US-08-839-008-2	Sequence 2, Appl
603	179	4.5	230	1	US-08-147-000B-2	Sequence 2, Appl	676	172.5	4.4	449	2	US-08-839-008-9	Sequence 9, Appl
604	179	4.5	230	2	US-08-889-078-2	Sequence 2, Appl	677	172.5	4.4	1248	3	US-08-882-046-6	Sequence 6, Appl
605	179	4.5	253	4	US-08-578-303-4	Sequence 4, Appl	678	172	4.4	721	3	US-08-981-392-5	Sequence 5, Appl
606	179	4.5	384	3	US-09-032-215-22	Sequence 22, Appl	679	171.5	4.3	238	3	US-08-944-483-39	Sequence 39, Appl
607	178.5	4.5	250	3	US-08-944-483-68	Sequence 68, Appl	680	171.5	4.3	259	3	US-08-906-769-190	Sequence 190, App
608	178.5	4.5	315	4	US-09-386-653A-9	Sequence 9, Appl	681	171.5	4.3	259	3	US-08-906-616-190	Sequence 190, App
609	178.5	4.5	401	2	US-08-839-008-5	Sequence 5, Appl	682	171.5	4.3	259	3	US-08-639-075A-190	Sequence 190, App
610	178.5	4.5	468	2	US-08-839-008-7	Sequence 7, Appl	683	171.5	4.3	259	3	US-09-004-731-85	Sequence 85, Appl
611	178.5	4.5	468	3	US-09-032-523-8	Sequence 8, Appl	684	171.5	4.3	259	3	US-09-012-431-190	Sequence 190, App

685 171.5 4.3 259 3 US-08-749-699-85 Sequence 85, Appl  
686 171.5 4.3 259 3 US-09-012-692-190 Sequence 190, App  
687 171.5 4.3 259 3 US-08-906-613-190 Sequence 190, App  
688 171.5 4.3 259 4 US-09-004-729-85 Sequence 85, Appl  
689 171.5 4.3 262 2 US-08-790-137-1 Sequence 1, Appl  
690 171.5 4.3 262 2 US-08-790-137-3 Sequence 3, Appl  
691 171.5 4.3 262 2 US-08-681-151-4 Sequence 4, Appl  
692 171.5 4.3 262 2 US-08-824-874-4 Sequence 4, Appl  
693 171.5 4.3 262 3 US-08-807-151-4 Sequence 4, Appl  
694 171.5 4.3 262 3 US-09-210-084-4 Sequence 4, Appl  
695 171.5 4.3 262 4 US-09-478-957-4 Sequence 4, Appl  
696 171.5 4.3 262 4 US-09-764-762-4 Sequence 4, Appl  
697 171.5 4.3 262 4 US-09-618-259-9 Sequence 9, Appl  
698 171.5 4.3 666 4 US-09-341-587-1 Sequence 1, Appl  
699 171.5 4.3 1785 4 US-09-341-587-3 Sequence 3, Appl  
700 171 4.3 262 3 US-09-025-059-4 Sequence 4, Appl

## ALIGNMENTS

## RESULT 1

US-08-296-014A-4  
; Sequence 4, Application US/08296014A  
; Patent No. 5716834  
; GENERAL INFORMATION:  
; APPLICANT: Ding, Jeak Ling  
; APPLICANT: Ho, Bow  
; TITLE OF INVENTION: The Cloned Factor C cDNA of the  
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius  
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch  
; STREET: 8110 Gatehouse Road, Suite 500 East  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22042  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/296,014A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murphy, Jr., Gerald M.  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 1781-105P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; TELEX: 248345  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1019 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-296-014A-4

Query Match 16.9%; Score 665; DB 1; Length 1019;  
Best Local Similarity 25.4%; Pred. No. 1.2e-46;  
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;  
QY 34 PGAEWIMRECCEYDQIEVCVCGKE-----VVGTYIPCCRNNEECDSCLIH 82  
DB 184 PNGQSNFFPKICR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSKDS----- 229  
QY 83 PGCTIFENCKSCR-NGSWGTL----- 103

230 PYLIGQETTLTCCQNGQNGQIPQCKNLVFCPDLDPVNAEHKVKIGVEQKVGPPQOTE 289  
104 -----DDFYVKGFCACR--AGMYGG--DCMR-----CGOVLK-- 133  
290 VTYTCGNYFLMGFDLTKCNPDSGWSGSPSCVKVADREVDCDSKAVDFLDVGVGPVRIH 349  
134 APKGQILLES-----YPLNAHCEWTIHA---KPGFVI----- 162  
350 CPAGCSLTAGTVMGTATYIHELSSVCRAAHAGKPLNSGAVHVVNNGPYSDFLGSDLNGI 409  
163 ---OLRFVMLSLEFDYM-----COYDVVEVRD-----GNRDQIIKRVCGN--E 202  
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203 RPAPIQS--IGSSLHVLPHSDG--SKNFDGFH-----AIYEETACSS 241  
470 RLAVLDKDVINSLSLTETLRGKGLATTWIGLHRLDAEKPFIWELMDRNSVNLNDNLTFWAS 529  
242 SPCFHDGTCVL-----DKAGS--YKCACLAGYTGQRCENLLEERN---CSDRGGPVNGYQKI 293  
530 GEPGNETNCTVYMDIQDQQLQSVWTKSCQPSFACMDLSRDKAKAKCDDPSLENGHATL 589  
294 TGGPGLINGRAKIGTVVSVFFCNNSYVLSGNEKRTCCQNGSWGSKQPICIK--ACREPKI 351  
590 HQQS--IDGFYA--GSSIRYSCEVLHLSGTETVYCTTNGTWSAPKPRCIKVIITCNPPV 645  
352 SDLVRRVLPQVQSRRETPHLQLYSAAFSKOKLO---SAPTKKPAALPFGD----- 398  
646 PSYGSVEIKP---PSRTNSISRVSFPFLRLPRLPLPLARAAKPPPKPRSSQPSSTVDLASK 702  
399 ---LPMGYOHLATQLOECISPFYRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP- 455  
703 VKLPEGHYRVGSRALYTCSRYELLGSGRRCDNSGNWSGRPASCIPVCGRSDSPRSPF 762  
456 -----KTQGLRMPQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNNRTVVVAACHVTDLG 510  
763 IWNGNSTEIGQWPMQAGISRWLA-----DHNMMFLQCGGSLNKEWIVTAAHCVTYSA 815  
511 KVTMIKTADLVKVLGKFYRDDDDREKTIQSIQISAILHPNYDPIILLDADTALLKLDKA 570  
816 TAEIIPDQPKMYLKKYRDDSDDDYVQVREALEIHVNPYNDPGLNFDLALQLKTPV 875  
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876 TLTRVQPICLPT--DITT---REHLKEGTLLAVTGWG-----LNENNTYSETIQOAVLPV 926  
625 VDSLLCEEQHEHDGIPSVTDNMFPCASWEPTAPSDICTAETGGIAAVSFPGRASPEPRWH 684  
927 VAASTCEGKYKADLPLVTENMFCAQYK-KGRYDACSDDSGG--PLVFADDSRTERRWV 983  
685 LMGLVSNYSYDKTCSH-RLSTAFTKVLFPKDWIER 717  
984 LEGIVSWGSPSGCGKANQYGGFTKVNVELSWIRQ 1017  
RESULT 2  
US-08-596-405-4  
; Sequence 4, Application US/08596405  
; Patent No. 5858706  
; GENERAL INFORMATION:  
; APPLICANT: Ding, Jeak Ling  
; APPLICANT: Ho, Bow  
; TITLE OF INVENTION: The Cloned Factor C cDNA of the  
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius  
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch & Birch  
; STREET: 8110 Gatehouse Road, Suite 500 East  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA



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; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1019 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-596-405-4

Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAEWNIMCECEYDQIEVCVCKRE-----VVGYYIPCCRNENECDSCLIH 82
DB 184 PNGQWNSFPKICR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSCDS----- 229
QY 83 PGCTIFENCKSCR-NGSWGTL----- 103
DB 230 PYLIGETITCQNGQWNGQIPCKNLVFCPLDPVNHAEHKVIGVEKYGQFPQGT 289
QY 104 -----DDFYVKGFCYACER--AGYGG--DCMR-----CGQVLR-- 133
DB 290 VTYTCNGYFLMGFDLTKCNPDGSGSGSPQSVKVADEVDKSDKAVDFLDVGEPIRIH 349
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DB 410 KSELKSLARSFREDYVRSSTAGSGGCPDGFWEVDENCYVYTSKQRAWERAQGVCTNMAA 469
QY 203 RPAPIQS--IGSSJHVLPHSDG--SKNFDGPH-----AYIEBITACSS 241
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QY 242 SPCHDGTCLV-----DKAGS--YKACACLAGYTGQRCENLLERN---CSDPGGPVNGYQKI 293
DB 530 GEPGNETNCVYMDIQDLQSVYKTKSCFPSSPACMDLSDRNKAKCDDPGLSLENGATL 589
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DB 590 HGQS--IDGFVA--GSSIRYSCEVLHYSGLTETVCTTNGTWSAPKRCIKVITCQNPV 645
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DB 646 PSYGSVEIKP---PSRTNSISRVGSPFLRLPLRLPLARAAPKPPKPSQSPVOLDLASK 702
QY 399 ---LPMGQHLHTQYECISPFYRLGSSRTCLRTGWSGRAPSCPICGKIENITAP- 455
DB 703 VKLPEGHYRVGSRAITYCESRYELLGSGQRCDNSNGWSGRPASCIPVCGRSNPSRPF 762
QY 456 -----KTQGLRPWQAAIYRTSGVHDSGLHKGAWFLVCSGALVNERTVVVAACHVTDLGL 510
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QY 511 KVTMIKTADLKVVLGKFXRDDRDEKTIQSLQISAILHPNYDPILLDDADIALKLLDKA 570
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QY 571 RISTRVOPICLAASRDLSFQESH-----TVAGMNVLADVRSPGPKNDTLRSQVSV 624
DB 876 TLTTRVQPICLPT--DITT---REHLKEGT LAVVTGNG---LNENNTYSETIQQAVLPV 926
QY 625 VDSLCLCEQHEHDGHPVSVTDNMFCASMEPTAPSDICTAETGCIAGVSPFGRASPEPRWH 684
DB 927 VAASTCEGYKEADLPLTVTENMFCAGYK-KGRYDACSGDSGG--PLVFADDSRTERRWV 983
QY 685 LMGLVSWSKYDKTCSH--RLSTAFTKVLPPFKDWIER 717
DB 984 LEGIVSWGSPSGCGKANQYGGFTKVNFLSWIRQ 1017

RESULT 3
US-08-877-620-4
; Sequence 4, Application US/08877620
; Patent No. 5985590
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: Ho, Bow
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolaesch & Birch
; STREET: 810 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,620
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/596,405
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1019 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-877-620-4

Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAEWNIMCECEYDQIEVCVCKRE-----VVGYYIPCCRNENECDSCLIH 82
DB 184 PNGQWNSFPKICR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSCDS----- 229
QY 83 PGCTIFENCKSCR-NGSWGTL----- 103
DB 230 PYLIGETITCQNGQWNGQIPCKNLVFCPLDPVNHAEHKVIGVEKYGQFPQGT 289
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QY 399 ---LPMGQHLHTQYECISPFYRLGSSRTCLRTGWSGRAPSCPICGKIENITAP- 455
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QY 203 RPATIOS--IGSSLHVLPHSDG--SKNPDGFH-----AIYEETACSS 241  
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QY 399 --LPMGYQHLHTQLOVECI--SPFYRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAP- 455  
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984 LEGIVSWGSPSGCGKANQYGF\*KNVFLSWIRQ 1017

## RESULT 4

US-09-287-368-4  
; Sequence 4, Application US/09287368A  
; Patent No. 6645724  
; GENERAL INFORMATION:  
; APPLICANT: DING, Jeak Ling  
; APPLICANT: HO, Bow  
; TITLE OF INVENTION: Assays for Endotoxin and Methods for Removal of Endotoxin  
; TITLE OF INVENTION: from a Sample Using Recombinant Factor C  
; FILE REFERENCES: 1781-0165P  
; CURRENT APPLICATION NUMBER: US/09/287,368A  
; CURRENT FILING DATE: 1999-04-07  
; EARLIER APPLICATION NUMBER: 09/201,786  
; EARLIER FILING DATE: 1998-12-01  
; EARLIER APPLICATION NUMBER: 09/081,767  
; EARLIER FILING DATE: 1998-05-21  
; EARLIER APPLICATION NUMBER: 60/058,816

; EARLIER FILING DATE: 1997-09-19  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1019  
; TYPE: PRT  
; ORGANISM: Carinocorpius rotundicauda  
; FEATURE:  
; OTHER INFORMATION: any n or Xaa = Unknown  
US-09-287-368-4  
  
Query Match 16.9%; Score 665; DB 4; Length 1019;  
Best Local Similarity 25.4%; Pred. No. 1.2e-46;  
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;  
  
QY 34 PGAENIMCRCECYDQIECVCPGKRE-----VVGYTIPCCRNEENECDCLIH 82  
Db 184 PNGQMSFPFKCIR---ECAMVSSPEHGKVALSGDMIEGATL-----RFSDDS----- 229  
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Db 410 KSEELKSLARSTRFDYRSSTAGSGCPDGWFEVDENCYVVTSKORAWERAGQVCTNMAA 469  
QY 203 RPATIOS--IGSSLHVLPHSDG--SKNPDGFH-----AIYEETACSS 241  
Db 470 RLAVLDKDVIPNSLTETLGLTWTWGLRLDAEKFPIWELMDRSNVVLDNLTFWAS 529  
QY 242 SPCFHDGTCVL-----DKAGS--YKACLAGYTGORCENLLEERN-----CSDPGGVNGYQKI 293  
Db 530 GEPGNETNCVYMDIQDQLQSVWKTSCFQPSGFACMDLSDRNKAKCDDPGSLENGHATL 589  
QY 294 TGGPGLINGRAHAKIGTVVVSFFCNNSYVLSGNEKRTCCQNGESGKQPICIK--ACREPKI 351  
Db 590 HQGS--IDGFYA--GSSIRYSEVLYHLSGTETVCTTNGTWSAPKPRCIKIVITQNPVP 645  
QY 352 SDLVRRRLVPMQVQSRRETPHLQLYSAAFSKQKLO--SAPTKKPALPFGD----- 398  
Db 646 PSYGSVEIKP--PSTNSISRVSFPFLRLPLPLPLARAAKPPPKPRSSQSPSTVDLASK 702  
QY 399 --LPMGYQHLHTQLOVECI--SPFYRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAP- 455  
Db 703 VKLPEGHYRVGSRATYTCESRYEYELLGSGRRCDNSNGMWSGRPASCIPIVCGRSDSRSPF 762  
QY 456 -----KTQGLRPMQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVAACHVTDLG 510  
Db 763 IWNGNSTEIGQWPQAGISRWLA-----DHNMFLOCGGSLNKKWIVTAACHVITYSA 815  
QY 511 KVTMIKTADLVKLVGFYRDDDDREKTIQSLQISAILHPNYDPTILLDADAILKLLDKA 570  
Db 816 TAEIIDPNQFKMYLGYKYYRDDSDDDYVQVREALEIHVNPNYDGNLNFDAIQLKTPV 875  
QY 571 RISTRVQPICLAASRDLSFQESHI-----TVAGNVLDVRSFGFNDLTRSGVSV 624  
Db 876 TLTRVQPICLPT--DITT--REHLKEGTLLAVVTG--LNENNTYSETIQOAVLPV 926  
QY 625 VDSLLCEEHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGCGIAAVSPFGGRASPEPRWH 684  
Db 927 VAASCTEEGKEADLPVTIENMFCAGYK--KGRYDACSDDSG--PLVFAADSRTERRWV 983  
QY 685 LMGLVSWSYDKTCSH--RLSTAFKVLPPFKDWIER 717

Db 984 LEGIVSWGSPGCGKANQYGGFTKVNFLSWIRQ 1017

RESULT 5

US-08-296-014A-2  
 ; Sequence 2, Application US/08296014A  
 ; Patent No. 5716834  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ding, Jeak Ling  
 ; APPLICANT: Ho, Bow  
 ; TITLE OF INVENTION: The Cloned Factor C cDNA of the  
 ; TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscopus  
 ; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Birch, Stewart, Kolasch & Birch  
 ; STREET: 8110 Gatehouse Road, Suite 500 East  
 ; CITY: Falls Church  
 ; STATE: Virginia  
 ; COUNTRY: USA  
 ; ZIP: 22042  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/296,014A  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Murphy, Jr., Gerald M.  
 ; REGISTRATION NUMBER: 28,977  
 ; REFERENCE/DOCKET NUMBER: 1781-105P  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703) 205-8000  
 ; TELEFAX: (703) 205-8050  
 ; TELEX: 248345  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1083 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-296-014A-2

Query Match 16.9%; Score 665; DB 1; Length 1083;  
 Best Local Similarity 25.4%; Pred. No. 1.3e-46;  
 Matched 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;  
 34 PGAEWNIMCECCBYDQIECVCPGKRE-----VVGTYTPCCRNENECDSCLIH 82  
 248 PNGQWSNFPKPCIR-----ECAMVSSPEHGKYNALSGDMIEGATL-----RFSCDS--- 293  
 83 PGCTIFENCKSCR-NGSWGTL----- 103  
 294 PYLLIGQETLTCOGNGONGQIPQCKNLVFCPLDPVNHAEHKVIGVEQKYGFPGQTE 353  
 104 -----DDFYVKGVCACR--AGWYGG--DCMR-----CGQVLR-- 133  
 354 VTYTCGNYFLMGFDTLKCPDGSWSGSPQCVKVADEVDKSKAVDFLDVGEVRIH 413  
 134 APKQIILLES-----YPLNAHCEWTIHA-----KPGFVI----- 162  
 414 CPAGCSLTAGTVMGTAIVHELSSVCRAAHAGKLPNSGGAVHVNNGPYSDFLGSDLNGI 473  
 163 ---QLRPFWLSLEFDYM-----COYDYVEYRD-----GDRDQIIRKVCN--E 202  
 474 KSEELKSLARFREDYVSSSTAGSKGCPDGFVEYDNCVYVTSKQAWERAQGVCTNMAA 533  
 203 RPAPIQS--IGSSLHLVLFHSDG--SKNFDGPH-----AIYEETACSS 241  
 534 RLAVLDKDVIFNSLTETLURGKGLTTTWIGLRLDAERKPFIMELMDSRVNLNDLITWAS 593

QY 242 SPCFHDGTCVLT-----DKAGS--YKACACLAGYTGQRCENILLEERN---CSDPGGVPNGYQKI 293  
 Db 594 GEPGNETNCYMDIQDQLQSVMTKSCFQSPSSFACWMDLSRKNKAKCDDPFGSLENGHATL 653  
 QY 294 TGGPGLNGRHAKIGTVVFFCNNSVYLSGNEKRTCOONGENWEGKQIPICIK--ACREPKI 351  
 Db 654 HGQS--IDGYA--GSSIRYSCEVLHYLSGTETVCTTNGTWSAPKRCIKVITQNPVP 709  
 QY 352 SDLVRRRLPMQVQSRTPHLQLYSAAFSKQKLQ---SAPTKKPALPFGD----- 398  
 Db 710 PSVGSVEIKP---PSRTNSISRVGSPFLRLPLRLPLARAAPKPPKPRSSQSPSTVDLASK 766  
 QY 399 --LPMGYQHILHLOQYECISPFYRRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAP- 455  
 Db 767 VKLPEGHYRVGSRAIYTCESRYEYELLGSGQRRCDNSNGWSGRDPASCIPVCGRSDSPSPF 826  
 QY 456 -----KTQGLRWPAQAIYRTSGVHDGSLHKAFLVCSGALVNVRTVVAACHVTDLG 510  
 Db 827 IWNGNSTEIQOWPQAGISRWLA-----DHNMFLOCGGSLNKKWIVTAACHVTYSA 879  
 QY 511 KVTMIKTADLKVVLGKPYRDDDEKTIQSLQISAILHPNYPILLDADIAILKLDKA 570  
 Db 880 TAEIIDPNQFMYLGYKYRDDSDDDVVOVREALEIHVWNYDFGNLNFIALIQLKTPV 939  
 QY 571 RISTRVQPICLAAASRLDSTSFQSHI-----TVAGNVLADVRSPGFKNDTLRSGVVSV 624  
 Db 940 TLTRVQPICLPT--DITT---REHLKEGTAVVVTGNG---LNENNTYSETIQQAVLPV 990  
 QY 625 VDSLLCEQHEHGHIPVSVTDNMFCAWSWEPTASDICTAETGGIAVSPFGRASPEPRWH 684  
 Db 991 VAASTCEEGYKEADPLVTVTENMFCAGYK--KGYDACSGDSGG--PLVFADDSRTERRV 1047  
 QY 685 LMGLVSWSYDKTCSH-RLSTAFKTVLPFFKDWIER 717  
 Db 1048 LEGIVSWGSPGCGKANQYGGFTKVNFLSWIRQ 1081  
 RESULT 6  
 US-08-596-405-2  
 ; Sequence 2, Application US/08596405  
 ; Patent No. 5858706  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ding, Jeak Ling  
 ; APPLICANT: Ho, Bow  
 ; TITLE OF INVENTION: The Cloned Factor C cDNA of the  
 ; TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscopus  
 ; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Birch, Stewart, Kolasch & Birch  
 ; STREET: 8110 Gatehouse Road, Suite 500 East  
 ; CITY: Falls Church  
 ; STATE: Virginia  
 ; COUNTRY: USA  
 ; ZIP: 22042  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/596,405  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Murphy, Jr., Gerald M.  
 ; REGISTRATION NUMBER: 28,977  
 ; REFERENCE/DOCKET NUMBER: 1781-105P  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703) 205-8000  
 ; TELEFAX: (703) 205-8050  
 ; TELEX: 248345

; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1083 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-596-405-2

Query Match 16.9%; Score 665; DB 2; Length 1083;  
 Best Local Similarity 25.4%; Pred. No. 1.3e-46;  
 Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;  
 QY 34 PGEWNNIMRECCEYDQIECVCPGKRE-----VVGTYTPCCRNEECDSCLIH 82  
 DB 248 PNGQSNFPKICR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSCHS-----293  
 QY 83 PGCTIFENCKSCR-NGSWGTL-----103  
 DB 294 FYLLIGQETLTCCGNGQNGQIPQCKNLVFCPLDPVNHAEHKVIGVEKYQGPFGTE 353  
 QY 104 -----DDPVYKGFYCAECR--AGWYGG--DCMR-----CGQVLR--133  
 DB 354 VTYTCGNYFLMGFTLKNPDGWSGSPSCVKVADREVDCCSKAVDFLDDVGFVRH 413  
 QY 134 APKQILLES-----YPLNAHCEWTIHA-----KPGFVI-----162  
 DB 414 CPAGCSLTAGTVMGTAIYHELSSVCRAAHAGKLPNSGGAVHVNNGPYSDFLGSLNGI 473  
 QY 163 ---QLRFVMLSLEFDYM-----COYDYVEVRD-----GDNRDGQIIKRVCGN--E 202  
 DB 474 KSEELKSLARSFRFDYVSSSTAGKSGCPDGFVENDENCYVYTSKORAWERAGQVCTNMAA 533  
 QY 203 RPAPIQS--IGSSLHVLPHSDG--SKNFDGFH-----AIYEETITACSS 241  
 DB 534 RLAVLDKDVIPNSLTETLRGKGLTTTWIGLHRLDAEKPFIMELMDSNVVLDNLTFWAS 593  
 QY 242 SPCFHDGTCLV-----DKAGS--YKACLAGYTGORCNLEERN-----CSDPGGPNVNGYK 293  
 DB 594 GEPGNETCVYMDIQDQLQSVWTKTSQFSSFPACMDLSRNTAKACDDPFGSLNGHATL 653  
 QY 294 TGGPGLINRHAKIGTVVFFCNNSVYLSGNEKRTCCQNGEWSGKQPIK--ACREP 351  
 DB 654 HQGS--IDGYA--GSIIRYSEVLHYLSTGTEVTCTTNGTWSAPKPRCIRKIVITQNPV 709  
 QY 352 SDLVRRVLPVQSRRETPHLQYLSAFAKQKIQ-----SAPTKKPALPFGD-----398  
 DB 710 PSYGSVEIKP---PSRTNSISRVGSPFLRLPLPLPLARAAPPPKPRSSQSPSTVDLASK 766  
 QY 399 --LPMGYQHLHTQLQYECISPFYRLGSSRRCLRTGKWSGRAPSCIPICGKIENITAP- 455  
 DB 767 VKLPEGHYRVGSRATYTCESRYELLGSGQRCDNSGNNWSGRPASCIPVCGRSDSPSPF 826  
 QY 456 -----KTQGLRWPMQAAIYRRSTGVHDGSLHKGAWFLVCGALVNERTVVAAHCVTDLG 510  
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 QY 511 KVTMIKTADLVKVLGKFRDORDEXTIOSAISAILHPNYDPILLDDADIALKLLDKA 570  
 DB 880 TAEIIPNQFQKYLGVYRDDSDDDVQVREALEIHNPNYDPGNLNFNFDIALIQLKTPV 939  
 QY 571 RSTRVQPICLAASRDLSFSQESHI-----TVAGNVAVLADVRSPGKNDILRSQVSV 624  
 DB 940 TLTRVQPICLPT--DITT---REHLKEGTLAVVTGWM-----LNENNTYSETIQQAVLVP 990  
 QY 625 VDSLLCEEHEDHGIPIVSTVDNMFCAWSEPTAPSDICTAETGTGIAAVSPFGRASPPRVH 684  
 DB 991 VAASTCEEGYKEADLPLTWTENMFCAGYK--KGRYDACSGDSGG--PLVADDSRTERRV 1047  
 QY 685 LMLGVSWSYDKTCSH--RLSTAFKTVLPFKDWIER 717  
 DB 1048 LEGIVSWGSPSGCGKANQYGGFTKVNFLSWIRQ 1081

RESULT 7  
 US-08-877-620-2  
 ; Sequence 2, Application US/08877620  
 ; Patent No. 5985590  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ding, Bow  
 ; APPLICANT: Ho, Bow  
 ; TITLE OF INVENTION: The Cloned Factor C cDNA of the  
 ; TITLE OF INVENTION: Singapore Horsehoe Crab, Carinoscorpius  
 ; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Birch, Stewart, Kolasch & Birch  
 ; STREET: 8110 Gatehouse Road, Suite 500 East  
 ; CITY: Falls Church  
 ; STATE: Virginia  
 ; COUNTRY: USA  
 ; ZIP: 22042  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA: 1781-105P  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA: 08/596,405  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Murphy, Jr., Gerald M.  
 ; REGISTRATION NUMBER: 28,977  
 ; REFERENCE/DOCKET NUMBER: 1781-105P  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703) 205-8000  
 ; TELEFAX: (703) 205-8050  
 ; TELEX: 248345  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1083 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-877-620-2

Query Match 16.9%; Score 665; DB 2; Length 1083;  
 Best Local Similarity 25.4%; Pred. No. 1.3e-46;  
 Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;  
 QY 34 PGEWNNIMRECCEYDQIECVCPGKRE-----VVGTYTPCCRNEECDSCLIH 82  
 DB 248 PNGQSNFPKICR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSCHS-----293  
 QY 83 PGCTIFENCKSCR-NGSWGTL-----103  
 DB 294 FYLLIGQETLTCCGNGQNGQIPQCKNLVFCPLDPVNHAEHKVIGVEKYQGPFGTE 353  
 QY 104 -----DDPVYKGFYCAECR--AGWYGG--DCMR-----CGQVLR--133  
 DB 354 VTYTCGNYFLMGFTLKNPDGWSGSPSCVKVADREVDCCSKAVDFLDDVGFVRH 413  
 QY 134 APKQILLES-----YPLNAHCEWTIHA-----KPGFVI-----162  
 DB 414 CPAGCSLTAGTVMGTAIYHELSSVCRAAHAGKLPNSGGAVHVNNGPYSDFLGSLNGI 473  
 QY 163 ---QLRFVMLSLEFDYM-----COYDYVEVRD-----GDNRDGQIIKRVCGN--E 202  
 DB 474 KSEELKSLARSFRFDYVSSSTAGKSGCPDGFVENDENCYVYTSKORAWERAGQVCTNMAA 533  
 QY 203 RPAPIQS--IGSSLHVLPHSDG--SKNFDGFH-----AIYEETITACSS 241  
 DB 534 RLAVLDKDVIPNSLTETLRGKGLTTTWIGLHRLDAEKPFIMELMDSNVVLDNLTFWAS 593

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QY 294 TGGPGLNGRHAKIGTVSFFCNSVYLSGNEKRTCOONGENSGKQPICIK--ACREPXI 351
Db 654 HGOS--IDGFYA--GSSIRYSCVHLHLSGTETVTCTTNGTWSAPKPRCIKVITQNPVPV 709
QY 352 SDLVRRRLPMQVQSRTPHLQLYSAAFSKQKLO---SAPTKKPALPFGD----- 398
Db 710 PSYGSVEIKP---PSRTNSISRVGSPFLRLPLPLPLARAAPKPPKPRSSQPSVTLASK 766
QY 399 --LPMGYQHLLHTQLOQECISPFYRRLGSSRRRTCLRTGKMSGRAPSCIPICGKIENITAP- 455
Db 767 VKLPEGHYRVGSRAIYTCESRYVELLSQGRRCDSNGNWSGRPASCIPIVCGRSDSPSP 826
QY 456 -----KTQGLRWPMQAAIYRTSGVHDGSLHKGAMFLVCSGALVNERTVVAAHCVTDLG 510
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QY 511 KVTMIKTADLKVVLGKPYRDDDEKTIQSLQISAILHPNYDPILLDADIALKLLDKA 570
Db 880 TAIIDPNQFMVLYGKYRDSRDDDDVQVREALEIHVNPYDGNLNFDFIALIQLKTPV 939
QY 571 RISTRVQPICLAASRLDSTSFQESHI-----TVAGNVLADVRSPGKNDTLRSVSV 624
Db 940 TLTRVQPICLPT--DITT---REHLKEGTAVVVTGWG----LNENNTYSETIQAQVLPV 990
QY 625 VDSLLCEEQHEHGIPIVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPRWH 684
Db 991 VAASTCEEGYKEADLPVTENNMFCAKY-KGRYDACSDDSGG--PLVFADDSRTERRV 1047
QY 685 LMGLVSWSDYKTCSH-RLSTAFTKVLFPFKDWIER 717
Db 1048 LEGIVSGSPGCGKANQYGGFTKVNFLSWIRQ 1081

RESULT 8
US-09-287-368-2
; Sequence 2, Application US/09287368A
; Patent No. 6645724
; GENERAL INFORMATION:
; APPLICANT: DING, Jeak Ling
; APPLICANT: HO, Bow
; TITLE OF INVENTION: Assays for Endotoxin and Methods for Removal of Endotoxin
; TITLE OF INVENTION: from a Sample Using Recombinant Factor C
; FILE REFERENCE: 1781-0165P
; CURRENT APPLICATION NUMBER: US/09/287,368A
; CURRENT FILING DATE: 1999-04-07
; EARLIER APPLICATION NUMBER: 09/201,786
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/081,767
; EARLIER FILING DATE: 1998-05-21
; EARLIER APPLICATION NUMBER: 60/058,816
; EARLIER FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Carinoscorpius rotundicauda
; FEATURE:
; OTHER INFORMATION: any n or xaa = Unknown
US-09-287-368-2

Query Match 16.98; Score 665; DB 4; Length 1083;
Best Local Similarity 25.48; Pred. No. 1.3e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;
QY 34 PGAEWNIMCECCEYDQIEVCVCPKRE-----VVGTYTIPCCRNEENECDSCLIH 82
Db 248 PNGQMSNFPKPCIR-----ECAMVSSPHGKNVLSGDMIEGATL-----RFSCDS----- 293

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QY 83 PGCTIFENCCKSCR-NGSWGTL----- 103
Db 294 PYYLIGQETLTTCOGNGOMNGQIPQCKNLVFCPLDVPVNAEHKVKIGVEQKYQFPQGTG 353
QY 104 -----DDPVYVGPYCAECR--AGWYGG--DCNR-----CGQVLR-- 133
Db 354 VYVTCGNTFLMGFDLTKCNPGSGWSGQSPCVKVVADREVDSCSKAVDFLDDVGEVPRIH 413
QY 134 APKGQILLES-----YPLNAHCEWTIHA-----KPGFVI----- 162
Db 414 CRAGCSLTAGTWGTATYHELSSVCRAATHAGKLPNSGGGAVHVNVNNGPYSDFLGSLNGI 473
QY 163 ---QLRFVWLSLEFDM-----CQDYVEVRD-----GDNRDQIIRKVCN--E 202
Db 474 KSEELKSLARSFRFDYVSSSTAGKSCGCPDGPWEVDENVVYVTSKQRAWERAQVCNTNMAA 533
QY 203 RPAPIOS--IGSSILHVLPHSDG-SKNFDCGFH-----AIYEIETACSS 241
Db 534 RLAVLDKQVIPSLSLTETLRGKGLTTTWIHLRLDABKPFIEWLMDRSNVVINDLTFWAS 593
QY 242 SPCHDGTGCVL-----DKAGS-YKACLAGYTGQRCENLLEERN---CSDPGGFWNGYQKI 293
Db 594 GEPGNETNCVMDIQDQLQSVKTKSCFQSPSPACWMDLSDRNKAKCDDPGSLENGHATL 653
QY 294 TGGPGLNGRHAKIGTVSFFCNSVYLSGNEKRTCOONGENSGKQPICIK--ACREPXI 351
Db 654 HGOS--IDGFYA--GSSIRYSCVHLHLSGTETVTCTTNGTWSAPKPRCIKVITQNPVPV 709
QY 352 SDLVRRRLPMQVQSRTPHLQLYSAAFSKQKLO---SAPTKKPALPFGD----- 398
Db 710 PSYGSVEIKP---PSRTNSISRVGSPFLRLPLPLARAAPKPPKPRSSQPSVTLASK 766
QY 399 --LPMGYQHLLHTQLOQECISPFYRRLGSSRRRTCLRTGKMSGRAPSCIPICGKIENITAP- 455
Db 767 VKLPEGHYRVGSRAIYTCESRYVELLSQGRRCDSNGNWSGRPASCIPIVCGRSDSPSP 826
QY 456 -----KTQGLRWPMQAAIYRTSGVHDGSLHKGAMFLVCSGALVNERTVVAAHCVTDLG 510
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QY 511 KVTMIKTADLKVVLGKPYRDDDEKTIQSLQISAILHPNYDPILLDADIALKLLDKA 570
Db 880 TAIIDPNQFMVLYGKYRDSRDDDDVQVREALEIHVNPYDGNLNFDFIALIQLKTPV 939
QY 571 RISTRVQPICLAASRLDSTSFQESHI-----TVAGNVLADVRSPGKNDTLRSVSV 624
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QY 625 VDSLLCEEQHEHGIPIVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPRWH 684
Db 991 VAASTCEEGYKEADLPVTENNMFCAKY-KGRYDACSDDSGG--PLVFADDSRTERRV 1047
QY 685 LMGLVSWSDYKTCSH-RLSTAFTKVLFPFKDWIER 717
Db 1048 LEGIVSGSPGCGKANQYGGFTKVNFLSWIRQ 1081

RESULT 9
US-09-027-337-2
; Sequence 2, Application US/09027337B
; Patent No. 5972616
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
; FILE REFERENCE: D6064
; CURRENT APPLICATION NUMBER: US/09/027,337B
; CURRENT FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 2
; LENGTH: 855

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; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of TAGD-15 encoded by nucleotides  
; Patent No. 5972616  
US-09-027-337-2

Query Match 8.3%; Score 327; DB 2; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-18;  
Matched 144; Conservative 69; Mismatches 224; Indels 230; Gaps 27;

QY 128 CGOVLRAKPGQI-----LLESYPLNAHCETTHAKPGFVIQLRFVNLSEFDYM----- 176  
DB 340 CGRLRKAQGTNSPYPGHYPPNIDCTWNE-----VFNQHVKVSKFYLLEPGVPA 394  
QY 177 --COYDVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSLHLVLFHSDGSKNFDGPHAIYE 234  
DB 395 GTCPKDYVEING-----EKYCGERSQFVVTNSNKITVRFHSDQSYTDTGFLAEY- 444  
QY 235 EITACSSSPCFHDGTC-----VLDKAGSYKCAACLAGY----- 266  
DB 445 -LSYDSSDPGPGFTCTGRCIRKELRCGWDADCTDHSDELNCSCDAGHQFTCKNFKCP 503  
QY 267 -----TGRCENLLEERNCSDPGPGVNGYQKITGGPGLNGHAKIGTVVFFCNSYV 320  
DB 504 LFWVCDVNDGNSDEQGCSCP-----AQTFRCSNGKC 537  
QY 321 LSG-----NEKRTCCQNGESGKQPICIKACREPKISDLVRRVLPVQVQSRTPHLQLYS 376  
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QY 377 AAFSKOKLASAPTKKPPALPFGDLPNGYQHLHTLOQYECISPFYRLGSSRRRTCLRTGKWS 436  
DB 568 -----TK-----HT--YRCLNGL-----CLSKGN-- 584  
QY 437 GRAPSCIPICGKIENITAPKTO-----GLR-----WPMQAAIYRRTS 473  
DB 585 -----PECCKEDCSDGSDKDCGLRSFTRQARVVGTTDAGEWPMQVSLHALGQ 637  
QY 474 GVHDGSLHKGAWFLVCSGALVNERTVVAACHCVDLKGKVTMIKTADLKVLGKFRYRDDDR 533  
DB 638 G-----H-----ICGASLISPNWLVSAAHCYIDDRGFRYSPTQWTAFLG-LHDQSOR 684  
QY 594 SH-ITVAGNVNVLADVRSPGKNDTLRSQVSVVSDLSLCEBQHDHGIPVSVTDNMFCAW 652  
DB 742 GKAIWVTGM---GHTQYGGTGALILQKGEIRVINQTCENL-----LPQOITPRMVCVGF 793  
QY 653 EPTAPSDICTAETGG-IAAVSPFGASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLPF 711  
DB 794 -LSGGVDSQCGSDGGLSSVEADGRI-----FQAGVWSWG-DGCAQRNKPQVYTRLPFLF 845  
QY 712 KDWIERN 718  
DB 846 RDWIKEN 852

## RESULT 10

US-09-644-600-2  
; Sequence 2, Application US/09644600  
; Patent No. 6451500  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; APPLICANT: Tanimoto, Hirotochi  
; TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease  
; FILE REFERENCE: Overexpressed in Carcinomas  
; CURRENT APPLICATION NUMBER: US/09/644,600  
; CURRENT FILING DATE: 2000-08-23

; PRIOR APPLICATION NUMBER: 09/421,213  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: 09/027,337  
; PRIOR FILING DATE: 1998-02-20  
; NUMBER OF SEQ ID NOS: 98  
; SEQ ID NO 2  
; LENGTH: 855  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: TAGD-15  
US-09-644-600-2

Query Match 8.3%; Score 327; DB 4; Length 855;

Best Local Similarity 21.6%; Pred. No. 1.3e-18;  
Matches 144; Conservative 69; Mismatches 224; Indels 230; Gaps 27;

QY 128 CGOVLRAKPGQI-----LLESYPLNAHCETTHAKPGFVIQLRFVNLSEFDYM----- 176  
DB 340 CGRLRKAQGTNSPYPGHYPPNIDCTWNE-----VFNQHVKVSKFYLLEPGVPA 394  
QY 177 --COYDVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSLHLVLFHSDGSKNFDGPHAIYE 234  
DB 395 GTCPKDYVEING-----EKYCGERSQFVVTNSNKITVRFHSDQSYTDTGFLAEY- 444  
QY 235 EITACSSSPCFHDGTC-----VLDKAGSYKCAACLAGY----- 266  
DB 445 -LSYDSSDPGPGFTCTGRCIRKELRCGWDADCTDHSDELNCSCDAGHQFTCKNFKCP 503  
QY 267 -----TGRCENLLEERNCSDPGPGVNGYQKITGGPGLNGHAKIGTVVFFCNSYV 320  
DB 504 LFWVCDVNDGNSDEQGCSCP-----AQTFRCSNGKC 537  
QY 321 LSG-----NEKRTCCQNGESGKQPICIKACREPKISDLVRRVLPVQVQSRTPHLQLYS 376  
DB 538 LSKSQCNKQDCGSDGSDASCPKVVVTC----- 567  
QY 377 AAFSKOKLASAPTKKPPALPFGDLPNGYQHLHTLOQYECISPFYRLGSSRRRTCLRTGKWS 436  
DB 568 -----TK-----HT--YRCLNGL-----CLSKGN-- 584  
QY 437 GRAPSCIPICGKIENITAPKTO-----GLR-----WPMQAAIYRRTS 473  
DB 585 -----PECCKEDCSDGSDKDCGLRSFTRQARVVGTTDAGEWPMQVSLHALGQ 637  
QY 474 GVHDGSLHKGAWFLVCSGALVNERTVVAACHCVDLKGKVTMIKTADLKVLGKFRYRDDDR 533  
DB 638 G-----H-----ICGASLISPNWLVSAAHCYIDDRGFRYSPTQWTAFLG-LHDQSOR 684  
QY 534 DEKTIQSLQISAILHPNVDPILLADIAILKLDKARISTRVQPICLAASRDLSFQE 593  
DB 685 SAPGVQERRLRIISHPPFNDFDYDIALLEKPAEYSSMVRPCLP---DASHVPPA 741  
QY 594 SH-ITVAGNVNVLADVRSPGKNDTLRSQVSVVSDLSLCEBQHDHGIPVSVTDNMFCAW 652  
DB 742 GKAIWVTGM---GHTQYGGTGALILQKGEIRVINQTCENL-----LPQOITPRMVCVGF 793  
QY 653 EPTAPSDICTAETGG-IAAVSPFGASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLPF 711  
DB 794 -LSGGVDSQCGSDGGLSSVEADGRI-----FQAGVWSWG-DGCAQRNKPQVYTRLPFLF 845  
QY 712 KDWIERN 718  
DB 846 RDWIKEN 852

## RESULT 11

US-09-654-600A-2  
; Sequence 2, Application US/09654600A  
; Patent No. 6649741  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; APPLICANT: Tanimoto, Hirotochi

;; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease  
;; FILE OF INVENTION: Overexpressed in Carcinomas  
;; REFERENCE: D6064CIP/D  
;; CURRENT APPLICATION NUMBER: US/09/654,600A  
;; CURRENT FILING DATE: 2000-09-01  
;; PRIOR APPLICATION NUMBER: 09/421,213  
;; 09/027,337  
;; PRIOR FILING DATE: 1999-10-20  
;; NUMBER OF SEQ ID NOS: 98  
;; SEQ ID NO 2  
;; LENGTH: 855  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: TADG-15  
US-09-654-600A-2

Query Match 8.3%; Score 327; DB 4; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-18;  
Matches 144; Conservative 69; Mismatches 224; Indels 230; Gaps 27;  
QY 128 CGVLRAPKGOI-----LLESYPLNAHCETTHAKPGFVIQLRFVYMLSLPEPYM----- 176  
Db 340 CGGLRKAQGFNSPYPGHPNIDCTWNE-----VNNQHVKVSKFYLLEPGVPA 394  
QY 177 --COYDYVEVDGNDQIIIRKVCGRNERPAPIQSIGSLHLVPHSDGSKNFDGFHAIYE 234  
Db 395 GTCPKDYVEING-----EKYCGERSQFVVTNSNKITVRFHSDQSYDTDTGFLAEY- 444  
QY 235 EITACSSSPCHDGTG-----VLDKAGSYKACLAGY----- 266  
Db 445 -LSYDSSDPGPGQFTCTGRCIRKELRCGDWADCTDHSDELNCSDAGHQBTCKNKFCKP 503  
QY 267 -----TGQRNLEERNCSDPGCPVNGYKITTGGPGLNGRHAKIGTVVSFFCNSYV 320  
Db 504 LFWCDSVNDGDSDEGGCCP-----AGTFRCSNGKC 537  
QY 321 LSG-----NEKRTCOONGSWGSKQIPICAKACREPISDLVRRVLPVMOVQSRRTCLRTGWS 376  
Db 538 LSKSQQCKGDKDCGSDGSEASCPKVVVTC-----YRCLNGL----- 567  
QY 377 AAFSKQKLSAPTCKPALPFGDLPMGYQHLLHTQIYECISPFYRLGSSRRRTCLRTGWS 436  
Db 568 -----TK-----HT-----YRCLNGL----- 584  
QY 437 GRAPSCIPICGKIENITAPKTQ-----GLR-----WPMQAAIYRRTS 473  
Db 585 -----PECDGKEDSCDSCGDEKCDCLRLRFTQARVVGTDADGEWPMQVSLHALGQ 637  
QY 474 GVHDSLHKGAWFLVCSGALVNERTVVVAHCVTDGLGKVTMIKTADLKVVLGKPYRDDDR 533  
Db 638 G-----H-----ICGASLISPNWLVSAAHCYIDDRGRYSDDPTQWTAFLG-LHDQSOR 684  
QY 534 DEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAAASRDLSSTFQE 593  
Db 685 SAPGVQERLRKRIISHPFNFDTFDYDIALLELEKPAEYSSMVRPCLP-----DASHVPPA 741  
QY 594 SH-ITVAGMNVLDVRSPPGKNDTLRSQVSVSDLSLCEEQHEDHGIPVSVTDNNMFCASW 652  
Db 742 GKALWVTGW-----GHTQYGGTALLQKEIRVINQTTCENT-----LPQOITPRMVCVF 793  
QY 653 EPTAPSDICTAETGG-IAAVFPPGRASPEPRHLMGLVSWSYDKTCSHRLSTAFTKVLPF 711  
Db 794 -LSGGVDSQCQDSGGPLSSVEADGRI-----FQAGVVSWG-DGCAQRNKPQVYTRPLPF 845  
QY 712 KDWIERN 718  
Db 846 RDWIKEN 852

RESULT 12  
5270178-16

;; Patent No. 5270178  
;; APPLICANT: GELITZ, BRUCE E.; GRINNELL, BRIAN W.  
;; TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION OF  
;; ZYMOGEN FORMS OF HUMAN PROTEIN C  
;; NUMBER OF SEQUENCES: 21  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/484,133  
;; FILING DATE: 23-FEB-1990  
;; SEQ ID NO:16:  
;; LENGTH: 460  
5270178-16

Query Match 8.1%; Score 321; DB 6; Length 460;  
Best Local Similarity 25.1%; Pred. No. 1.8e-18;  
Matches 138; Conservative 62; Mismatches 170; Indels 180; Gaps 27;  
QY 193 QIIKRVCGNERPAPI-QSIGSLHLVLFHSDGSKNFDGFHAIYEEIT-ACSSSPCFHDGTC 250  
Db 58 ECIEEICDFEEAKEIFQVDDTL-----AFWSKHVDGQCLVPLEHPCASLCCGH-GTC 111  
QY 251 VLDKAGSYKACLAGYTGQRNLEERNCSDPGGPN-----GYQKITGGPGLNGR 303  
Db 112 I-DGIGSFCDCRSWEGRCQREVSLNCLDNGGCTHYCLEEVGWRCSCAPGY----- 166  
QY 304 HAKIG-----TVVSFFCNSVYLSGNEKRTCOONGSWGSKQIPICAKACREPISDLVR 356  
Db 167 --KLGDLLQCHPAVPCGRPW-----KR-----MEKRSHL-- 197  
QY 357 RRVLPMOVQSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRMPWQAAIYRRTSGVH 476  
Db 198 -----KEDTELH-----KQI----- 208  
QY 417 PFYRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRMPWQAAIYRRTSGVH 476  
Db 209 --YPRL-----NGKMTRRGDS-----PWQVLL----- 229  
QY 477 DGSILHKGAWFLVCSGALVNERTVVVAHCVTDGLGKVTMIKTADLKVVLGKPYRDDDRDEK 536  
Db 230 -DSKCK-----LAGAVLIHPSWVLTAAHCDSEK-----LIVRIGY--DLRWEK 274  
QY 537 TIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICL-----AASRDLSSTFQ 592  
Db 275 WELDDDIKEVFPVHPNYSKSTTDNDIALHLAQPATLSQITVPICLPDSGLAERLNAQGO 334  
QY 593 ESHITVAGMNVLDVRSPPGKNDT--LRSGVSVSDLSLCEEQHEDHGIPVSVTDNNMFC 650  
Db 335 ETLVT--GMGYHSSREKEAKRNTFVLNFIKIPVPHNECSEVMN-----MVSENNMLCA 387  
QY 651 SWEPTAPSDICTAETGGIAAVSPGRASPEPRHLMGLVSWSYDKTCSHRLSTAFTKVLP 710  
Db 388 GILGDR-QDACEGDSGGPWSVAFHG-----TWFLVGLVSWGEGCGLLHNVG-VYTHVSR 439  
QY 711 FKDWIERNK 720  
Db 440 YLDWIHGHIR 449

RESULT 13  
US-08-200-900A-2  
;; Sequence 2, Application US/08200900A  
;; Patent No. 5655566  
;; GENERAL INFORMATION:  
;; APPLICANT:  
;; TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE  
;; NUMBER OF SEQUENCES: 38  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Genetics Institute, Inc. - Legal Affairs  
;; STREET: 87 CambridgePark Drive  
;; CITY: Cambridge  
;; STATE: MA  
;; COUNTRY: USA  
;; ZIP: 02140  
;; COMPUTER READABLE FORM:



/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/200,900A  
/ FILING DATE: 23-FEB-1994  
/ CLASSIFICATION: 435  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Meiner, Maureen C.  
/ REGISTRATION NUMBER: 31,544  
/ REFERENCE/DOCKET NUMBER: GI 5201-FWC  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (617) 876-1170 X8574  
/ TELEFAX: (617) 876-5851  
/ INFORMATION FOR SEQ ID NO: 2:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 798 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ PCT-US-08-200-900A-2

Query Match 8.0%; Score 317.5; DB 1; Length 798;  
Best Local Similarity 24.6%; Pred. No. 7.4e-18;  
Matches 146; Conservative 80; Mismatches 225; Indels 143; Gaps 30;

QY 143 SYPLNAHCEWTHAKPGFVIQIRFVMSLEFDYMCQYDVEVRDGNRDNQIIRKVCNE 202  
DB 324 SYPNQAFICMNLNAQKGNQIQLHF-----QEPDENIADVVEIRDGDDSLFLAVYTG-- 377  
QY 203 RPAPIQSGSS---LHVLFDHSGSKNFDGFHAIYEITACS--SSPCFHDG--TCVLDDKAGS 257  
DB 378 -PGPVNDFSTNRTMTVLTIDNMLAKQGFKANFTTGYGLGPIPECKEDNFQC---KQG- 432  
QY 258 YKACLAGTGTGRCENLLEERNCSDEGPGVNGYQKITGGPGLNGHAKIGTVVFFCANN 317  
DB 433 -ECIPLVNL-----CDGPFPHCKDGSDEAHCVRLEFNGTTDSSGLVQFRIQSIWHV- 480  
QY 318 SYVLSGNEKRTCOQNGEWSGKQICIKACREPKISDLVRRVRLPMQVQSRETPHLQLYSA 377  
DB 481 -----ACAEN--WT-----TQISDDVCQLL----- 498  
QY 378 AFSKOKLOSAPTKKPPALPGDLPMGYOHLHTQLOVEICISPFYRRLGSSRRRTCLRTGKWSG 437  
DB 499 -----GLGTGNSVPTFTSTGGP--YVNLNT-----APNGSLILTPSQOCLE----- 538  
QY 438 RAPSCIP1-----CGK--IENITAPKTQG-----LRWPQAAIYRRTSGVHDGSLHKG 483  
DB 539 --DSLILLQCNKYKSCGKLVTOEVSPIKVGSDSREGAWPVWVALY-----FDDQ----- 586  
QY 484 AWFVCSGALVNERTVVAAHCVTDLGKVTMKTADLVKLVGKFFYRDDDRDEKTIQSLQI 543  
DB 587 ---QVCGASLSVRDLVSAACHV--YGR--NMEPSKWKAVLG-LHMASNLTSFQIETRLI 638  
QY 544 SAILHPNVDPIILDADIAIKLLDKARISTRVQPICLAASRDLSSTFQESH1-TVAGWN 602  
DB 639 DQIVINPHYNKRNKNDIAMHLEMKVNTDYIPICLPEENQV---FPPGRICSIAGWG 695  
QY 603 VLADVRSPGFKNIDTLRSGVSVVDSLLCEQHEHDGIPVSVTDNMFCAWETAPSDICT 662  
DB 696 ALI---YQGSTADVLQEADVPLLSNEKQQQMPEY-----NITENMVCAGYE--AGGVDSQC 747  
QY 663 AETGGIAAVSPPGRASPEPRHLMGLVSWSYDKTCSHRLSTAFTKVLPFKOMIE 716  
DB 748 GDSGG-----PLMCQENNRWLLAGVTSFGYQCALPNR-PGVYARVPRFTWMIQ 794

RESULT 14  
PCT-US94-00616-2  
; Sequence 2, Application PC/TUS9400616  
; GENERAL INFORMATION:

/ APPLICANT:  
/ TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE  
/ NUMBER OF SEQUENCES: 33  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: PCT/US94/00616  
/ FILING DATE:  
/ CLASSIFICATION:  
/ INFORMATION FOR SEQ ID NO: 2:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 798 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ PCT-US94-00616-2

Query Match 8.0%; Score 317.5; DB 5; Length 798;  
Best Local Similarity 24.6%; Pred. No. 7.4e-18;  
Matches 146; Conservative 80; Mismatches 225; Indels 143; Gaps 30;

QY 143 SYPLNAHCEWTHAKPGFVIQIRFVMSLEFDYMCQYDVEVRDGNRDNQIIRKVCNE 202  
DB 324 SYPNQAFICMNLNAQKGNQIQLHF-----QEPDENIADVVEIRDGDDSLFLAVYTG-- 377  
QY 203 RPAPIQSGSS---LHVLFDHSGSKNFDGFHAIYEITACS--SSPCFHDG--TCVLDDKAGS 257  
DB 378 -PGPVNDFSTNRTMTVLTIDNMLAKQGFKANFTTGYGLGPIPECKEDNFQC---KQG- 432  
QY 258 YKACLAGTGTGRCENLLEERNCSDEGPGVNGYQKITGGPGLNGHAKIGTVVFFCANN 317  
DB 433 -ECIPLVNL-----CDGPFPHCKDGSDEAHCVRLEFNGTTDSSGLVQFRIQSIWHV- 480  
QY 318 SYVLSGNEKRTCOQNGEWSGKQICIKACREPKISDLVRRVRLPMQVQSRETPHLQLYSA 377  
DB 481 -----ACAEN--WT-----TQISDDVCQLL----- 498  
QY 378 AFSKOKLOSAPTKKPPALPGDLPMGYOHLHTQLOVEICISPFYRRLGSSRRRTCLRTGKWSG 437  
DB 499 -----GLGTGNSVPTFTSTGGP--YVNLNT-----APNGSLILTPSQOCLE----- 538  
QY 438 RAPSCIP1-----CGK--IENITAPKTQG-----LRWPQAAIYRRTSGVHDGSLHKG 483  
DB 539 --DSLILLQCNKYKSCGKLVTOEVSPIKVGSDSREGAWPVWVALY-----FDDQ----- 586  
QY 484 AWFVCSGALVNERTVVAAHCVTDLGKVTMKTADLVKLVGKFFYRDDDRDEKTIQSLQI 543  
DB 587 ---QVCGASLSVRDLVSAACHV--YGR--NMEPSKWKAVLG-LHMASNLTSFQIETRLI 638  
QY 544 SAILHPNVDPIILDADIAIKLLDKARISTRVQPICLAASRDLSSTFQESH1-TVAGWN 602  
DB 639 DQIVINPHYNKRNKNDIAMHLEMKVNTDYIPICLPEENQV---FPPGRICSIAGWG 695  
QY 603 VLADVRSPGFKNIDTLRSGVSVVDSLLCEQHEHDGIPVSVTDNMFCAWETAPSDICT 662  
DB 696 ALI---YQGSTADVLQEADVPLLSNEKQQQMPEY-----NITENMVCAGYE--AGGVDSQC 747  
QY 663 AETGGIAAVSPPGRASPEPRHLMGLVSWSYDKTCSHRLSTAFTKVLPFKOMIE 716  
DB 748 GDSGG-----PLMCQENNRWLLAGVTSFGYQCALPNR-PGVYARVPRFTWMIQ 794

RESULT 15  
5460953-3  
; Patent No. 5460953  
; APPLICANT: GERLITZ, BRUCE E.; GRINNELL, BRIAN W.  
; TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION OF  
; GLYCOSYLATION MUTANTS OF HUMAN PROTEIN C  
; NUMBER OF SEQUENCES: 3



Starch out

91.3%  
 Tangas  
 100%

The antibody of Claim 1 which specifically binds to the polypeptide shown in

The antibody of Claim 1 which is an antibody fragment.

The antibody of Claim 1 which is a monoclonal antibody.

An antibody that binds to the polypeptide shown in Figure 38 (SEQ ID NO:38).

## Claims

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MELGCTQTLGLFTLQLTLTLSSLPREYTVINEACPGAEWNIIMCRCECEYDQIECVCPGKRELVGYT  
 IPRCNRNEENECDSCLIHPCCTIIFENCKSCRNCSWGSLDLDYVKGFYCAECRAAGWYGGDCMRGQ  
 VLRAPKGOILLSESYPLMAHCEWTHAKPGFVIQTLRFVMTLSLEFDYKQCQYDYVEVRDGDNRDGOII  
 KRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHHDGTCVLDKAGSYKC  
 ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGGLINGRHAHAKIGITVVSFFCNNSYVLSGNE  
 KRTCCQNGEWSGKQPIKACREPKISDLVRRRVLPMDQVQSFRETPLHLHQLYSAAFSKQKLQSAPTK  
 KPALPFGDLPMGYQHLHTQLQYECISPFYRRRLGSSRRCTCRLTGKWSGRRAPSCIPICGKIENITAP  
 KTQGLRWQPAIYRRTSGVHDSLHKGAWFLVCSGALVNERITVVAHACVTDLGGKVTMIKTADL  
 KVLGKFEYRDDDRDEKTIQSLQISAIILHPNYDPIILLDADIAIKLLDKARISTRVQPIICLAASR  
 DLSTSFQESHITVAAGWNLADVRSPGFKNDTLRSGVSVVSDSLCEEQHEHDHGIPVSVITDNMFCA  
 SWEPYAPSDICITAEETGGIAAVSFPGRASEPFRWHLMGLVSWMSYCKTCSHRSLTAFTKVLPEKDWI  
 ERNMK

Important features of the protein:

Signal peptide:  
 amino acids 1-23

EGF-like domain cysteine pattern signature.  
 amino acids 260-272

N-glycosylation sites.  
 amino acids 96-100, 279-283, 316-320, 451-455, 614-618

N-myristoylation sites.  
 amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,  
 474-480, 491-497, 638-644, 666-672

Amidation site.  
 amino acids 56-60

Serine proteases, trypsin family.  
 amino acids 489-506

CUB domain proteins profile.  
 amino acids 150-167

FIGURE 38

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